

O'Bryen, Barbara

From: Seharaseyon, Jegatheesan
Sent: Tuesday, December 21, 2004 1:33 PM
To: O'Bryen, Barbara
Subject: RE: PR01550

Hi,

Please search SEQ ID NOs: 121 (NA) and 122 (AA) in 10/063734,
In issued and commercial databases.

Also,

Please search the nucleotide encoding SEQ ID NO: 122.

Please do a word search of the nucleic acid with a word size of 10 nucleotides and
a word search of the protein, with a word size of 6 amino acids.

AND on the EST databases, in particular, I need enough hits to get at old art (~50).

Thanks,
Seyon.

J. Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 22:49:14 ; Search time 5526 Seconds
(without alignments)
10756.995 Million cell updates/sec

Title: US-10-063-734-121

Perfect score: 1257
Sequence: 1 ggaagagagcgcgcggtcga.....aataaaattattccacaa 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenBank1:*
1: gb_bai:*
2: gb_hlg:*
3: gb_in:*
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6: gb_pac:*
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9: gb_pr:*
10: gb_pro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1257	100.0	1257	6	AX092390 Sequence
2	1257	100.0	1257	6	AX376298 Sequence
3	1257	100.0	1257	6	AX454660 Sequence
4	1257	100.0	1257	6	AX459648 Sequence
5	1257	100.0	1257	6	AX491138 Sequence
6	1257	100.0	1257	6	AX697362 Sequence
7	1257	100.0	1257	6	AY358914 Homo sapi
8	1253.8	99.7	1284	6	AX829144 Sequence
9	1236.8	98.4	1257	6	BD269636 Human sec
10	1231.6	98.0	1342	6	BD223153 98 human
11	1231.6	98.0	1342	6	AR243851 Sequence
12	1222.8	97.3	1286	6	BD223185 98 human
13	1222.8	97.3	1286	6	AR243886 Sequence
14	1215.8	96.7	1236	9	BC014245 Homo sapi
15	1199.8	95.4	1220	6	AR405953 Sequence
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80	182.4	14.5	398	6	CQ664298 Sequence
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93 68.4 5.4 154391 2 CR388412
C 94 5.4 110000 2 PEMAL13.09
C 95 5.4 318221 2 PEMAL13.F3
C 96 67.8 5.4 224322 2 CR450711
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ALIGNMENTS

RESULT 1
AX092390
LOCUS AX092390
DEFINITION Sequence 121 from Patent WO0116318.
ACCESSION AX092390
VERSION AX092390.1 GI:13444509
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
TITLE Secrected and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 121 08-MAR-2001;
Genentech, Inc. (US)

FEATURES
source
1..1257
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1257; DB 6; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-213;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 GCTCTCTGCT 240
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DB 1021 ATCTAGCATTTATTTGATTTTGTCTCAATCAAAAGTGTGATTTTAAATGATTTT 1080
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QY 1201 AATTGTAATGTTAAGATTTTAAATTTTAAATGATTTTAAATTTTAAATTTTAAATTT 1257
DB 1201 AATTGTAATGTTAAGATTTTAAATTTTAAATGATTTTAAATTTTAAATTTTAAATTT 1257

RESULT 2
AX376298
LOCUS AX376298
DEFINITION Sequence 365 from Patent WO0168848.
ACCESSION AX376298
VERSION AX376298.1 GI:19170540
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secrected and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 365 20-SEP-2001;

Genentech, Inc. (US)	Location/Qualifiers
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DEFINITION	Sequence 245 from Patent WO0208284.		linear
ACCESSION	AX454660		
VERSION	AX454660.1	GI:21713954	

REFERENCE
AUTHORS
1
Baker, K.P., Ferrara, N., Gerber, H., Gerlitsen, M.E., Goddard, A.,

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 245 31-JAN-2002;

FEATURES	Location/Qualifiers
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RESULT 4	AX459648	LOCUS	AX459648	1257 bp	DNA	linear	PAT 08-JUL-2002
DEFINITION	Sequence 2 from Patent WO0216602.						
ACCESSION	AX459648						
VERSION	AX459648.1		GI:21725519				
KEYWORDS							
SOURCE							
ORGANISM	Homo sapiens (human)						
REFERENCE	Homo sapiens						
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
TITLE	Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Polakis, P., Williams, P.M., Wood, W.I., Wu, T.D. and Zhang, Z.						
JOURNAL	Compositions and methods for the diagnosis and treatment of tumor Patent: WO 0216602-A 2 28-FEB-2002;						
FEATURES	GENENTECH, INC. (US)						
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SOURCE	1:..1257						
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 REFERENCE
 AUTHORS
 1 Baker, K.P., Ferraz, N., Gerber, H., Gerlitsen, M.B., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
 and Ye, W.
 Compositions and methods for the diagnosis and treatment of
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 Genentech, Inc. (US)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 AUTHORS
 1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
 Baton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,
 Godowski, P.J., Guiney, A.L., Smith, V., Tumas, D., Wood, W.I.,
 Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.
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 REFERENCE
 AUTHORS
 1 Clark, H.F., Guiney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chu, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Baton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.B.,
 Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
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 Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,

TITLE
Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment

JOURNAL
Genome Res. 13 (10), 2265-2270 (2003)

PubMed
12975309

REFERENCE
2 (bases 1 to 1257)

AUTHORS
Clark, H.F.

TITLE
Direct Submission

JOURNAL
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
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ORIGIN

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REFERENCE
1 Mack, D.H., Gish, K.C. and Afar, D.
Methods of diagnosis of breast cancer, compositions and methods of
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Patent: WO 02059377-A 37 01-AUG-2002;
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 ORGANISM
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 REFERENCE
 Komatsoulis, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A.,
 Shi, Y., LaFleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P.,
 Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and
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ORIGIN

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Db	731	GGAAGCACTTGTGTAGAGAAATGGTGTCTGTGATTAGTGGATGTGCTATCTGGTGGAC	790
Qy	788	TTGTTCAGATTACCCAAAAGAGATGCTTCTACCTGATGGAATTCAGTTTCTCGCATAT	847
Db	791	TTGTTCAGATTACCCAAAAGAGATGCTTCTACCTGATGGAATTCAGTTTCTCGCATAT	850
Qy	848	TATGGAAGACATACCAAAATAAATGCTTAAATTTTCATTGCTACCTCTTTTTTAAATAT	907
Db	851	TATGGAAGACATACCAAAATAAATGCTTAAATTTTCATTGCTACCTCTTTTTTAAATAT	910
Qy	908	GCCTTGAATGGTTCACCTTAAATGACATTTTAAATAGTTATATGATACATCTGAAATGA	967
Db	911	GCCTTGAATGGTTCACCTTAAATGACATTTTAAATAGTTATATGATACATCTGAAATGA	970
Qy	968	AAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTTTTTAAATCTAGC	1027
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Qy	1088	TTTCTCTTAGTGCACATCTCTGCAACCTATATATTTGGATATATGTTGTGTCTTTGT	1147
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Qy	1208	AAAGTTAGAAATTTTTTTTATATCTGTAAATAAAAATTTATCCACA	1257
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RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	COMMENT
BD223185	BD223185	98 human secretory proteins.	BD223185	BD223185.1	GI:33032955	JP 2002521055-A/120.	Homo sapiens (human)	1 (bases, 1 to 1286)	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	98 human secretory proteins	Patent: JP 2002521055-A 120 16-JUL-2002;
											HUMAN GENOME SCIENCES, INC
											OS Homo sapiens (human)
											PN JP 2002521055-A/120
											PD 16-JUL-2002
											PF 29-JUL-1999 JP 2000562480
											PR 30-JUL-1998 US 60/094657, 05-AUG-1998 US 60/095486 PR
											06-AUG-1998 US 60/095455, 06-AUG-1998 US 60/095454 PR
											12-AUG-1998 US 60/096319
											PI GEORGE A KOMATSCOUIS, CRAIG A ROSEN, STEVEN
											M RUBEN ROXANNE DUAN
											PI PAUL A MOORE, YANGSU SHI, DAVID LAFLEUR, YING PEI WEI, JIAN NT, PHILIP
											KIMBERLY A FLORENCE, PAUL E YOUNG, LAURIE A BREWER, DANIEL R PI
											SOPET, GREGORY A ENDRESS, REINHARD BENER, HENRIK S OLSEN, MICHAEL PI

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ORIGINAL
FEATURES
source
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					2	Gaps
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QY	68	AGAGCGTACACAGTTCCTCTCCCTGAGTCTCCTCGGCTCCAGACTCCGGCTGCCGGCA	127			
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QY	128	GCCGGAGCCATGCGACGCCCAAGGCGCCGCGCTCCCGCAGCGGCTCCGCGGCTCT	187			
DB	121	GCCGGAGCCATGCGACGCCCAAGGCGCCGCGCTCCCGCAGCGGCTCCGCGGCTCT	180			
QY	188	GCTGTCTCTGTCTGCTGACGCTCCGCGCCCTGCGAGCGCTTGTGATATCCCAAGGGAA	247			
DB	181	GCTGTCTCTGTCTGCTGACGCTCCGCGCCCTGCGAGCGCTTGTGATATCCCAAGGGAA	240			
QY	248	GCAAAAGCGCAGCTCCCGCAGAGGGAGGTGTGACCTGTATTAATGAAATGCTTACA	307			
DB	241	GCAAAAGCGCAGCTCCCGCAGAGGGAGGTGTGACCTGTATTAATGAAATGCTTACA	299			
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QY	368	ACCTGGATCCAGAGTCCGGATGATTCAAAGAGAGAAAAGGGGGAATGCTGAGGAGAA	427			
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QY	428	CTTGGAGAGTCTGTGACACCCAACTACAGAGGTTCATGAGTCTTGAATTAATG	487			
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QY	488	CATGAGTCTTGGGAAATTTGGCGAGTGTACATTTCAAAAGATGCGTTCAATATGTCCT	547			
DB	480	CATGAGTCTTGGGAAATTTGGCGAGTGTACATTTCAAAAGATGCGTTCAATATGTCCT	539			
QY	548	AAGAGTTTGTTCAGTGCCTCATTCGCGTAAATGCAAAATGCAATGCTGTACGCTTG	607			
DB	540	AAGAGTTTGTTCAGTGCCTCATTCGCGTAAATGCAAAATGCAATGCTGTACGCTTG	599			
QY	608	GTAATTTCATTCATGAGCTGAAATGTTACGAGACTCTTCCCATTTAGATATATTTA	667			
DB	600	GTAATTTCATTCATGAGCTGAAATGTTACGAGACTCTTCCCATTTAGATATATTTA	659			

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OY	728	GGAGAAGCACTTTGTGAAGGAATGGTCTGTGATAGTGAAGTGTGCATCTGGGTGGAC	787
Db	720	GGAGAAGCACTTTGTGAAGGAATGGTCTGTGATAGTGAAGTGTGCATCTGGGTGGAC	779
OY	788	TTGTTCAATTCACCAAAAGAGATGCTTCATCTGATGGAATTCAGTTTCTGCATCAT	847
Db	780	TTGTTCAATTCACCAAAAGAGATGCTTCATCTGATGGAATTCAGTTTCTGCATCAT	839
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Db	900	GCGTTGAGATGGTTCACCTTAATAGACATTTTAAATAGTTTATGTAATCATCTGATGTA	959
OY	968	AAACCAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACACTGTTTTTAAATCTAGC	1027
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Db	1020	ATTATTCATTTGGCTTCATCAATCAAAAGTGGTTCAATATTTTATTTAGTGGTTAGAATAC	1079
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Db	1080	TTTCTTCATAGTCACATTCCTCAACCTAATATTTGGAAATATTTGTGTGGTCTTTTGTGT	1133
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OY	1208	AAATGTATAGAAATTTTTTTTATATCTGTAAATATAAAAATATATTTTCCACA	1257
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LOCUS	AR243886
DEFINITION	AR243886 1286 bp DNA
ACCESSION	Sequence 124 from patent US 6476195.
VERSION	AR243886
KEYWORDS	AR243886.1 GI:27291379
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1286)
TITLE	Konatsoulis,G., Rosen,C.A., Ruben,S.M., Duan,R.D., Moore,P.A., Shi,Y., LaFleur,D.W., Wei,Y.-F., Ni,J., Florence,K.A., Young,P., Brewer,L.A., Soppel,D.R., Endress,G.A., Ebner,R., Olsen,H. and Mucenski,M.
JOURNAL	Secreted protein HNFGF20
FEATURES	Patent: US 6476195-A 124 05-NOV-2002;
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Query Match	97.3%	Score 1222.8;	DB 6;	Length 1286;
Best Local Similarity	99.7%	Pred. No. 2.8e-207;		
Matches 1246; Conservative	0;	Mismatches 2;	Indels 2;	Gaps 2;

QY 8 GGCGCGGGGTGAAAGGCGCATTTGATGCAAGCTTGCGCGCGCTCGAGACCGCGCGAGACC 67
Dd 2 GGCGCGGGGTGAAAGGCGCATTTGATGCAAGCTTGCGCGCGCTCGAGACCGCGCGAG-C 60
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RESULT 14
BC014245

LOCUS 1236 bp mRNA linear PRI 29-JUN-2004

DEFINITION Homo sapiens collagen triple helix repeat containing 1, mRNA (CDNA

ACCESSION BC014245

VERSION BC014245.2 GI:33878497

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1236)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F., Dietzenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebelin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kaha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.M., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalske, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1236)

Strausberg, R.

Direct Submission

Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Aug 19, 2003 this sequence version replaced gi:15559789.

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: DCTD/BTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov>

Contact: nisc_mgc@hgrl.nih.gov

Akher, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Diackley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blakesley, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaapi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantipop, S., Thomas, P.J., Touchman, J.W., Turegon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

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Location/Qualifiers

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Best local similarity 99.8%; Pred. No. 4.9e-206;

Matches 1217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 99 CTCCGCTTCACGCTCCGCGCTCCGCGAGCGCGGAGCGATCGACCGAGGCGCGCC 158

DB 61 CTCCGCTTCACGCTCCGCGCTCCGCGAGCGCGGAGCGATCGACCGAGGCGCGCC 120

QY 159 GCCTCCCGAGCGGCTCCGCGGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 218

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QY 579 AATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638

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LOCUS AR405953
DEFINITION Sequence 3 from patent US 6630325.
ACCESSION AR405953
VERSION AR405953.1 GI:40155009
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1220)
AUTHORS Lindner,V. and Friesel,R.E.
TITLE Compositions, methods and kits relating to remodel
JOURNAL Patent: US 6630325-A 3 07-OCT-2003;
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Query Match 95.4%; Score 1199.8; DB 6; Length 1220;
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Matches 1212; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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OY	1243	AAATTATTTCCACA	1257
Dd	1205	AAATTATTTCCACA	1219
 RESULT 16 AY136825 1221 bp mRNA linear PRI 01-DEC-2002 Homo sapiens collagen triple helix repeat-containing protein 1 (CTHRCl) mRNA, complete cds. Accession AY136825 Version AY136825.1 GI:25989620 Keywords Source Homo sapiens (human) Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Reference Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Authors Lehner, W., Moore, D.P., Harmon, K.J., Mancini, M.L. and Lindner, V. Title Expression of the novel collagen triple helix repeat-containing gene (Cthrcl) suggests functions in multiple organ systems Journal Unpublished Reference 2 (bases 1 to 1221) Authors Lindner, V. Title Direct Submision Journal Submitted (29-JUL-2002) Center for Molecular Medicine, Maine Medical Center Research Institute, 81 Research Drive, Scarborough, ME 04074, USA Features source Location/Qualifiers 1..1221 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="8" /tissue_type="aorta smooth muscle" 1..1221 /gene="CTHRCl" 104..835 /note="matrix protein" /codon_start=1 /product="collagen triple helix repeat-containing protein 1" /protein_id="AAAN5749.1" /db_xref="GI:25989621" /translation="MRPGPAPSPQRRLGLLLLLLPAPSASSEIPKQKQLRQ REVVLYNMGICLGPAVGRDGSNGANGIGETGIPERDGFKGEGCLAESFESES TPNKQCSMSILANYGIDLGKLAECTFTMRNSALRVVPSGLRKCNACCORWYF FNAGEGSLPLIEAIIVLDGSGSPENSTINIHRTSVSGLDEGIGAGLVDAIWMGT SDYKGDASTGMNSVRITIEELPK"			
 ORIGIN Query Match 95.4%; Score 1198.8; DB 9; Length 1221; Best Local Similarity 99.8%; Pred. NO. 5.1e-203; Matches 1211; Conservative 0; Mismatches 2; Indels 1; Gaps 1;			
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OY	163	CCCCGCAGCGGCTCGCGGAGCTCTCGTGCTCTCTGCTGTCGACGTGCGCGGCGGCTGA	222
Dd	129	CCCCGCAGCGGCTCGCGGAGCTCTCGTGCTCTCTGCTGTCGACGTGCGCGGCGGCTGA	188
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Db	189	GC	CGCTCTG	ATC	CCCAAGGG	GAAGCAAAAGG	CGAGCTCCGG	CAAGGGAGGTG	GTGG	248
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Qy	463	GT	TCA	GAGT	CTCA	TGAA	TTA	TGGCA	TAGACTT	522
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Qy	823	G	ATGA	AT	TGCA	ATTC	TCGAT	CACTTA	TATGAGAA	882
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BD193030
LOCUS 1288 bp DNA linear PAT 17-JUL-2003
DEFINITION 207 human secreted proteins.
ACCESSION BD193030
VERSION BD193030.1 GI:33002769
KEYWORDS JP 2002516573-A/124.
SOURCE
ORGANISM
synthetic construct
artificial sequences.
1 (bases 1 to 1288)
REFERENCE
AUTHORS Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,
Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y.,
Florence, C., Florence, K., Lafleur, D.W., Ni, U., Fan, P., Wei, Y.F.,
Dillon, P.J., Andress, G.A., and Carter, K.C.
207 human secreted proteins
Patent: JP 2002516573-A 124 04-JUN-2002;
TITLE
JOURNAL HUMAN GENOME SCIENCES INC
PN JP 2002516573-A/124
COMMENT
PR 04-JUN-1998 JP 1999502815
PR 06-JUN-1997 US 60/048915, 06-JUN-1997 US 60/048882 PR
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05-SEP-1997 US 60/057661, 05-SEP-1997 US 60/057647 PR
18-DEC-1997 US 60/070923
PI PAUL, YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A
PI ROSEN,
PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER, PI
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PI PING FAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SOPPET, YI LI,
PI ZHIHEN ZENG,
PI HLA KIAM, GUO, LIANG YU, PING FENG, PATRICK J DILLON, GREGORY A PI
ENDRESS,
PI KENNETH C CARTER
PC A01N37/18, A01N43/04, C12Q1/00, C12Q1/02, C12Q1/68, C12N5/00 PC
C12N5/06, C12N15/00,
PC C12N15/06, C12N15/09, C12N15/10, C12N15/11, G01N33/53 CC
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CC Topology: Linear;
FH Key Location/Qualifiers.
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Best Local Similarity 99.3%; Pred. No. 1.1e-202;
Matches 1442; Conservative 2; Mismatches 2; Indels 5; Gaps 4;
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QY 128 GGCGGAGCGCATGCGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 187
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DB 598 GTATTTTCACTTCAATGAGGTGAATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
QY 668 TTTGAGACCAAG 727
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LOCUS	CO822026
DEFINITION	Sequence 125 from Patent EP1428933.
ACCESSION	CO822026
VERSION	CO822026.1
KEYWORDS	GI:49020742
SOURCE	.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Young,P., Greene,J.M., Ferrie,A.M., Ruben,S.M., Rosen,C.A., Hu,J.S., Olsen,H.S., Ehner,R., Brewer,L.A., More,P.A., Shi,Y., Florence,C., Florence,K., Lafleur,D.W., Ni,J., Fan,P., Wei,Y.F., Fischer,C.L., Soppet,D.R., Li,Y., Zeng,Z., Kyav,H., Yu,G.L., Feng,P., Dillon,P.J., Endreses,G.A. and Carter,K.C. 207 human secreted proteins Patent: EP 1428933-A 125 16-JUN-2004;
TITLE	Human Genome Sciences, Inc. (US)
JOURNAL	Location/Qualifiers
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Best Local Similarity	99.3%; Pred. No. 1.1e-202;
Matches 1242; Conservative	2; Mismatches 2; Indels 5; Gaps 4;
OY	8 GCCGCGGGGTGAAGGGCCCATTTATGCAGCTTCGGGGGGCTCCGAGCGCGGCCGAGCC 67
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DEFINITION Homo sapiens cDNA FLJ26553 fis, clone LNF01690.
ACCESSION AKJ30063
VERSION AKJ30063.1 GI:34526801
KEYWORDS oligo cloning; fis (Full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Taahiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
Nakazumi, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H.,
Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,
Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,
Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1190)
AUTHORS Sugano, S. and Suzuki, Y.
JOURNAL Direct Submission
TITLE Submitted (31-JUN-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
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(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
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Best Local Similarity 92.9%; Pred. No. 4,3e-180;
Matches 1168; Conservative 0; Mismatches 2; Indels 87; Gaps 1;
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QY 301 GCTTACAAAGGCGCAGAGAGTGTCTGTGAGACGCGAGAGCCCTGCGGCAATGTTATTC 360
DB 229 GCTTACAAAGGCGCAGAGAGTGTCTGTGAGACGCGAGAGCCCTGCGGCAATGCGATTC 288
QY 361 CGGTTACACCTGGAGATCCAGGTGGGATGATTTAAAGAGAAAGGGGGAATCTTGA 420

DB 289 CGGTTACACCTGGAGATCCAGGTGGGATGATTTAAAGAGAAAGGGGGAATGTCGA 348
QY 421 GGAAGAGCTTTGAGAGGCTCTGACACCCCACTCAAGCACTGTTCAATGAGTTCATTA 480
DB 349 GGAAGAGCTTTGAGAGGCTCTGACACCCCACTCAAGCACTGTTCAATGAGTTCATTA 408
QY 481 ATTATGAGATGATCTTGGGAAAATTGGAGGTGTGACATTTACCAAGATCGTTCAATA 540
DB 409 ATTATGAGATGATCTTGGGAAAATTGGAGGTGTGACATTTACCAAGATCGTTCAATA 468
QY 541 GTGCTCTAAGAGTTTGTCTGAGTGCTCATCTTGGGCTTAAATGCAAGATGATGCTGTC 600
DB 469 GTGCTCTAAGAGTTTGTCTGAGTGCTCATCTTGGGCTTAAATGCAAGATGATGCTGTC 528
QY 601 AGCGTTGATTTTACATTCATGAGAGTGAATGTCAGAGCCCTCCCATGAGCTA 660
DB 529 AGCGTTGATTTTACATTCATGAGAGTGAATGTCAGAGCCCTCCCATGAGCTA 588
QY 661 TAATTTATTTGACCAAGAGAGCCCTGAAATGAAATTCACATTAATTAATTCATGCACTT 720
DB 589 TAATTTATTTGACCAAGAGAGCCCTGAAATGAAATTCACATTAATTAATTCATGCACTT 648
QY 721 CTTCGTGAGAGACTTTGTGAAGAAATGCTGTGATTAAGTATGATGTTGCTATCTGG 780
DB 649 CTTCGTGAGAGACTTTGTGAAGAAATGCTGTGATTAAGTATGATGTTGCTATCTGG 708
QY 781 TTGGCACTTTTCAAGATTAACCAAGAGAGTGTCTTACCTGGAGTGAATTCAGTTCTC 840
DB 709 TTGGCACTTTTCAAGATTAACCAAGAGAGTGTCTTACCTGGAGTGAATTCAGTTCTC 768
QY 841 GCATCATTTATTAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
DB 769 GCATCATTTATTAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 828
QY 901 TTATTAATGCTTTGAAAGTGTCTTCAATTAAGCAATTTAATTAAGTATTAATTAATCT 960
DB 829 TTATTAATGCTTTGAAAGTGTCTTCAATTAAGCAATTTAATTAAGTATTAATTAATCT 888
QY 961 GAATGAAGAGAAAGCTTAATATGTTTATACAGACCAAGGTGATTCACACTGTTTAA 1020
DB 889 GAATGAAGAGAAAGCTTAATATGTTTATACAGACCAAGGTGATTCACACTGTTTAA 948
QY 1021 ATTACATTAATTAATTTTGTCTCAATCAAAAGTGTCTTCAATTTTATTAATTTT 1080
DB 949 ATTACATTAATTAATTTTGTCTCAATCAAAAGTGTCTTCAATTTTATTAATTTT 1008
QY 1081 AGAATACCTTTCTTATATGATCATTTCTCAACCTTAATTTTGAATATTTGTGCTCT 1140
DB 1009 AGAATACCTTTCTTATATGATCATTTCTCAACCTTAATTTTGAATATTTGTGCTCT 1068
QY 1141 TTTGTTTTTCTCTTATATGATCATTTTAAAAAATATAAAGCTAACCAATCTTTGTAC 1200
DB 1069 TTTGTTTTTCTCTTATATGATCATTTTAAAAAATATAAAGCTAACCAATCTTTGTAC 1128
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAATTAATTAATTTTCCACA 1257
DB 1129 AATTTGTAATGTTAAGAAATTTTATATCTGTTAATTAATTAATTTTCCACA 1185
RESULT 20
AF395488
LOCUS AF395488 1215 bp mRNA linear PRI 07-JUN-2003
DEFINITION Homo sapiens NTWC1 mRNA, complete cds.
ACCESSION AF395488
VERSION AF395488.1 GI:27525623
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens (human)
REFERENCE
AUTHORS Sanuki, N., Fujiki, K., Kanai, A., Tanaka, Y. and Iwata, T.
TITLE Novel polypeptide found in human cornea cDNA library

JOURNAL Unpublished
 REFERENCES 2 (bases 1 to 1215)
 AUTHORS Sanki N., Fujiki K., Kanai A., Tanaka Y. and Iwata T.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) National Center for Senory Organs,
 National Tokyo Medical Center, 2-5-1 Higashiyaoka, Meguro, Tokyo
 152-8902, Japan

FEATURES Location/Qualifiers
 source 1..1215

CDS

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 121..819
 /codon_start=1
 /product="NTMCI"
 /protein_id="AA017919.1"
 /db_xref="GI:27525624"
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 PAGVPGDPSPGANGIPTGPIPGDGPKEGECLESPESWTENYKQSGSLNY
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ORIGIN

Query Match 76.7%; Score 964.6; DB 9; Length 1215;
 Best Local Similarity 99.6%; Pred. No. 2,1e-161; Indels 0; Gaps 0;
 Matches 967; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 287 GTATAATGGAATGCTTCAAGAGCCAGAGAGTGCCTGTCAGACGGAGCCCTGG 346
 DB 228 GTATAATGGAATGCTTCAAGAGCCAGAGAGTGCCTGTCAGACGGAGCCCTGG 287
 QY 347 GGGCAATGTTATCCGGGTACACCTGGATCCCAAGTCCGAGATGATTTCAAGAGAGAA 406
 DB 288 GGGCAATGCTTCCGGGTACACCTGGATCCCAAGTCCGAGATGATTTCAAGAGAGAA 347
 QY 407 GGGGGAATGCTGAGGGAAGCTTTGAGAGTCTTGGACACCAACTACAGAGAGTTC 466
 DB 348 GGGGGAATGCTGAGGGAAGCTTTGAGAGTCTTGGACACCAACTACAGAGAGTTC 407
 QY 467 ATGAGATTCATTAATTAATGAGATGATCTTGGAGAAATTCGAGATGATTTCAAA 526
 DB 408 ATGAGATTCATTAATTAATGAGATGATCTTGGAGAAATTCGAGATGATTTCAAA 467
 QY 527 GATGCGTCAAAATGCTCTTAAGAGTTCCTGAGTCTGCTTCCGCTAAATAGCAG 586
 DB 468 GATGCGTCAAAATGCTCTTAAGAGTTCCTGAGTCTGCTTCCGCTAAATAGCAG 527
 QY 587 AAATGATGCTGAGGCTGATATTTCAATTCATGAGTGAATGTTCAAGACCTCT 646
 DB 528 AAATGATGCTGAGGCTGATATTTCAATTCATGAGTGAATGTTCAAGACCTCT 587
 QY 647 TCCCATTAAGATTAATTAATTAATGAGCAAGAGAGCCCTGAATGATTTCAAA 706
 DB 588 TCCCATTAAGATTAATTAATTAATGAGCAAGAGAGCCCTGAATGATTTCAAA 647
 QY 707 TATTCATGCACTTCTTCTGAGAGACTTTTGAAGAAATGCTGCTGATTAAGTGA 766
 DB 648 TATTCATGCACTTCTTCTGAGAGACTTTTGAAGAAATGCTGCTGATTAAGTGA 707
 QY 767 TGTTCATCTGAGGTTGAGCACTTTCAGATTAACCAAGAGAGATCTTCACTGATG 826
 DB 708 TGTTCATCTGAGGTTGAGCACTTTCAGATTAACCAAGAGAGATCTTCACTGATG 767
 QY 827 GAATTCAGTTCTCGCATCTTAATGAAGACTAACCAAAATTAATGCTTAATTTTCA 886
 DB 768 GAATTCAGTTCTCGCATCTTAATGAAGACTAACCAAAATTAATGCTTAATTTTCA 827
 QY 887 TGTCTACTCTTTTATTAATGCTTGGATGTTGATCTTAATGATTTTAAATAGT 946
 DB 828 TGTCTACTCTTTTATTAATGCTTGGATGTTGATCTTAATGATTTTAAATAGT 887
 QY 947 TTATGATATCATGATGAAGCAAGCAATTAATATGTTTACAGACCAAGTGTGATTT 1006

DB 888 TTATGATATCATGATGAAGCAAGCAATTAATATGTTTACAGACCAAGTGTGATTT 947
 QY 1007 CACACTGTTTTAAATCTAGATTTATTCATTTTGGTTCAATTAAGAGTTTCAATAT 1066
 DB 948 CACACTGTTTTAAATCTAGATTTATTCATTTTGGTTCAATTAAGAGTTTCAATAT 1007
 QY 1067 TTTTATGATGTTGATGAATCTTCTTCAATGATCATCTTCTCAACCTAATATTGAA 1126
 DB 1008 TTTTATGATGTTGATGAATCTTCTTCAATGATCATCTTCTCAACCTAATATTGAA 1067
 QY 1127 TATGTTGATGCTTTTGTGTTTCTTCTTCAATGATCATCTTCTCAACCTAATATTGAA 1186
 DB 1068 TATGTTGATGCTTTTGTGTTTCTTCTTCAATGATCATCTTCTCAACCTAATATTGAA 1127
 QY 1187 ACCAATCTTTGATCAATTTGTAATGTTAAGATTTTATATCTGTTAATTAATAT 1246
 DB 1128 ACCAATCTTTGATCAATTTGTAATGTTAAGATTTTATATCTGTTAATTAATAT 1187
 QY 1247 TATTTCCACA 1257
 DB 1188 TATTTCCACA 1198

RESULT 21

AR454024 837 bp DNA linear PAT 20-FEB-2004

LOCUS AR454024 Sequence 512 from patent US 6680197.

DEFINITION AR454024

ACCESSION AR454024

VERSION AR454024.1 GI:42686814

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

1 (bases 1 to 837)

Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,

Hepner, W.T. and Henderson, R.A.

Compositions and methods for the therapy and diagnosis of breast

cancer Patent: US 6680197-A 512 20-JAN-2004;

Location/Qualifiers

1..837

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 65.7%; Score 826; DB 6; Length 837;
 Best Local Similarity 99.9%; Pred. No. 8,6e-137;
 Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 332 ATGCACTCTGCGCGGCTTCGAGAGCGCGGAGCCAGACGCTGACCAAGTTCTCTCT 91
 DB 1 ATGCACTCTGCGCGGCTTCGAGAGCGCGGAGCCAGACGCTGACCAAGTTCTCTCT 59
 QY 92 CGGTCCTCTCGGCTCTCACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 151
 DB 60 CGGTCCTCTCGGCTCTCACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 119
 QY 152 CCGCGCGGCTCTCGGCTCTCACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 211
 DB 120 CCGCGCGGCTCTCGGCTCTCACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 179
 QY 212 CCGCGCGGCTCTCGGCTCTCACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 271
 DB 180 CCGCGCGGCTCTCGGCTCTCACTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 239
 QY 272 GGAAGTGTGAGACTGTATTAATGAAATGCTTACCAAGGCGCAGAGAGAGTCTGCTG 331
 DB 240 GGAAGTGTGAGACTGTATTAATGAAATGCTTACCAAGGCGCAGAGAGAGTCTGCTG 299
 QY 332 AGACGGAGACCTTGGGGCAATGTTATTCGGGATACCTTGGATCCAGTTCGGATGG 391
 DB 300 AGACGGAGACCTTGGGGCAATGTTATTCGGGATACCTTGGATCCAGTTCGGATGG 359

Db 828 TCATGAGAGTTCAATTGAAATTATGCAATAGATCTTTGGAAAAATTCGGAGATGTAATTACA 769
Qy 525 AAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGC 584
Db 768 AAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGC 709
Qy 585 AAAAAATGATGCGTGAAGGTTGTATTCACATTCATGAGCTGAATGTCAGAGCT 644
Db 708 AAAAAATGATGCGTGAAGGTTGTATTCACATTCATGAGCTGAATGTCAGAGCT 649
Qy 645 CTTCCTCAATGAAGCTAATATTTATTTGGAACCAAGAGCCCTGAATGTAATCAACAT 704
Db 648 CTTCCTCAATGAAGCTAATATTTATTTGGAACCAAGAGCCCTGAATGTAATCAACAT 589
Qy 705 AATATTCATGCACTTCTCTGTGGAAGACCTTTGGAAGAAATGTGCTGATTAAGTG 764
Db 588 AATATTCATGCACTTCTCTGTGGAAGACCTTTGGAAGAAATGTGCTGATTAAGTG 529
Qy 765 GATGTTGCTATCGGGTGGCACTTGTGAGATTACCAAAAGAGATGCTTCACTGGA 824
Db 528 GATGTTGCTATCGGGTGGCACTTGTGAGATTACCAAAAGAGATGCTTCACTGGA 469
Qy 825 TGAATTCAGTTCTTCGCAATCAATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTGA 884
Db 468 TGAATTCAGTTCTTCGCAATCAATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTGA 409
Qy 885 TTGCTACCTCTTTTATTTATTTATGCTTGAATGTTCACTTAATGACATTTAAATA 944
Db 408 TTGCTACCTCTTTTATTTATTTATGCTTGAATGTTCACTTAATGACATTTAAATA 349
Qy 945 GTTATGATATCATTCGAATGAAGAAAGCAAGCTAATATGTTTACGACCAAGTGTAT 1004
Db 348 GTTATGATATCATTCGAATGAAGAAAGCAAGCTAATATGTTTACGACCAAGTGTAT 289
Qy 1005 TTCAACATGTTTAAATCTAGCATTAATCTTTCTTCAATCAAAAGTGTTCATA 1064
Db 288 TTCAACATGTTTAAATCTAGCATTAATCTTTCTTCAATCAAAAGTGTTCATA 229
Qy 1065 TTTTATTTAGTGTGTAAGAAATCTTCTTCATAGTCAATCTCTCAACCTAATATTTGG 1124
Db 228 TTTTATTTAGTGTGTAAGAAATCTTCTTCATAGTCAATCTCTCAACCTAATATTTGG 169
Qy 1125 AATATGTTGTGCTCTTTGTTTCTCTTACTATAGCATTTTAAATAATATAAG 1184
Db 168 AATATGTTGTGCTCTTTGTTTCTCTTACTATAGCATTTTAAATAATATAAG 109
Qy 1185 CTACCAATCTTTGTAATTTGTAATGTTAAGATTTTATATCTGTTAAATATA 1244
Db 108 CTACCAATCTTTGTAATTTGTAATGTTAAGATTTTATATCTGTTAAATATA 49
Qy 1245 ATTATTTCCACA 1257
Db 48 ATTATTTCCACA 36

RESULT 24
AR454022 732 bp DNA linear PAT 20-FEB-2004
LOCUS AR454022
DEFINITION Sequence 510 from patent US 6680197.
ACCESSION AR454022
VERSION AR454022.1 GI:42686812
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 732)
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,
Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: US 6680197-A 510 20-JAN-2004;
FEATURES location/Qualifiers

source 1..732
/organism="unknown"
/mol_type="genomic DNA"

Query Match 58.2%; Score 732; DB 6; Length 732;
Best Local Similarity 100.0%; Pred. No. 4.3e-120;
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 ATGCAACCCAGAGGCCCCCGCCCTCCCGCAGCGGCTCCGAGGCTCTGTGCTCTG 197
Db 1 ATGCAACCCAGAGGCCCCCGCCCTCCCGCAGCGGCTCCGAGGCTCTGTGCTCTG 60
Qy 198 CTGCTGACGCTCCGCGCCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 257
Db 61 CTGCTGACGCTCCGCGCCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 120
Qy 258 CAGCTCCGCGCAGAGGAGGTGTGAGCTGTATTAATGGAATGTGCTTCAAGGCGCAGCA 317
Db 121 CAGCTCCGCGCAGAGGAGGTGTGAGCTGTATTAATGGAATGTGCTTCAAGGCGCAGCA 180
Qy 318 GGAATGCTGTGTGAGAGCGGAGCCCTGGGCGCAATGTTATTCGGGTTACACTTGGATC 377
Db 181 GGAATGCTGTGTGAGAGCGGAGCCCTGGGCGCAATGTTATTCGGGTTACACTTGGATC 240
Qy 378 CAGGTCGGGATGATTTCAAGAGAAAGGGGGAATGCTGAGGGAAGCTTGGAGAG 437
Db 241 CAGGTCGGGATGATTTCAAGAGAAAGGGGGAATGCTGAGGGAAGCTTGGAGAG 300
Qy 438 TCCTGACACCCCACTACAGAGATGTTCAATGAGTTCAATGAAATTAATGCAATGATCTT 497
Db 301 TCCTGACACCCCACTACAGAGATGTTCAATGAGTTCAATGAAATTAATGCAATGATCTT 360
Qy 498 GGAATATTCGGAAGTTCATTTACAAAGATGCGTTCAATATGCTTTAAGATTGG 557
Db 361 GGAATATTCGGAAGTTCATTTACAAAGATGCGTTCAATATGCTTTAAGATTGG 420
Qy 558 TTCAGTGCCTCACTTCGCTAATAATGCAAGATGCTGACGCTGTGATTTACA 617
Db 421 TTCAGTGCCTCACTTCGCTAATAATGCAAGATGCTGACGCTGTGATTTACA 480
Qy 618 TTCATAGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGTATTAATTTTGAACCA 677
Db 481 TTCATAGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGTATTAATTTTGAACCA 540
Qy 678 GGAAGCTCGAATGATTCACAAATTAATTAATTCATTCGACCTTCTTGTGGAAGACTT 737
Db 541 GGAAGCTCGAATGATTCACAAATTAATTAATTCATTCGACCTTCTTGTGGAAGACTT 600
Qy 738 TGTGAAGGAATGTGTCGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGCAGAT 797
Db 601 TGTGAAGGAATGTGTCGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGCAGAT 660
Qy 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGATCATTTATTAAGA 857
Db 661 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGATCATTTATTAAGA 720
Qy 858 CTACCAAAATTA 869
Db 721 CTACCAAAATTA 732

RESULT 25
AR454023 729 bp DNA linear PAT 20-FEB-2004
LOCUS AR454023
DEFINITION Sequence 511 from patent US 6680197.
ACCESSION AR454023
VERSION AR454023.1 GI:42686813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 729)

AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,
 TITLE Hepler, W.T. and Henderson, R.A.
 Compositions and methods for the therapy and diagnosis of breast
 cancer
 JOURNAL Patent: US 6680197-A 511 20-JAN-2004;
 FEATURES Location/Qualifiers
 source 1..729
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 58.0%; Score 729; DB 6; Length 729;
 Best Local Similarity 100.0%; Pred. No. 1.5e-119;
 Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 ATGCACCCCGAGGGGCCCCCGCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCTG 197
 Db 1 ATGCACCCCGAGGGGCCCCCGCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCTG 60
 QY 198 CTGCTGCAAGCTCCCGCGCGCTGCAAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 257
 Db 61 CTGCTGCAAGCTCCCGCGCGCTGCAAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 120
 QY 258 CAGCTCCGCGAGAGGAGGTGTGTGAAGCTGTATATATGATGATGCTTACAGGGCCAGCA 317
 Db 121 CAGCTCCGCGAGAGGAGGTGTGTGAAGCTGTATATATGATGATGCTTACAGGGCCAGCA 180
 QY 318 GAGAGGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACTGGAGATC 377
 Db 181 GAGAGGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACTGGAGATC 240
 QY 378 CCAGGTCCGGATGATTTCAAGAGAAAGGGGATGTCTGAGGAAAGCTTTGAGAG 437
 Db 241 CCAGGTCCGGATGATTTCAAGAGAAAGGGGATGTCTGAGGAAAGCTTTGAGAG 300
 QY 438 TCCTGGAACCCACTACAGAGAGTGTATGAGATTCATTAATTAATGCAATGATCTT 497
 Db 301 TCCTGGAACCCACTACAGAGAGTGTATGAGATTCATTAATTAATGCAATGATCTT 360
 QY 498 GGAAGAAATGGGAGATGATTTCAAGAGATGCTTCAAAATGCTTAAAGCTTAAAGATTTG 557
 Db 361 GGAAGAAATGGGAGATGATTTCAAGAGATGCTTCAAAATGCTTAAAGATTTG 420
 QY 558 TTCAGTGTCTCACTTCGCTAAATGCAAGAAATGCAATGCTGTGAGGTTGATTTTACA 617
 Db 421 TTCAGTGTCTCACTTCGCTAAATGCAAGAAATGCAATGCTGTGAGGTTGATTTTACA 480
 QY 618 TTCATGAGAGTGAATGTTCAAGACCTCTTCCATTGAAGCTATTAATTTTGAACCA 677
 Db 481 TTCATGAGAGTGAATGTTCAAGACCTCTTCCATTGAAGCTATTAATTTTGAACCA 540
 QY 678 GGAAGCCCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737
 Db 541 GGAAGCCCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 600
 QY 738 TGTGAAGGAATGTGTGATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 797
 Db 601 TGTGAAGGAATGTGTGATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 798 TACCCAAAGAGAGATGCTTTTCACTGATGATGATGATGATGATGATGATGATGATGAT 857
 Db 661 TACCCAAAGAGAGATGCTTTTCACTGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 858 CTACCAAAA 866
 Db 721 CTACCAAAA 729

RESULT 26
 BD006704
 LOCUS BD006704
 DEFINITION Novel polypeptide.
 ACCESSION BD006704 732 bp DNA linear PAT 31-JAN-2002

VERSION BD006704.1 GI:18635075
 KEYWORDS JP 2001029090-A/7.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 732)
 Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.
 TITLE Novel polypeptide
 JOURNAL Patent: JP 2001029090-A 7 06-FEB-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Homo sapiens (human)
 PN JP 2001029090-A/7
 PD 06-FEB-2001
 PF 19-MAY-2000 JP 2000147530
 PR
 PI YASUAKI ITO, SHINICHI MOGI, HIDEYUKI TANAKA, SHOICHI OKUBO, PI
 KAZUHIRO OGI
 PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
 PC A61P1/00
 PC A61P5/00, A61P9/00, A61P11/00, A61P25/00, A61P25/18, A61P31/00, PC
 A61P35/00,
 PC A61P37/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15, G01N33/50,
 PC G01N33/566//
 PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, (C12P21/02, PC
 C12R1.91),
 PC (C12N5/10, C12R1.91), (C12P21/08, C12R1.91), C12N15/00, A61K37/02,
 PC C12N5/00,
 PC (C12N5/00, C12R1.91)
 CC
 FT
 FH Key Location/Qualifiers
 FT source 1..732
 FT /organism="Homo sapiens (human)".
 FT /mol_type="genomic DNA"
 FT /db_xref="taxon:9606"

ORIGIN

Query Match 58.0%; Score 728.8; DB 6; Length 732;
 Best Local Similarity 99.7%; Pred. No. 1.6e-119;
 Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 ATGCACCCCGAGGGGCCCCCGCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCTG 197
 Db 1 ATGCACCCCGAGGGGCCCCCGCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCTG 60
 QY 198 CTGCTGCAAGCTCCCGCGCGCTGCAAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 257
 Db 61 CTGCTGCAAGCTCCCGCGCGCTGCAAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 120
 QY 258 CAGCTCCGCGAGAGAGTGTGTGAAGCTGTATATATGATGATGCTTACAGGGCCAGCA 317
 Db 121 CAGCTCCGCGAGAGAGTGTGTGAAGCTGTATATATGATGATGCTTACAGGGCCAGCA 180
 QY 318 GAGAGGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACTGGAGATC 377
 Db 181 GAGAGGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACTGGAGATC 240
 QY 378 CCAGGTCCGGATGATTTCAAGAGAAAGGGGATGTCTGAGGAAAGCTTTGAGAG 437
 Db 241 CCAGGTCCGGATGATTTCAAGAGAAAGGGGATGTCTGAGGAAAGCTTTGAGAG 300
 QY 438 TCCTGGAACCCACTACAGAGAGTGTATGAGATTCATTAATTAATGCAATGATCTT 497
 Db 301 TCCTGGAACCCACTACAGAGAGTGTATGAGATTCATTAATTAATGCAATGATCTT 360
 QY 498 GGAAGAAATGGGAGATGATTTCAAGAGATGCTTCAAAATGCTTAAAGCTTAAAGATTTG 557
 Db 361 GGAAGAAATGGGAGATGATTTCAAGAGATGCTTCAAAATGCTTAAAGATTTG 420
 QY 558 TTCAGTGTCTCACTTCGCTAAATGCAAGAAATGCAATGCTGTGAGGTTGATTTTACA 617

|||||
Db 421 TTCAAGGCTCACTTGCGCTAAATGACAAATGACGCTGACGGTGTATTTGACA 480
Qy 618 TTCAATGAGCTGAATGTTGACAGACCTCTTCCCATGAGCTATATTTATTTGACCA 677
Db 481 TTCAATGAGCTGAATGTTGACAGACCTCTTCCCATGAGCTATATTTATTTGACCA 540
Qy 678 GGAAGCCCTGAATGAAATCAACAATTATTCATGCACTCTTCTGTGAGAGACTT 737
Db 541 GGAAGCCCTGAATGAAATCAACAATTATTCATGCACTCTTCTGTGAGAGACTT 600
Qy 738 TGTGAAGAAATGCTGCTGATTAAGTGAATGTTGCTATCTGAGGTGCACTTTGAGAT 797
Db 601 TGTGAAGAAATGCTGCTGATTAAGTGAATGTTGCTATCTGAGGTGCACTTTGAGAT 660
Qy 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCACTATTTAGAGA 857
Db 661 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCACTATTTAGAGA 720
Qy 858 CTACCAAAATTA 869
Db 721 CTACCAAAATTA 732

RESULT 27
LOCUS CQ714369 732 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 303 from Patent WO02068579.
ACCESSION CQ714369
VERSION CQ714369.1 GI:42275226
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of humenexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 303 06-SEP-2002;
PE Corporation (NY) (US)
LOCATION/Qualifiers
1..732
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 57.9%; Score 727.2; DB 6; Length 732;
Best Local Similarity 99.6%; Pred. No. 3.1e-119; Mismatches 3; Indels 0; Gaps 0;
Matches 729; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 138 ATGCGACCCCGAGGGCCCGCGCTCCCGCAGCGGCTCCGCTCTGCTGCTCTG 197
Db 1 ATGCGACCCCGAGGGCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTCTGCTG 60
Qy 198 CTGCTGCAAGTCTCCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGCGG 257
Db 61 CTGCTGCAAGTCTCCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGCGG 120
Qy 258 CAGCTCCGCGAGGGAGGTGTGAGACTGTATTAATGGAATGTGCTTACAGGGCCAGCA 317
Db 121 CAGCTCCGCGAGGGAGGTGTGAGACTGTATTAATGGAATGTGCTTACAGGGCCAGCA 180
Qy 318 GGAAGTCTGCTGAGACGGAGCCCTGAGGCAATGTATTCGGGTACACCTGGGATC 377
Db 181 GGAAGTCTGCTGAGACGGAGCCCTGAGGCAATGTATTCGGGTACACCTGGGATC 240
Qy 378 CCAAGTCTGGGATGATTTCAAGAGAAAAGGGGAAATGTCTGAGGGAAGCTTTGAGAG 437
Db 241 CCAAGTCTGGGATGATTTCAAGAGAAAAGGGGAAATGTCTGAGGGAAGCTTTGAGAG 300

Qy 438 TCTTGACACCCCACTACAGCAGTCTTCATGAGTTCATTTAATTTAGCATATGCTT 497
Db 301 TCTTGACACCCCACTACAGCAGTCTTCATGAGTTCATTTAATTTAGCATATGCTT 360
Qy 498 GGGAAAATTTGGGAGTGTACATTTTACAAAGATGCGTTCAAATAGCTTCTAGAGTTTG 557
Db 361 GGGAAAATTTGGGAGTGTACATTTTACAAAGATGCGTTCAAATAGCTTCTAGAGTTTG 420
Qy 558 TTCAAGTCTCACTTCCGCTAAATGACAAATGACATGCTGACGGTGTATTTGACA 617
Db 421 TTCAAGTCTCACTTCCGCTAAATGACAAATGACATGCTGACGGTGTATTTGACA 480
Qy 618 TTCAATGAGCTGAATGTTGACAGACCTCTTCCCATGAGCTATATTTATTTGACCA 677
Db 481 TTCAATGAGCTGAATGTTGACAGACCTCTTCCCATGAGCTATATTTATTTGACCA 540
Qy 678 GGAAGCCCTGAATGAAATCAACAATTATTCATGCACTCTTCTGTGAGAGACTT 737
Db 541 GGAAGCCCTGAATGAAATCAACAATTATTCATGCACTCTTCTGTGAGAGACTT 600
Qy 738 TGTGAAGAAATGCTGCTGATTAAGTGAATGTTGCTATCTGAGGTGCACTTTGAGAT 797
Db 601 TGTGAAGAAATGCTGCTGATTAAGTGAATGTTGCTATCTGAGGTGCACTTTGAGAT 660
Qy 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCACTATTTAGAGA 857
Db 661 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCACTATTTAGAGA 720
Qy 858 CTACCAAAATTA 869
Db 721 CTACCAAAATTA 732

RESULT 28
LOCUS AX375790/c 683 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 3 from Patent WO0173031.
ACCESSION AX375790
VERSION AX375790.1 GI:19170293
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Xu, J., and Stolk, J.A.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: WO 0173031-A 3 04-OCT-2001;
CORIXA CORPORATION (US)
LOCATION/Qualifiers
1..683
source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 54.3%; Score 682.2; DB 6; Length 683;
Best Local Similarity 99.7%; Pred. No. 3e-111; Mismatches 2; Indels 0; Gaps 0;
Matches 681; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 516 AATTTTACAAAGATGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 AATTTTACAAAGATGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624
Qy 576 CTAAATGAGAAATGATGCTGTGAGCGTGTGATTTTCAATTCAATGAGCTGATGT 635
Db 623 CTAAATGAGAAATGATGCTGTGAGCGTGTGATTTTCAATTCAATGAGCTGATGT 564
Qy 636 TGAAGACTTCTTCCATGAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAT 695
Db 563 TGAAGACTTCTTCCATGAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAT 504

QY 696 TCAACATTAATATTCATGACCTTCTGTGGAAGACTTTGTGAAGAAATTTGGTCT 755
Db 503 TCAACATTAATATTCATGACCTTCTGTGGAAGACTTTGTGAAGAAATTTGGTCT 444
QY 756 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTTTCAATACCAAAAGAGATGCT 815
Db 443 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTTTCAATACCAAAAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCT 875
Db 383 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCT 324
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCAATTAATGACAT 935
Db 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCAATTAATGACAT 264
QY 936 TTTAAATAGTTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATTTTACAGACA 995
Db 263 TTTAAATAGTTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATTTTACAGACA 204
QY 996 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATTCATTTTGTTCATCAACAAAGTG 1055
Db 203 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATTCATTTTGTTCATCAACAAAGTG 144
QY 1056 GTTTCATATTTTATTTAGTTGTTGAATACCTTTCTTCAATGACATTTCTCAACT 1115
Db 143 GTTTCATATTTTATTTAGTTGTTGAATACCTTTCTTCAATGACATTTCTCAACT 84
QY 1116 ATAATTTGGAATATTTGTTGCTTTTCTTTTCTTCTAGATATGACATTTTAAATA 1175
Db 83 ATAATTTGGAATATTTGTTGCTTTTCTTTTCTTCTAGATATGACATTTTAAATA 24
QY 1176 ATATTAAGCTACCAATCTTTGT 1198
Db 23 ATATTAAGCTACCAATCTTTGT 1

RESULT 29
AR280558/c 683 bp DNA linear PAT 10-APR-2003
LOCUS AR280558
DEFINITION Sequence 63 from patent US 6518237.
ACCESSION AR280558
VERSION AR280558.1 GI:29716028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Yuglu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.
TITLE Compositions for treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6518237-A 63 11-FEB-2003;
FEATURES Location/Qualifiers
source 1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTTACAAAGAGCGTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 ACATTTTACAAAGAGCGTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624
QY 576 CTTAAATAGCAAAATGATGCTGTCAGGCTGTATTTCAATTAAGAGAGCTAAATGCT 635
Db 623 CTTAAATAGCAAAATGATGCTGTCAGGCTGTATTTCAATTAAGAGAGCTAAATGCT 564
QY 636 TCAGAGCTCTTCCCATTTGAAGCTAATATTTATTTTGAACCAAGAGAGCTGAATGAT 695
Db 563 TCAGAGCTCTTCCCATTTGAAGCTAATATTTATTTTGAACCAAGAGAGCTGAATGAT 504

QY 696 TCAACATTAATATTCATGACCTTCTGTGGAAGAACTTTGTAAGAAATTTGGTCT 755
Db 503 TCAACATTAATATTCATGACCTTCTGTGGAAGAACTTTGTAAGAAATTTGGTCT 444
QY 756 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTTTCAATACCAAAAGAGATGCT 815
Db 443 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTTTCAATACCAAAAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCT 875
Db 383 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCT 324
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCAATTAATGACAT 935
Db 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCAATTAATGACAT 264
QY 936 TTTAAATAGTTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATTTTACAGACA 995
Db 263 TTTAAATAGTTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATTTTACAGACA 204
QY 996 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATTCATTTTGTTCATCAACAAAGTG 1055
Db 203 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATTCATTTTGTTCATCAACAAAGTG 144
QY 1056 GTTTCATATTTTATTTAGTTGTTGAATACCTTTCTTCAATGACATTTCTCAACT 1115
Db 143 GTTTCATATTTTATTTAGTTGTTGAATACCTTTCTTCAATGACATTTCTCAACT 84
QY 1116 ATAATTTGGAATATTTGTTGCTTTTCTTTTCTTCTAGATATGACATTTTAAATA 1175
Db 83 ATAATTTGGAATATTTGTTGCTTTTCTTTTCTTCTAGATATGACATTTTAAATA 24
QY 1176 ATATTAAGCTACCAATCTTTGT 1198
Db 23 ATATTAAGCTACCAATCTTTGT 1

RESULT 30
AR283054/c 683 bp DNA linear PAT 10-APR-2003
LOCUS AR283054
DEFINITION Sequence 63 from patent US 6528054.
ACCESSION AR283054
VERSION AR283054.1 GI:29719881
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6528054-A 63 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTTACAAAGAGCGTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 ACATTTTACAAAGAGCGTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624
QY 576 CTTAAATAGCAAAATGATGCTGTCAGGCTGTATTTCAATTAAGAGAGCTAAATGCT 635
Db 623 CTTAAATAGCAAAATGATGCTGTCAGGCTGTATTTCAATTAAGAGAGCTAAATGCT 564
QY 636 TCAGAGCTCTTCCCATTTGAAGCTAATATTTATTTTGAACCAAGAGAGCTGAATGAT 695

|||||
Db 563 TAGGACCTCTCCCATTTGAAGCTATATTTATTTGGACCAAGAGCCCTGAAATGAAT 504
|||
Qy 696 TCACCAATTAATATTCATGCACTCTTCTGTGGAAGACTTTGGAAGAAATGGTGCT 755
|||
Db 503 TCACCAATTAATATTCATGCACTCTTCTGTGGAAGACTTTGGAAGAAATGGTGCT 444
|||
Qy 756 GGATTAGGAGATGTGCTATCTGGGTGGCACTTGTGAGTAAACCAAGAGATGCT 815
|||
Db 443 GGATTAGGAGATGTGCTATCTGGGTGGCACTTGTGAGTAAACCAAGAGATGCT 384
|||
Qy 816 TCTACTGATGGAATTCAGTTTCTCCCATCATTTATGGAAGAACTACCAAAATTAATGCTT 875
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Db 383 TCTACTGATGGAATTCAGTTTCTCCCATCATTTATGGAAGAACTACCAAAATTAATGCTT 324
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Qy 876 TAATTTCAATTTGCTACTCTTTTATTTATGAGCTTGGAAATGCTCACTTAATGACAT 935
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Db 323 TAATTTCAATTTGCTACTCTTTTATTTATGAGCTTGGAAATGCTCACTTAATGACAT 264
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Qy 936 TTTAAATTAAGTTATGATATCATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 995
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Db 263 TTTAAATTAAGTTATGATATCATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 204
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Qy 996 AAGTGTGATTTGACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 1055
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Db 203 AAGTGTGATTTGACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 144
|||
Qy 1056 GTTTCAAATATTTTTTTAGTTGGTTAGAAATACCTTCTTCATGACATTCCTCAACCT 1115
|||
Db 143 GTTTCAAATATTTTTTTAGTTGGTTAGAAATACCTTCTTCATGACATTCCTCAACCT 84
|||
Qy 1116 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 1175
|||
Db 83 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 24
|||
Qy 1176 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 1198
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Db 23 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 1

RESULT 31
AR341827/c 683 bp DNA linear PAT 17-AUG-2003
LOCUS AR341827 Sequence 63 from patent US 6573368.
DEFINITION AR341827
ACCESSION AR341827 GI:33736404
VERSION AR341827.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 683)
AUTHORS Yugi,J., Dillon,D.C., Mitcham,J.L. and Xu,J.
TITLES Compositions for the treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6573368-A 63 03-JUN-2003;
FEATURES
source Location/Qualifiers
1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 516 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
|||
Db 683 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
|||
Qy 576 CTAAATGCGAAGATGCGTGTCTGACGCGTTGGTATTTCACTTCAATGAGCTGAATGT 635
|||
Db 623 CTAAATGCGAAGATGCGTGTCTGACGCGTTGGTATTTCACTTCAATGAGCTGAATGT 564

|||||
Qy 636 TCAGACCTCTCCCATTTGAAGCTATTAATTTATTTGGACCAAGAGCCCTGAAATGAAT 695
|||
Db 563 TAGGACCTCTCCCATTTGAAGCTATTAATTTATTTGGACCAAGAGCCCTGAAATGAAT 504
|||
Qy 696 TCACCAATTAATATTCATGCACTCTTCTGTGGAAGACTTTGGAAGAAATGGTGCT 755
|||
Db 503 TCACCAATTAATATTCATGCACTCTTCTGTGGAAGACTTTGGAAGAAATGGTGCT 444
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Qy 756 GGATTAGGAGATGTGCTATCTGGGTGGCACTTGTGAGTAAACCAAGAGATGCT 815
|||
Db 443 GGATTAGGAGATGTGCTATCTGGGTGGCACTTGTGAGTAAACCAAGAGATGCT 384
|||
Qy 816 TCTACTGATGGAATTCAGTTTCTCCCATCATTTATGGAAGAACTACCAAAATTAATGCTT 875
|||
Db 383 TCTACTGATGGAATTCAGTTTCTCCCATCATTTATGGAAGAACTACCAAAATTAATGCTT 324
|||
Qy 876 TAATTTCAATTTGCTACTCTTTTATTTATGAGCTTGGAAATGCTCACTTAATGACAT 935
|||
Db 323 TAATTTCAATTTGCTACTCTTTTATTTATGAGCTTGGAAATGCTCACTTAATGACAT 264
|||
Qy 936 TTTAAATTAAGTTATGATATCATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 995
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Db 263 TTTAAATTAAGTTATGATATCATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 204
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Qy 996 AAGTGTGATTTGACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 1055
|||
Db 203 AAGTGTGATTTGACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 144
|||
Qy 1056 GTTTCAAATATTTTTTTAGTTGGTTAGAAATACCTTCTTCATGACATTCCTCAACCT 1115
|||
Db 143 GTTTCAAATATTTTTTTAGTTGGTTAGAAATACCTTCTTCATGACATTCCTCAACCT 84
|||
Qy 1116 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 1175
|||
Db 83 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 24
|||
Qy 1176 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 1198
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Db 23 ATAAATTTGAATATGTTGGTCTTTTGTCTTTCTTAAATAGCATTTTAAATTA 1

RESULT 32
AR343822/c 683 bp DNA linear PAT 17-AUG-2003
LOCUS AR343822 Sequence 63 from patent US 6579973.
DEFINITION AR343822
ACCESSION AR343822
VERSION AR343822.1 GI:33739722
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 683)
AUTHORS Yugi,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.
TITLES Compositions for the treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6579973-A 63 17-JUN-2003;
FEATURES
source Location/Qualifiers
1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 516 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
|||
Db 683 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
|||
Qy 576 CTAAATGCGAAGATGCGTGTCTGACGCGTTGGTATTTCACTTCAATGAGCTGAATGT 635
|||
Db 623 CTAAATGCGAAGATGCGTGTCTGACGCGTTGGTATTTCACTTCAATGAGCTGAATGT 564

QY 636 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 695
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 504
QY 636 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 755
DB 503 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 444
QY 756 GGATTAAGTGAAGTGTCTATCTGGGTTGGACCTGTTCAGATTAACCAAGAGAGATGCT 815
DB 443 GGATTAAGTGAAGTGTCTATCTGGGTTGGACCTGTTCAGATTAACCAAGAGAGATGCT 384
QY 816 TCTACTGATGAGATTCAGTTTCTCGCATCATTAATTAAGAACTACCAAAATTAATGCTT 875
DB 383 TCTACTGATGAGATTCAGTTTCTCGCATCATTAATTAAGAACTACCAAAATTAATGCTT 324
QY 876 TTAATTTTCACTTGTCTACCTCTTTTATTAATGCTTGAAGTGTCACTTAATGACAT 935
DB 323 TTAATTTTCACTTGTCTACCTCTTTTATTAATGCTTGAAGTGTCACTTAATGACAT 264
QY 936 TTTAATAATAGTTTATGATATACATCTGATGAAAGCAAGCTAATATGTTTACAGACA 995
DB 263 TTTAATAATAGTTTATGATATACATCTGATGAAAGCAAGCTAATATGTTTACAGACA 204
QY 996 AAGTGTGATTTACACCTGTTTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 1055
DB 203 AAGTGTGATTTACACCTGTTTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 144
QY 1056 GTTTCAATATTTTTTTTAACTGTTAGTAAATACCTTTTCAATGACATTTCTCAACCT 1115
DB 143 GTTTCAATATTTTTTTTAACTGTTAGTAAATACCTTTTCAATGACATTTCTCAACCT 84
QY 1116 ATAATTTGGAATATGTTGTGCTTTTGTCTTTTCTTGAATGACATTTTAAAAA 1175
DB 83 ATAATTTGGAATATGTTGTGCTTTTGTCTTTTCTTGAATGACATTTTAAAAA 24
QY 1176 ATAATAAGCTACCAATCTTTGT 1198
DB 23 ATAATAAGCTACCAATCTTTGT 1

RESULT 33
AR351023/c
LOCUS AR351023 683 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6586572.
ACCESSION AR351023
VERSION AR351023.1 GI:33752702
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and
Hepler, W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
Patent: US 6586572-A 63 01-JUN-2003;
JOURNAL Location/Qualifiers
FEATURES
1..683
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 576 CTAAATAGCAAAATGATGCTGTCAAGCGTTGTATTTCACTTAATGAGAGCTGAATGT 635

DB 623 CTAAATAGCAAAATGATGCTGTCAAGCGTTGTATTTCACTTAATGAGAGCTGAATGT 564
QY 636 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 695
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 504
QY 696 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 755
DB 503 TCAGGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAGACCCTGAATGAAT 444
QY 756 GGATTAAGTGAAGTGTCTATCTGGGTTGGACCTGTTCAGATTAACCAAGAGAGATGCT 815
DB 443 GGATTAAGTGAAGTGTCTATCTGGGTTGGACCTGTTCAGATTAACCAAGAGAGATGCT 384
QY 816 TCTACTGATGAGATTCAGTTTCTCGCATCATTAATTAAGAACTACCAAAATTAATGCTT 875
DB 383 TCTACTGATGAGATTCAGTTTCTCGCATCATTAATTAAGAACTACCAAAATTAATGCTT 324
QY 876 TTAATTTTCACTTGTCTACCTCTTTTATTAATGCTTGAAGTGTCACTTAATGACAT 935
DB 323 TTAATTTTCACTTGTCTACCTCTTTTATTAATGCTTGAAGTGTCACTTAATGACAT 264
QY 936 TTTAATAATAGTTTATGATATACATCTGATGAAAGCAAGCTAATATGTTTACAGACA 995
DB 263 TTTAATAATAGTTTATGATATACATCTGATGAAAGCAAGCTAATATGTTTACAGACA 204
QY 996 AAGTGTGATTTACACCTGTTTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 1055
DB 203 AAGTGTGATTTACACCTGTTTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 144
QY 1056 GTTTCAATATTTTTTTTAACTGTTAGTAAATACCTTTTCAATGACATTTCTCAACCT 1115
DB 143 GTTTCAATATTTTTTTTAACTGTTAGTAAATACCTTTTCAATGACATTTCTCAACCT 84
QY 1116 ATAATTTGGAATATGTTGTGCTTTTGTCTTTTCTTGAATGACATTTTAAAAA 1175
DB 83 ATAATTTGGAATATGTTGTGCTTTTGTCTTTTCTTGAATGACATTTTAAAAA 24
QY 1176 ATAATAAGCTACCAATCTTTGT 1198
DB 23 ATAATAAGCTACCAATCTTTGT 1

RESULT 34
AR352789/c
LOCUS AR352789 683 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6590076.
ACCESSION AR352789
VERSION AR352789.1 GI:33758194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Yunglu, J., Dillon, D.C., Mitcham, J.L. and Xu, J.
TITLE Compositions for the treatment and diagnosis of breast cancer and
methods for their use
Patent: US 6590076-A 63 08-JUL-2003;
JOURNAL Location/Qualifiers
FEATURES
1..683
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGG 624

QY 576 CTAATAAGCAAGAAATGCATGCTGTGACGGTGGTATTTCACTTCAATGAGAGCTGAATGT 635
DB 623 CTAAATATGCAAGAAATGCATGCTGTGACGGTGGTATTTCACTTCAATGAGAGCTGAATGT 564
QY 636 TCAGGACCTCTTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695
DB 563 TCAGGACCTCTTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 504
QY 696 TCACAAATTAATATTCATGCACTCTTCTGTGGAAAGACCTTGTGAAGAAATGGTGCT 755
DB 503 TCACAAATTAATATTCATGCACTCTTCTGTGGAAAGACCTTGTGAAGAAATGGTGCT 444
QY 756 GGAATTAAGGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGAGATGCT 815
DB 443 GGAATTAAGGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTCTGCGATCATTTATGAGAACTACCAAAATTAATGCTT 875
DB 383 TCTACTGATGGAATTCAGTTCTGCGATCATTTATGAGAACTACCAAAATTAATGCTT 324
QY 876 TAATTTTCATTTGCTACCTCTTTTATTTATGAGAACTGAAATGCTTCACTTAATGACAT 935
DB 323 TAATTTTCATTTGCTACCTCTTTTATTTATGAGAACTGAAATGCTTCACTTAATGACAT 264
QY 936 TTTAAATTAAGTTATGTATACATCTGAATGAAAGCAAGCTAATATGTTTACAGACA 995
DB 263 TTTAAATTAAGTTATGTATACATCTGAATGAAAGCAAGCTAATATGTTTACAGACA 204
QY 996 AAGTGTGATTTACACCTGTTTTTAAATCTAGCAATTAATGCTTCACTTAATGAGTG 1055
DB 203 AAGTGTGATTTACACCTGTTTTTAAATCTAGCAATTAATGCTTCACTTAATGAGTG 144
QY 1056 GTTTCAAATTTTTTTTATGTTAGTGAATACCTTTCTCAATGCTCACTTCTCAACT 1115
DB 143 GTTTCAAATTTTTTTTATGTTAGTGAATACCTTTCTCAATGCTCACTTCTCAACT 84
QY 1116 ATAAATTTGGAATATGTGTGCTTTTGTGTTTTCTCTTATGATAGCAATTTTAAAAAA 1175
DB 83 ATAAATTTGGAATATGTGTGCTTTTGTGTTTTCTCTTATGATAGCAATTTTAAAAAA 24
QY 1176 ATATAAAGCTACCAATCTTTGT 1198
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 35
AR453603/c 683 bp DNA linear PAT 20-FEB-2004
LOCUS AR453603
DEFINITION Sequence 63 from patent US 6680197.
ACCESSION AR453603
VERSION AR453603.1 GI:42686393
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: US 6680197-A 63 20-JAN-2004;
FEATURES
source Location/Qualifiers
1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred.No.3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
516 ACATTTACAAAGATGCTTCAATATGCTCTAAGATTTTGTTCAGTGCTCACTTCG 575

DB 683 ACATTTACAAAGATGCTTCAATATGCTCTAAGATTTTGTTCAGTGCTCACTTCG 624
QY 576 CTAATAAGCAAGAAATGCATGCTGTGACGGTGGTATTTCACTTCAATGAGAGCTGAATGT 635
DB 623 CTAAATATGCAAGAAATGCATGCTGTGACGGTGGTATTTCACTTCAATGAGAGCTGAATGT 564
QY 636 TCAGGACCTCTTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695
DB 563 TCAGGACCTCTTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 504
QY 696 TCACAAATTAATATTCATGCACTCTTCTGTGGAAAGACCTTGTGAAGAAATGGTGCT 755
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QY 756 GGAATTAAGGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGAGATGCT 815
DB 443 GGAATTAAGGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTCTGCGATCATTTATGAGAACTACCAAAATTAATGCTT 875
DB 383 TCTACTGATGGAATTCAGTTCTGCGATCATTTATGAGAACTACCAAAATTAATGCTT 324
QY 876 TAATTTTCATTTGCTACCTCTTTTATTTATGAGAACTGAAATGCTTCACTTAATGACAT 935
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DB 263 TTTAAATTAAGTTATGTATACATCTGAATGAAAGCAAGCTAATATGTTTACAGACA 204
QY 996 AAGTGTGATTTACACCTGTTTTTAAATCTAGCAATTAATGCTTCACTTAATGAGTG 1055
DB 203 AAGTGTGATTTACACCTGTTTTTAAATCTAGCAATTAATGCTTCACTTAATGAGTG 144
QY 1056 GTTTCAAATTTTTTTTATGTTAGTGAATACCTTTCTCAATGCTCACTTCTCAACT 1115
DB 143 GTTTCAAATTTTTTTTATGTTAGTGAATACCTTTCTCAATGCTCACTTCTCAACT 84
QY 1116 ATAAATTTGGAATATGTGTGCTTTTGTGTTTTCTCTTATGATAGCAATTTTAAAAAA 1175
DB 83 ATAAATTTGGAATATGTGTGCTTTTGTGTTTTCTCTTATGATAGCAATTTTAAAAAA 24
QY 1176 ATATAAAGCTACCAATCTTTGT 1198
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 36
AX302743/c 683 bp DNA linear PAT 30-NOV-2001
LOCUS AX302743
DEFINITION Sequence 63 from Patent WO0179286.
ACCESSION AX302743
VERSION AX302743.1 GI:17383244
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and
Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: WO 0179286-A 63 25-OCT-2001;
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;


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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature
1..687
/note="n = A,T,C or G"
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Query Match      51.0%; Score 640.8; DB 6; Length 687;
Best Local Similarity 97.5%; Pred. No. 6.9e-104;
Matches 659; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

QY 570 CTTGGCTAAATGAGAAATGATGCTGTCAGCGGTGATTTTCATTCATGAGAGCT 629
Db 1 CTTGGCTAAATGAGAAATGATGCTGTCAGCGGTGATTTTCATTCATGAGAGCT 60
QY 630 GAATGTTGAGAGCTCTTCCCATTTGAGCTATTAATTTGAGACCAAGAAAGCCCTGAA 689
Db 61 GAATGTTGAGAGCTCTTCCCATTTGAGCTATTAATTTGAGACCAAGAAAGCCCTGAA 120
QY 690 ATGATTCAACATTAATTAATTCATGCACTTCTGCTGAGAGAGACTTTGTAAGGAAT 749
Db 121 ATGATTCAACATTAATTAATTCATGCACTTCTGCTGAGAGAGACTTTGTAAGGAAT 180
QY 750 GGTGCTGATTAAGTGAATGTTGCTATCTGGTTGGCACTTGTTCAGATTACCAAGAA 809
Db 181 GGTGCTGATTAAGTGAATGTTGCTATCTGGTTGGCACTTGTTCAGATTACCAAGAA 240
QY 810 GATGCTTCTACTGATGGAATTCAGTTTCTGCATCATTAATTTGAAGAACTACCAAAATA 869
Db 241 GATGCTTCTACTGATGGAATTCAGTTTCTGCATCATTAATTTGAAGAACTACCAAAATA 300
QY 870 ATGCTTAATTTTCACTTGTGCTACCTCTTTTATTAATGCTTGAATGCTTCACTTAA 929
Db 301 ATGCTTAATTTTCACTTGTGCTACCTCTTTTATTAATGCTTGAATGCTTCACTTAA 360
QY 930 TGACATTTTAATAAGTTATGATATACATCTGAATGAGAAAGCAAGCTAAATATGTTAC 989
Db 361 TGACATTTTAATAAGTTATGATATACATCTGAATGAGAAAGCAAGCTAAATATGTTAC 420
QY 990 AGACCAAGTGTGATTTTCACTGTTTAAATCTAGCAATTAATTCATTTTGTCTTCAATCA 1049
Db 421 AGACCAAGTGTGATTTTCACTGTTTAAATCTAGCAATTAATTCATTTTGTCTTCAATCA 480
QY 1050 AAATGCTTCAATTTTATTTTATGTTAGTTGATGAATATCTTCTCATAGTCACTTCTCT 1109
Db 481 AAATGCTTCAATTTTATTTTATGTTAGTTGATGAATATCTTCTCATAGTCACTTCTCT 540
QY 1110 CAACCTTAATTTGGAATATGTTGTGCTCTTTGTGTTTCTCTTAAATGAGCAATTTT 1169
Db 541 CAACCTTAATTTGGAATATGTTGTGCTCTTTGTGTTTCTCTTAAATGAGCAATTTT 599
QY 1170 AAAAAAATATAAGCTACCAATCTTGTGAACAATTTGTAAATGTTAAGAAATTTTAT 1229
Db 600 AAAAAAATATAAGCTACCAATCTTGTGAACAATTTGTAAATGTTAAGAAATTTTAT 659
QY 1230 ATCTGTTAAATATAAA 1245
Db 660 ATCTGTTAAATATAAA 675

RESULT 40
AR405955 734 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 9 from patent US 6630325.
DEFINITION AR405955
ACCESSION AR405955.1 GI:40155011
VERSION AR405955.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 734)
Lindner,V. and Friesel,R.E.
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TITLE Compositions, methods and kits relating to remodel
JOURNAL Patent: US 6630325-A 9 07-OCT-2003;
FEATURES Location/Qualifiers
source
1..734
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match      45.1%; Score 566.6; DB 6; Length 734;
Best Local Similarity 87.0%; Pred. No. 1.1e-90;
Matches 636; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 142 GACCCACAGGCGCCGCGCTCCCGAGGAGCTCCGAGGCTCC-----TGCTGCTCC 195
Db 4 GCCCCACAGGCGCGCCGCTCCCGAGGAGCTCCGAGGAGCTCCGAGGCTCC 63
QY 196 TGTGCTGCACTGCGCGCGCGCTGAGCGGCTCTGAGATCCCAAGGAGCAAAAG 255
Db 64 TGTGCTGCACTGCGCGCGCGCTGAGCGGCTCTGAGATCCCAAGGAGCAAAAG 123
QY 256 CGCAGCTCCGCAAGAGAGAGTGTGATGCTGTATTAATGGAATGTCTTCAAGGCGCAG 315
Db 124 CGCAGATCCGCAAGAGAGAGTGTGATGCTGTATTAATGGAATGTCTTCAAGGAGCAG 183
QY 316 CAGAGTGCCTGCTGTCGAGACGAGAGCCCTGGGAGCAATGTTAATTCGGGTACACTGGGA 375
Db 184 CAGAGATGCTGCTGTCGATGAGAGAGCCCTGGGAGCAATGTTAATTCGGGTACACTGGGA 243
QY 376 TCCAGAGTGGGATGATTTCAAGAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAG 435
Db 244 TCCAGAGTGGGATGATTTCAAGAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAG 303
QY 436 AGTCTGCAACCCCACTCAACAAGAGTGTATGATGAGTTCATGAATTAATGAGCATAGATC 495
Db 304 AATCTGCAACCCCACTCAACAAGAGTGTATGATGAGTTCATGAATTAATGAGCATAGATC 363
QY 496 TTGGGAAATTTGCGGAGTGTACATTTACAAAGATGCTTCAAAATGAGTCTTAAGAGTT 555
Db 364 TTGGGAAATTTGCGGAGTGTACATTTACAAAGATGCTTCAAAATGAGTCTTAAGAGTT 423
QY 556 TGTTCAGTGCCTCACTTGCGCTAAATATGCAAGAAATGCAATGCTGCTGAGTGTGATTTCA 615
Db 424 TGTTCAGTGCCTCACTTGCGCTAAATATGCAAGAAATGCTGCTGAGTGTGATTTCA 483
QY 616 CATTCGAATGAGCTGAATGTTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGAGAC 675
Db 484 CATTCGAATGAGCTGAATGTTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGAGAC 543
QY 676 AAGGAGCCCTGAATGATTCACAAATTAATTAATTCATGCACTTCTCTGTGGAAGAG 735
Db 544 AAGGAGCCCTGAATGATTCACAAATTAATTAATTCATGCACTTCTCTGTGGAAGAG 603
QY 736 TTTGTGAAGAAATTTGCTGTGATTAATGATGTTGCTATCTGAGTGTGAGCACTTTGAC 795
Db 604 TCTGTGAAGAAATTTGCTGTGATTAATGATGTTGCTATCTGAGTGTGAGCACTTTGAC 663
QY 796 ATTAACCAAAAGAGATGCTTCTACATGAGATGGAATTCAGTTTCTCGATCATTAATGAAG 855
Db 664 ATTAACCAAAAGAGATGCTTCTACATGAGATGGAATTCAGTTTCTCGATCATTAATGAAG 723
QY 856 AACTACCAAAA 866
Db 724 AACTACCAAAA 734

RESULT 41
AP004221 160197 bp DNA linear PRI 02-OCT-2001
LOCUS Homo sapiens genomic DNA, chromosome 8q23, clone: KB1896D3.
DEFINITION AP004221
ACCESSION AP004221.1 GI:15824052
VERSION AP004221.1
KEYWORDS
SOURCE Homo sapiens (human)
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Best Local Similarity 93.8%; Pred. No. 1.4e-85;
Matches 562; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY  719  TCTCTCTGTGAAGACCTTTGTGAAGATTGCTGATTAAGTGAATGTTGCTATCTG  778
DB  123076 TCTTGCAGTGAAGACCTTTGTGAAGATTGCTGATTAAGTGAATGTTGCTATCTG  123135
QY  779  GGTTGGACCTGTTTCAGATTACCCCAAAAGAGATGCTCTACTGATGAGATTCAGTTTC  838
DB  123136 GGTTGGACCTGTTTCAGATTACCCCAAAAGAGATGCTCTACTGATGAGATTCAGTTTC  123195
QY  839  TCGCATCATTTAAGAACTACCAAAATTAATGCTTAATTTTCAATTTGCTACTCTTT  898
DB  123196 TCGCATCATTTAAGAACTACCAAAATTAATGCTTAATTTTCAATTTGCTACTCTTT  123255
QY  899  TTTTATTAATGCTTGAATGCTTCACTTAATTAATGATTTTAATTAATGATTAATCAT  958
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QY  959  CTGAATGAAGAAAGCAAGCTAATATGTTTACAGACCAAGTGATTTTACACGTCTTT  1018
DB  123316 CTGAATGAAGAAAGCAAGCTAATATGTTTACAGACCAAGTGATTTTACACGTCTTT  123375
QY  1019  AAATTCAGCATTTATTCATTTTGTCTTCAATCAAAAGTGCTTCAATATTTTATGTTGG  1078
DB  123376 AAATTCAGCATTTATTCATTTTGTCTTCAATCAAAAGTGCTTCAATATTTTATGTTGG  123435
QY  1079  TTAGAATCTTCTTCATAGCACATTCCTCAACCTATAATTTGGAAATTTGTGTGT  1138
DB  123436 TTAGAATCTTCTTCATAGCACATTCCTCAACCTATAATTTGGAAATTTGTGTGT  123495
QY  1139  CTTTGTCTTCTCTTATAGTATAGCATTTTAAAAAATATAAAGCTACCAATCTTTGT  1198
DB  123496 CTTTGTCTTCTCTTATAGTATAGCATTTTAAAAAATATAAAGCTACCAATCTTTGT  123555
QY  1199  ACAATTTGTAATGTTAAGATTTTATTTATCTGTTAAATATAATTTATTCACACA  1257
DB  123556 ACAATTTGTAATGTTAAGATTTTATTTATCTGTTAAATATAATTTATTCACACA  123614

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RESULT 42
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LOCUS      AC012213      176922 bp      DNA      linear      PRI 07-FEB-2002
DEFINITION Homo sapiens chromosome , clone RP11-1C8, complete sequence.
ACCESSION  AC012213
VERSION    AC012213.8  GI:18598769
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 176922)
            Birren,B., Linton,L., Nusbaum,C., Allen,N., Anderson,M.,
            Baldwin,D., Barna,N., Beckert,R., Boguslavsky,L., Bouhassira,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., Dekrellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hages,B., Heathord,A., Horton,L.,
            Howland,D., Johnson,R., Jones,C., Kann,L., Karates,A., Klein,J.,
            Lehocaky,J., Liu,C., Locke,K., Macdonald,P., Margulis,N.,
            McEwan,P., McGurk,A., McKernan,K., McDonald,I., Meldrum,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talama,J.,
            Teefaye,S., Tittrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
            Direct Submission
            Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            3 (bases 1 to 176922)
REFERENCE  3
AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
            Anderson,M., Barna,N., Bastien,V., Boguslavsky,L., Bouhassira,B.,
            Brown,A., Camarata,J., Campioano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., Dekrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Gindes,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hages,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kann,A., Karates,A., Kells,C., Labocque,K., Lamazeres,R.,
            Landers,T., Lehocaky,J., Levine,R., Liu,G., Maclean,C.,
            Macdonald,P., Major,J., Margulis,N., Matthews,C., McCarthy,M.,
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            Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
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            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

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TITLE
JOURNAL

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, W. J., Young, G.,
Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission

COMMENT

Submitted (07-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 7, 2002 this sequence version replaced gi:18129443.
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Genome Center

Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu
Project Information

Center project name: L1765
Center clone name: 1_C_8

FEATURES

source

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Query Match      42.9%; Score 539.8; DB 9; Length 176922;
Best Local Similarity 93.8%; Pred. No. 1.4e-85;
Matches 562; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

659 TATAATTTATTTGGACCAAGAAAGCCCTGAATGAAATTCACATTAATATTCATGCGAC 718
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QY 719 TTTCTGTGGAAGACCTTTGTGAAGAAATGCTGTGATTAATGATGATGCTTACTC 778
Db 136343 TCTTGACATGGAAGACCTTTGTGAAGAAATGCTGTGATTAATGATGATGCTTACTC 136284

QY 779 GGTGGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGGAATTCAGTTTC 838
Db 136283 GGTGGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGGAATTCAGTTTC 136224

QY 839 TCGCATCATTAATTTGAAGAACTACCAAAATTAATGCTTAAATTTTCATTTGCTACCTCTT 898
Db 136223 TCGCATCATTAATTTGAAGAACTACCAAAATTAATGCTTAAATTTTCATTTGCTACCTCTT 136164

QY 899 TTTTATTAATGCTTGAAGATGTTCACTTAATGACATTTTAAATTAAGTTTATGATACAT 958
Db 136163 TTTTATTAATGCTTGAAGATGTTCACTTAATGACATTTTAAATTAAGTTTATGATACAT 136104

QY 959 CTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTTACCTGTTTTT 1018
Db 136103 CTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTTACCTGTTTTT 136044

QY 1019 AAATTCACATTAATTCATTTTCTTCATCAATCAAAAGTGTTCATATTTTATTTTGTG 1078
Db 136043 AAATTCACATTAATTCATTTTCTTCATCAATCAAAAGTGTTCATATTTTATTTTGTG 135984

QY 1079 TTGAATACCTTCTTCATGACATTCCTGCAACCTTAATTTGGAATATTTGTTGTGT 1138
Db 135983 TTGAATACCTTCTTCATGACATTCCTGCAACCTTAATTTGGAATATTTGTTGTGT 135924

QY 1139 CTTTGTGTTTTCTTGTGATAGATTTTAAATTAATTAAGCTTCCATCTTTGT 1198
Db 135923 CTTTGTGTTTTCTTGTGATAGATTTTAAATTAATTAAGCTTCCATCTTTGT 135864

QY 1199 ACAATTTGTAATGTTAAGATTTTATTAATCTGTTAATTAATTAATTTTCCAA 1257
Db 135863 ACAATTTGTAATGTTAAGATTTTATTAATCTGTTAATTAATTAATTTTCCAA 135805

RESULT 43
AX339938/c 560 bp DNA linear PAT 10-JAN-2002
LOCUS Sequence 185 from Patent W00196388.
DEFINITION AX339938
ACCESSION AX339938
VERSION AX339938.1 GI:18135919
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Jiang, Y., Harlocker, S.L. and Secrist, H.
TITL E Compositions and methods for the therapy and diagnosis of colon
JOURNAL Patent: WO 0196388-A 185 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
LOCATION/Qualifiers
SOURCE 1..560
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
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Query Match      42.3%; Score 532.2; DB 6; Length 560;
Best Local Similarity 99.3%; Pred. No. 1.3e-84;
Matches 554; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

643 CTCCTCCCATTTGAAGCTATAA-TTATTTGGACCAAGAAAGCCCTGAATGAATTCACA 701
Db 558 HCTCTCCCATTTGAAGCTATAA-TTATTTGGACCAAGAAAGCCCTGAATGAATTCACA 499

QY 702 AATTAATTAATTCAGACCTTCTGTGGAAGACCTTTGTAAGAAATTTGCTGTGATTA 761
Db 498 AATTAATTAATTCAGACCTTCTGTGGAAGACCTTTGTAAGAAATTTGCTGTGATTA 439

QY 762 GTGATGTTGCTATCTGGGTTGGACCTTGTTCAGATTAACCAAAAGAGATGCTTACT 821
Db 438 GTGATGTTGCTATCTGGGTTGGACCTTGTTCAGATTAACCAAAAGAGATGCTTACT 379

QY 822 GGATGAATTAAGATTTCTGCAATCAATTTGAAGAACTACCAAAATTAATGCTTTAATTT 881
Db 378 GGATGAATTAAGATTTCTGCAATCAATTTGAAGAACTACCAAAATTAATGCTTTAATTT 319

QY 882 TCATTTGCTACCTC-TTTTTTATTAATGCTTGAAGATGCTTCAATTAATGACATTTTA 940
Db 318 TCATTTGCTACCTC-TTTTTTATTAATGCTTGAAGATGCTTCAATTAATGACATTTTA 259

QY 941 ATAAGTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTG 1000
Db 258 ATAAGTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTG 199

QY 1001 TGATTTCACTGTTTTTAAATCTAGACATTAATTCATTTTGTCTTCATCAAAAGTGTTC 1060
Db 198 TGATTTCACTGTTTTTAAATCTAGACATTAATTCATTTTGTCTTCATCAAAAGTGTTC 139

QY 1061 AATTTTTTTTATGTTGTTGAATGATCTTCTTCATGTCACATCTTCCTCACTTAAT 1120
Db 138 AATTTTTTTTATGTTGTTGAATGATCTTCTTCATGTCACATCTTCCTCACTTAAT 79

QY 1121 TTGAATATTTGTTGCTTTTGTGTTTCTCTTATGATAGATTTTAAAAAATA 1180
Db 78 TTGAATATTTGTTGCTTTTGTGTTTCTCTTATGATAGATTTTAAAAAATA 19

QY 1181 AAAGCTACCAATCTTTGT 1198
Db 18 AAAGCTACCAATCTTTGT 1

RESULT 44
CQ463279 485 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 6057 from Patent W00192581.
DEFINITION CQ463279
ACCESSION CQ463279
VERSION CQ463279.1 GI:41428898
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Algate, P.A., Harlocker, S.L. and Jones, R.
TITL E Compositions and methods for the therapy and diagnosis of
JOURNAL Patent: WO 0192581-A 6057 06-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
LOCATION/Qualifiers
SOURCE 1..485
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match      38.3%; Score 481.8; DB 6; Length 485;
Best Local Similarity 99.6%; Pred. No. 1.2e-75;
Matches 483; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 734 ACTTGGGAAGAAATTGTCGTGATTAAGNAGATGTTGCTATCGGGTTGGCACTTGTTC 793
DB 1 ACTTTGGAGAAATGGTGTGATTAAGNAGATGTTGCTATCGGGTTGGCACTTGTTC 60
QY 794 AGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTCGCATCTTAATGA 853
DB 61 AGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTCGCATCTTAATGA 120
QY 854 AGAATACCCAAATTAATGCTTTAATTTTCACTTGTCTTTTCTTTTAAATGCTTG 913
DB 121 AGAATACCCAAATTAATGCTTTAATTTTCACTTGTCTTTTCTTTTAAATGCTTG 180
QY 914 GAATGGTCACTTAATTAATGATCTTTAATTAATTAATTAATTAATTAATTAATTAAT 973
DB 181 GAATGGTCACTTAATTAATGATCTTTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 974 AGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGCATTAAT 1033
DB 241 AGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGCATTAAT 300
QY 1034 CATTTTGCTTCAATCAAAAGTGTTCATATTTTCTTTTGTGTTAGAAATCTTTCTT 1093
DB 301 CATTTTGCTTCAATCAAAAGTGTTCATATTTTCTTTTGTGTTAGAAATCTTTCTT 360
QY 1094 CATAGTCATCTCTCAACCTTAATTTTGAATATTTGTTGTTTCTTTTCTTCTC 1153
DB 361 CATAGTCATCTCTCAACCTTAATTTTGAATATTTGTTGTTTCTTTTCTTCTC 420
QY 1154 TTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1213
DB 421 TTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 1214 TAAGA 1218
DB 481 TAAGA 485

RESULT 45
CQ463299/c
LOCUS CQ463299 464 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6077 from Patent WO0192581.
ACCESSION CQ463299
VERSION CQ463299.1 GI:41428918
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Aligate, P.A., Harlocker, S.L. and Jones, R.
Compositions and methods for the therapy and diagnosis of
ovarian cancer
Patent: WO 0192581-A 6077 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source 1..464
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match: 36.5%; Score 459.2; DB 6; Length 464;
Best Local Similarity 99.4%; Pred. No. 1.2e-71;
Matches 461; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 793 CAGATTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTCGCATCTTAATG 852
DB 464 CAGATTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTCGCATCTTAATG 405
QY 853 AAGAATACCAAAATTAATGCTTTAATTTTCACTTGTCTTTTCTTTTAAATGCTT 912
DB 404 AAGAATACCAAAATTAATGCTTTAATTTTCACTTGTCTTTTCTTTTAAATGCTT 345

QY 913 GGAATGTTCACTTAATGACATTTTAATTAATTAATTAATTAATTAATTAATTAAT 972
DB 344 GGAATGTTCACTTAATTAATGACATTTTAATTAATTAATTAATTAATTAATTAAT 285
QY 973 AAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGCATTAAT 1032
DB 284 AAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGCATTAAT 225
QY 1033 TCATTTTGCTTCAATCAAAAGTGTTCATATTTTCTTTTAAATTAATTAATTAAT 1092
DB 224 TCATTTTGCTTCAATCAAAAGTGTTCATATTTTCTTTTAAATTAATTAATTAAT 165
QY 1093 TCATTTTGCTTCAATCAAAAGTGTTCATATTTTCTTTTAAATTAATTAATTAAT 1152
DB 164 TCATTTTGCTTCAATCAAAAGTGTTCATATTTTCTTTTAAATTAATTAATTAAT 105
QY 1153 CTTAGTATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1212
DB 104 CTTAGTATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 45
QY 1213 TTAGAATTTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1256
DB 44 TTAGAATTTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1

RESULT 46
CQ712169
LOCUS CQ712169 466 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 57095 from Patent WO2070737.
ACCESSION CQ712169
VERSION CQ712169.1 GI:42273026
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Liew, C.C., Marshall, W.B. and Zhang, H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 57095 12-SEP-2002;
JOURNAL ChondroGene Inc. (CA)
FEATURES
source 1..466
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match: 34.7%; Score 435.8; DB 6; Length 466;
Best Local Similarity 98.9%; Pred. No. 1.7e-67;
Matches 448; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 693 AATTCAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 752
DB 14 AATTCAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 73
QY 753 GCTGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAGAGAT 812
DB 74 GCTGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAGAGAT 133
QY 813 GCTTCACTGAGATGGAATTCAGTTTCTCGCATCTTAATTAATTAATTAATTAATTAAT 871
DB 134 GCTTCACTGAGATGGAATTCAGTTTCTCGCATCTTAATTAATTAATTAATTAATTAAT 193
QY 872 GCTTCACTGAGATGGAATTCAGTTTCTCGCATCTTAATTAATTAATTAATTAATTAAT 931
DB 194 GCTTCACTGAGATGGAATTCAGTTTCTCGCATCTTAATTAATTAATTAATTAATTAAT 253
QY 932 AATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 991
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QY 992 ACCAAGTGTGATTTGACACTGTTTTAAATCTAGCATTTATCTTGTGCTCATCAAA 1051
DB 314 ACCAAGTGTGATTTGACACTGTTTTAAATCTAGCATTTATCTTGTGCTCATCAAA 373
QY 1052 AGTGTGTTCAATTTTTTTTTAGTGTGATTAAGTACTTTCTTCAATGTCATCTCTCA 1111
DB 374 AGTGTGTTCAATTTTTTTTTAGTGTGATTAAGTACTTTCTTCAATGTCATCTCTCA 433
QY 1112 ACCATTAATTTGGAATATTTGTTGGTCTTTTG 1144
DB 434 ACCATTAATTTGGAATATTTGTTGGTCTTTTG 466

RESULT 47
AX351434/C 460 bp DNA linear PAT 06-FEB-2002
LOCUS AX351434
DEFINITION Sequence 181 from Patent WO0196390.
ACCESSION AX351434
VERSION AX351434.1 GI:18616781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Jiang, Y., Hepler, W.T., Clapper, J.D., Wang, A. and Secrist, H.
AUTHORS Compositions and methods for the therapy and diagnosis of colon
TITLE Cancer
JOURNAL Patent: WO 0196390-A 181 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..460
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 98.9%; Pred. No. 5e-67;
Matches 457; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 737 TTGTAAGGAATTTGTCGTGATTTAGTGAATTTGCTATCTGGTGTGACATTTGTCACA 796
DB 460 TTGTAAGGAATTTGTCGTGATTTAGTGAATTTGCTATCTGGTGTGACATTTGTCACA 403
QY 797 TTACCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTCGCATCATTTGGAAGA 856
DB 402 TTACCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTCGCATCATTTGGAAGA 343
QY 857 ACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTTATATATGCTTGAA 916
DB 342 ACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTTATATATGCTTGAA 283
QY 917 TGGTCACTTAATAATGATTTTAAATTAAGTTATGATATCATCTGAATGAAGAAAGC 976
DB 282 TGGTCACTTAATAATGATTTTAAATTAAGTTATGATATCATCTGAATGAAGAAAGC 223
QY 977 TAAATATGTTTACAGACCAAGTGTGATTTCACTGTTTAAATCTAGCATTTATTCAT 1036
DB 222 TAAATATGTTTACAGACCAAGTGTGATTTCACTGTTTAAATCTAGCATTTATTCAT 163
QY 1037 TTTGCTTCAATCAAAAGTGTGATTTTATTTTATGTTGATTAATCTTTCTTCAT 1096
DB 162 TTTGCTTCAATCAAAAGTGTGATTTTATTTTATGTTGATTAATCTTTCTTCAT 103
QY 1097 AGTCAATTTCTCTCAACCTAATTAATTTGGAATTTGTTGGTCTTTGTTTCTCTCA 1156
DB 102 AGTCAATTTCTCTCAACCTAATTTGGAATTTGTTGGTCTTTGTTTCTCTCA 43
QY 1157 GTATAGCATTTTAAAAAATATAAAGTACCAATCTTTGT 1198
DB 42 GTATAGCATTTTAAAAAATATAAAGTACCAATCTTTGT 1

RESULT 48
AX340025 471 bp DNA linear PAT 10-JAN-2002
LOCUS AX340025
DEFINITION Sequence 272 from Patent WO0196388.
ACCESSION AX340025
VERSION AX340025.1 GI:18136006
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Jiang, Y., Harlocker, S.L. and Secrist, H.
AUTHORS Compositions and methods for the therapy and diagnosis of colon
TITLE Cancer
JOURNAL Patent: WO 0196388-A 272 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..471
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN
Query Match 34.3%; Score 431.2; DB 6; Length 471;
Best Local Similarity 98.9%; Pred. No. 1.1e-66;
Matches 464; Conservative 1; Mismatches 1; Indels 3; Gaps 3;

QY 516 ACATTACAAAGATGCGTTCAATATGCTCTAGAGTTTGTCTAGTGTGCTCACTTCG 575
DB 1 ACATTACAAAGATGCGTTCAATATGCTCTAGAGTTTGTCTAGTGTGCTCACTTCG 60
QY 576 CTAAATGCAAAATGATGCTGCTGACGCTTGTGATTTTCACTTCAATGAGCTGAATGT 635
DB 61 CTAAATGCAAAATGATGCTGCTGACGCTTGTGATTTTCACTTCAATGAGCTGAATGT 120
QY 636 TCAGACCTCTTCCCATTTGAAGCTATATTTATTTGACCAAGAGCCCTGAATGAAT 695
DB 121 TCAGACCTCTTCCCATTTGAAGCTATATTTATTTGACCAAGAGCCCTGAATGAAT 180
QY 696 TCAACATTAATTAATTCATGCACTTCTTGTGTGAGAGACTTTGTGAGAAATGCTGT 755
DB 181 TCAACATTAATTAATTCATGCACTTCTTGTGTGAGAGACTTTGTGAGAAATGCTGT 240
QY 756 GGAATAGGATGATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
DB 241 GGAATAGGATGATGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 816 TCTACTGATGATTAATGATGCTTCTGCACTTATTTGAAAGTACCAAAATTAATGCTT 875
DB 301 TCTACTGATGATTAATGATGCTTCTGCACTTATTTGAAAGTACCAAAATTAATGCTT 360
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAAT-GGTTCACTTAATGACA 934
DB 361 TAAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAATGGTTCACTTAATGACA 420
QY 935 TTTTAAATTAAG-TTATGTAATACA-TCTGAATGAAGCAAACTAAT 981
DB 421 TTTTAAATTAAGTTATGTAATACA-TCTGAATGAAGCAAACTAAT 469

RESULT 49
BX935556 1009 bp mRNA linear VMT 30-MAR-2004
LOCUS BX935556
DEFINITION Gallus gallus finished cDNA, clone ChEST92913.
ACCESSION BX935556
VERSION BX935556.2 GI:46018669
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 1821985908 residues

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Post-processing: Listing first 45 summaries

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9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1104	87.8	1288	3	BC021025 Homo sapi
2	1054	83.9	1207	3	CR605392 full-length
3	1036	82.4	1189	3	CR596030 full-length
4	958	76.2	1111	3	CR612318 full-length
5	950	75.6	1103	3	CR594803 full-length
6	700	55.7	1098	1	AL532456 full-length
7	693	55.1	747	6	CA415410 full-length
8	693	55.1	796	5	BQ008675 full-length
9	691	55.0	1102	1	AL575307 full-length
10	682	54.3	702	1	BQ010155 full-length
11	668	53.1	1100	1	AL551834 full-length
12	640	50.9	723	6	CA431413 full-length
13	636	50.6	683	2	BE607413 full-length
14	632	50.3	683	2	BQ425256 full-length
15	603	48.0	902	5	BQ424201 full-length
16	602	47.9	827	1	AL544722 full-length
17	595	47.3	922	5	BQ425098 full-length
18	588	46.8	730	7	BU729033 full-length
19	587	46.7	700	7	CN394776 full-length
20	581	46.2	724	9	BQ009009 full-length
21	579	46.1	732	9	AY399084 full-length
22	572	44.7	610	5	BQ013605 full-length
23	562	44.7	610	5	BQ013605 full-length
24	558	44.4	903	4	BT763235 full-length

25	557	44.3	710	3	CR592899 full-length
26	552	43.9	556	1	AT162109 full-length
27	548	43.6	567	6	CA686366 full-length
28	538	42.8	671	5	BUG24465 full-length
29	535	42.6	654	5	BUG24261 full-length
30	532	42.3	549	1	A1085616 full-length
31	532	42.3	1132	6	BMS60093 full-length
32	531	42.2	716	4	CA413294 full-length
33	518	41.2	569	2	AM071610 full-length
34	512	40.7	512	4	BM887835 full-length
35	508	40.4	723	5	BQ005403 full-length
36	500	39.8	986	5	BQ648112 full-length
37	476	37.9	1064	1	AL564395 full-length
38	474	37.7	528	2	BES50475 full-length
39	472	37.5	492	2	BF000103 full-length
40	472	37.5	504	2	AM16980 full-length
41	472	37.5	511	1	A1422726 full-length
42	469	37.3	571	7	CN394775 full-length
43	462	36.8	507	1	A1809642 full-length
44	461	36.7	466	1	A1359844 full-length
45	457	36.4	463	1	A1379443 full-length

ALIGNMENTS

RESULT 1	BC021025	1288 bp	mRNA	linear	HTC 04-AUG-2004
LOCUS	BC021025				
DEFINITION	Homo sapiens collagen triple helix repeat containing 1, mRNA (CDNA clone IMAGE:3617432).				
ACCESSION	BC021025				
VERSION	BC021025.1	GI:18045042			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marisano, K., Farmer, A.A., Rubin, G.M., Hong, L., Stepien, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., USCIN, T.B., Toshimaki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McMan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shoykhetko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shoykhetko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, V.S., Krzywicki, M.I., Skalka, U., Smillie, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
TITLE	human and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
AUTHORS	2 (bases 1 to 1288)				
REFERENCE	Director MGC Project.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTF CDNA Library Preparation: Rubin Laboratory				


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source
1. .1207
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/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

Query Match 83.9%; Score 1054; DB 3; Length 1207;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1204; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 45 CGGCTCCGAGGCGCGGCGAGCGAGCGTGAACGATTCCTCTCTCGGTCTCTCCGCG 104
DB 1 CGGCTCCGAGGCGCGGCGAGCGAGCGTGAACGATTCCTCTCTCGGTCTCTCCGCG 60
QY 105 CTCAGCTCCGCGCTGCGCGGAGCGCGGAGCCATGCGACCCGAGGCGCGCGCTCC 164
DB 61 CTCAGCTCCGCGCTGCGCGGAGCGCGGAGCCATGCGACCCGAGGCGCGCGCTCC 120
QY 165 CCGCAGCGGCTCGCGGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224
DB 121 CCGCAGCGGCTCGCGGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 225 GGCTCTGAGATCCCGAAGGAGGAGCAAAAGGCGGAGCTCCGCGAGGAGGAGGTGTGAG 284
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QY 465 TCATGAGATTCATTAATTAATGAGCATGATCTTGGGAAATGCGAGTGTACATTACA 524
DB 421 TCATGAGATTCATTAATTAATGAGCATGATCTTGGGAAATGCGAGTGTACATTACA 480
QY 525 AAGATGCGTTCAAAATGCTCTTAAGAGTTTGTCACTGGGCTCACTTGGCTAAATGC 584
DB 481 AAGATGCGTTCAAAATGCTCTTAAGAGTTTGTCACTGGGCTCACTTGGCTAAATGC 540
QY 585 AAAAAAGCATGCTGAGGCTGTGATTTTCACTTGAAGAGTGAATGTTGAGAGCTT 644
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DB 601 CTTCCTCATGGAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 660
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DB 661 AATATTCATGCACTTCTCTGTGAGAGGAGCTTGTGAAGAGTGTGTGTGAGTTAGTG 720
QY 765 GATGTTGCTATCTGAGGCTGTGATTTTCACTTGAAGAGTGAATGTTGATCTGAG 824
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QY 1125 AATATTTGTTGCTTTTGTGTTTCTTTCTTGTAGTATGATTTTAAATTAATTAAG 1184
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QY 1245 AATATTT 1251
DB 1201 AATATTT 1207

RESULT 3
CRS96030 1189 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS01061YA20 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CRS96030
VERSION CRS96030.1 GI:50476837
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1189)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation 1600
Paraday Avenue
2 (bases 1 to 1189)

REFERENCE
Genoscope.
Direct Submision
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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Query Match 82.4%; Score 1036; DB 3; Length 1189;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 45 CGGCTCCGAGGCGCGGCGAGCGAGCGTGAACGATTCCTCTCTCGGTCTCTCCGCG 104
DB 1 CGGCTCCGAGGCGCGGCGAGCGAGCGTGAACGATTCCTCTCTCGGTCTCTCCGCG 60

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QY	105	CTCAGCTCCGCGCTGCGCGGACGCGGAGCCATGGAACCCAGAGGCGCCGCGCTCC	164
Db	61	CTCCAGCTCCGCGCTGCGCGGACGCGGAGCCATGGAACCCAGAGGCGCCGCGCTCC	120
QY	165	CCGAGCGGCTCCGCGGCTCTGCTGCTCTGCTGCTGCAAGTCCCGCGCGTGCAGC	224
Db	121	CCCGAGCGGCTCCGCGGCTCTGCTGCTCTGCTGCTGCAAGTCCCGCGCGTGCAGC	180
QY	225	GCCTCGAGATCCCGAAGGGGAGCAAAAGCCGAGTCCGCGAGAGGAGGTGTGTGAC	284
Db	181	GCCTCGAGATCCCGAAGGGGAGCAAAAGCCGAGTCCGCGAGAGGAGGTGTGTGAC	240
QY	285	CTGTATATGGAATGTGCTTACAGAGGCCAGCAGAGTGCCTGTGCAGACGGAGCCCT	344
Db	241	CTGTATATGGAATGTGCTTACAGAGGCCAGCAGAGTGCCTGTGCAGACGGAGCCCT	300
QY	345	GGGGCCAAATGTATTCGCGGCTACACTGGGATCCGAGTCCGAGTGGATTCAAGAGAA	404
Db	301	GGGGCCAAATGTATTCGCGGCTACACTGGGATCCGAGTCCGAGTGGATTCAAGAGAA	360
QY	405	AAGGGGAAATGTCTGAGGGGAAACCTTTGAGAGTCCCTGACACCCAACTTACAGCAGT	464
Db	361	AAGGGGAAATGTCTGAGGGGAAACCTTTGAGAGTCCCTGACACCCAACTTACAGCAGT	420
QY	465	TCAATGAGTTCATTGAATTATGCAATGATCTTTGGAAAATTCGGAGTGTACATTTACA	524
Db	421	TCAATGAGTTCATTGAATTATGCAATGATCTTTGGAAAATTCGGAGTGTACATTTACA	480
QY	525	AAGATCGATTCAATATGTGCTCTAGAGTTTGTTCAGTGGCTCACCTGGGCTAAAATGC	584
Db	481	AAGATCGATTCAATATGTGCTCTAGAGTTTGTTCAGTGGCTCACCTGGGCTAAAATGC	540
QY	585	AGAAATGCATGCTGTGACGTTGGTATTTTCACATTCATGAGCTGAATGTTCAAGACCT	644
Db	541	AGAAATGCATGCTGTGACGTTGGTATTTTCACATTCATGAGCTGAATGTTCAAGACCT	600
QY	645	CTTCCCATGGAAGCTAATATTTATTTTGACCAAGGAAGCCCTGAAATGAATTCACAAAT	704
Db	601	CTTCCCATGGAAGCTAATATTTATTTTGACCAAGGAAGCCCTGAAATGAATTCACAAAT	660
QY	705	AATATTCAATCGACCTTCTGTGGAAGACTTTTGAAGAAATGTGCTGGATTAGTG	764
Db	661	AATATTCAATCGACCTTCTGTGGAAGACTTTTGAAGAAATGTGCTGGATTAGTG	720
QY	765	GATGTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGAGACTCTTCACTGGA	824
Db	721	GATGTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGAGACTCTTCACTGGA	780
QY	825	TGGAATTCAGTTTCTGCGATCAATTATTGAAGAACTACCAAAATTAATGCTTTAATTTGA	884
Db	781	TGGAATTCAGTTTCTGCGATCAANTATTGAAGAACTACCAAAATTAATGCTTTAATTTGA	840
QY	885	TTTGTCACTCTTTTTTTTATATGCTTGAATGGTCACTTAAATGACATTTTAAATTA	944
Db	841	TTTGTCACTCTTTTTTTTATATGCTTGAATGGTCACTTAAATGACATTTTAAATTA	900
QY	945	GTTTATGTATCATCTGATGAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTAT	1004
Db	901	GTTTATGTATCATCTGATGAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTAT	960
QY	1005	TTCACACTGTTTTTAATCTAGCATTTTCAATTTTGCTTCAATCAAAAGTGTTCAAAT	1064
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QY	1065	TTTTTTTATGTTGGTAGAATCTTCTTCAATGACACTTCTTCAACTTATTTTGG	1124
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Db	1081	AATATGTGTGTGCTTTTGTTTTTTCTCTTAGATAGCAATTTTAAAAAATATTAAG	1140
QY	1185	CTACCAATCTTTGTACAAATTTGTAAATGTTTAAAGAAATTTTTTTATATCT	1233

Db	1141	CTACCAATCTGTGACAAATTTGTAATGTAAGTAATTTTATTATATCT	1189
RESULT 4	CR612318	1111 bp	mRNA linear HTC 21-JUL-2004
LOCUS	CR612318	full-length cDNA clone CS0DM014YN20 of Fetal Liver of Homo sapiens (human).	
ACCESSION	CR612318	GI:50493125	
VERSION	HTC; CNSLT cDNA.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1111)		
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1111)		
REFERENCE	Genoscope.		
AUTHORS	Direct Submission		
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr		
JOURNAL	- Web : www.genoscope.cns.fr)		
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen		
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	/tissue_type="Fetal liver"		
	/plasmid="pCMVSPORT_6"		
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Query Match	76.2%; Score 958; DB 3; Length 1111;		
Best Local Similarity	99.7%; Pred. No. 0;		
Matches 1108; Conservative	0; Mismatches 3; Indels 0; Gaps 0;		
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QY	200	GCTGACGCTGCGCCGCGCCGCTGACGCGCTTGAAGATCCCAAGGAGAAAGACGCA	259
DB	61	GCTGACGCTGCGCCGCGCCGCTGACGCGCTTGAAGATCCCAAGGAGAAAGACGCA	120
QY	260	GCTCCGCGAAGGAGGAGTGCTGACCTGTATATGAAATGTGCTTACAAGGCCAGCAG	319
DB	121	GCTCCGCGAAGGAGGAGTGCTGACCTGTATATGAAATGTGCTTACAAGGCCAGCAG	180
QY	320	AGTCGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACTGGGATCC	379
DB	181	AGTCGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACTGGGATCC	240
QY	380	AGTCGCGATGATTTCAAAGAGAAAAGGGGAATGTTCTGAGGGAAGCTTTGAGAGTC	439
DB	241	AGTCGCGATGATTTCAAAGAGAAAAGGGGAATGTTCTGAGGGAAGCTTTGAGAGTC	300
QY	440	CTGGAACACCCAACTACAGCAGTGTTATGAGATTTCAATGATTTATGCAATGATCTTG	499
DB	301	CTGGAACACCCAACTACAGCAGTGTTATGAGATTTCAATGATTTATGCAATGATCTTG	360
QY	500	GAATAATTCGGAGTGATCAATTTCAAAGATGCGTTCAAATAGTGTCTTAAGAGTTTGT	559

Db	361	GAATATTCGGAGTGTACATTTACAAAGTGGTTCAATATAGTGTCTTAAGAGTTTGT	420		
Qy	560	CAGTGGCTCACTTGGCTTAAATGCGAAATGCAATGCTGTGCAAGCCTTGATTTTCACATT	619		
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Qy	680	AAGCCCTGAATGAAATTCACATTAATTCATGCGACTTCTTGAGGAAGACTTGG	739		
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Qy	740	TGAAGGAATTTGGTGTGATTTAGTGGATTTGCTATCTGAGTTGGCACTTTGCAGATTA	799		
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Qy	860	ACCAAAATTAATNGCTTTAATTTTCAATTTGCTACCTCTTTTATTTATGCGCTGGAATGG	919		
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Qy	980	ATATGTTTACAGACCAAAAGTGTGATTTCACTGTGTTTTAAATCTAGACATTAATTCATTT	1039		
Db	841	ATATGTTTACAGACCAAAAGTGTGATTTCACTGTGTTTTAAATCTAGACATTAATTCATTT	900		
Qy	1040	GCTTCAATCAAAAGTGTTCATTAATTTTCTTTTAACTGGTAGAATACCTTCTCATAGT	1099		
Db	901	GCTTCAATCAAAAGTGTTCATTAATTTTCTTTTAACTGGTAGAATACCTTCTCATAGT	960		
Qy	1100	CACATTTCTGCAACTATTAATTTGGAATATTTGTTGGCTTTGTTTTCTCTTAGTA	1158		
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Qy	1160	TAGCATTTTAAAAAATAATAAAGCTACCAATCTTTGTACAAATTTGTAAATGTTAAGA	1219		
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Db	1081	TTTTTTTTTATCTGTCTTAAATTAATTAATTT 1111			
RESULT 5					
LOCUS	CR594803	1103 bp	mRNA linear HTC 21-JUL-2004		
DEFINITION	full-length cDNA clone CS0D1022YF04 of Placenta Cot 25-normalized of Homo sapiens (human).				
ACCESSION	CR594803				
VERSION	CR594803.1	GI:50475610			
KEYWORDS	HTC; CNSLT_cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
REMARK	Unpublished				
REFERENCE	Contact : Feng Liang Email : fliang@lifetech.com URL :				
AUTHORS	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600				
	Paradise Avenue				
	2 (bases 1 to 1103)				
	Genoscope.				

FEATURES	source
COMMENT	<p>Direct Submission</p> <p>Submitted (20-UTB-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(AT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.</p>
FEATURES	<p>Location/Qualifiers</p> <p>1. 1103</p> <p>/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1022YF04" /tissue type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6"</p>
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Query Match	75.6%; Score 950; DB 3; Length 1103;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 1100; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Db	<p>69 GAGCGTACCAACGTTCCCTCTGAGTCTCTCCGCGTCCGACGTCGCGGCGCCCGGAG 128</p> <p> </p> <p>1 GAGCGTGACACGTTCTCTCTGAGTCTCTCCGCGTCCGACGTCGCGGCGCCCGGAG 60</p>
QY	<p>129 CCGGAGACGATGACACCCGAGGGCCCGCGCTCCCGACAGGATTCGCGGCTCTCTG 188</p> <p> </p> <p>61 CCGGAGACGATGACACCCGAGGGCCCGCGCTCCCGACAGGATTCGCGGCTCTCTG 120</p>
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Db	
QY	<p>309 GGGCCAGACGAGTGCCTGCTGACAGCGGAGCCTGGGGCCAAATGTTATCCGGGTACA 368</p> <p> </p> <p>241 GGGCCAGACGAGTGCCTGCTGACAGCGGAGCCTGGGGCCAAATGTTATCCGGGTACA 300</p>
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QY	<p>429 TTTGAGAGTCTGTGACACCCCACTACAGAGTGTTCATGTGAGTTCTATGATTTATGCGC 488</p> <p> </p> <p>361 TTTGAGAGTCTGTGACACCCCACTACAGAGTGTTCATGTGAGTTCTATGATTTATGCGC 420</p>
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QY	<p>789 TGTTCAGTTATCCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATCATTT 848</p> <p> </p>

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RESULT 6 1098 bp mRNA linear EST 24-MAR-2004
AL532456 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
LOCUS CS0DM014YN20 5-PRIME, mRNA sequence.
DEFINITION
ACCESSION AL532456
VERSION AL532456.3 GI:45707373
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteleostomi; Primates; Carnivora; Hominoidea; Homo.
TITLE 1 (bases 1 to 1098)
JOURNAL Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31070288.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DM014DGI0QPIec=4941.f.
FEATURES
LOCATION/Qualifiers
1..1098
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM014YN20"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_id="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dt) primer. Five prime end
enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match

55.7%; Score 700; DB 1; Length 1098;

Best Local Similarity 100.0%; Pred. No. 0; Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 ATTCGGGATACCTCGGATCCAGTCCGAGTGAATCAAGAGAAAAGGGGAATGT 416
Db 217 ATTCGGGATACCTCGGATCCAGTCCGAGTGAATCAAGAGAAAAGGGGAATGT 276
Qy 417 CTGAGGAAAGGTTGAGAGAGCTCGACCCCAACTCAAGAGAGTGTATGAGTTCA 476
Db 277 CTGAGGAAAGGTTGAGAGAGCTCGACCCCAACTCAAGAGAGTGTATGAGTTCA 336
Qy 477 TTGAATTAATGACATCTTGGGAAAATTCGAGAGTCAATTTCAAAAGATGCTTCA 536
Db 337 TTGAATTAATGACATCTTGGGAAAATTCGAGAGTCAATTTCAAAAGATGCTTCA 396
Qy 537 AATAGTGTCTTAAGAGTTTGTTCAGTGGCTCATTTGGGCTTAATAATGCAATGCTGC 596
Db 397 AATAGTGTCTTAAGAGTTTGTTCAGTGGCTCATTTGGGCTTAATAATGCAATGCTGC 456
Qy 597 TGTACGCTGGATTTTCAATCAATGAGCTGAATGTTCAAGACCTTCCCATTTGAA 656
Db 457 TGTACGCTGGATTTTCAATCAATGAGCTGAATGTTCAAGACCTTCCCATTTGAA 516
Qy 657 GCTATTAATTAATTTGAGCAAGAGAGCCCTGAATGAATTCACAAATTAATTTATCGC 716
Db 517 GCTATTAATTAATTTGAGCAAGAGAGCCCTGAATGAATTCACAAATTAATTTATCGC 576
Qy 717 ACTTCTCTGAGGAAAGAGCTTTGAGAGAAATTTGCTGATTTAGTGAATGCTTATC 776
Db 577 ACTTCTCTGAGGAAAGAGCTTTGAGAGAAATTTGCTGATTTAGTGAATGCTTATC 636
Qy 777 TGGGTTGACCTTTGTCAGATTTACCAAAAGAGATGCTTCACTGATGGAATTCAGTT 836
Db 637 TGGGTTGACCTTTGTCAGATTTACCAAAAGAGATGCTTCACTGATGGAATTCAGTT 696
Qy 837 TCTGCATCATTTATGAAAGAGCTACCAAAATTAATGCTTAAATTTTCAATTTGCTACT 896
Db 697 TCTGCATCATTTATGAAAGAGCTACCAAAATTAATGCTTAAATTTTCAATTTGCTACT 756
Qy 897 TTTTATTAATGAGCTTGAATGCTTCACTTAATGACATTTTAAATGATTAATGATAC 956
Db 757 TTTTATTAATGAGCTTGAATGCTTCACTTAATGACATTTTAAATGATTAATGATAC 816
Qy 957 ATCTGAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTT 1016
Db 817 ATCTGAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTT 876
Qy 1017 TTAATCTAGATTAATTTCTTCTCAATCAAAAGTGG 1056
Db 877 TTAATCTAGATTAATTTCTTCTCAATCAAAAGTGG 916

RESULT 7 747 bp mRNA linear EST 07-NOV-2002
LOCUS CA415410/c
DEFINITION UI-H-E20-baw-n-12-0-UI.s1 NCI CGAP Ch1 Homo sapiens CDNA clone
LOCUS CA415410
DEFINITION UI-H-E20-baw-n-12-0-UI 3', mRNA sequence.
ACCESSION CA415410.1 GI:24778061
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteleostomi; Primates; Carnivora; Hominoidea; Homo.
TITLE 1 (bases 1 to 747)
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Straube, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics

CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-60, >AT rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1. 747
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E20-baw-n-12-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch1"
 /note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI_CGAP_Ch1 is a cDNA library containing the following
 tissue(s): Chondrosarcoma Grade II. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into p773-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 TGATCAGCT.
 TAG_TISSUE=grade-2-chondrosarcoma
 TAG_LIB=UI-H-E20
 TAG_SEQ=ACTAATATG"

ORIGIN

Query Match 55.1%; Score 693; DB 6; Length 747;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 565 GCTCAGCTGGGCGAAATGAGAAATGCAATGCTGAGCGTTGTTTCACTTCAAG 624
 DB 713 GCTCAGCTGGGCGAAATGAGAAATGCAATGCTGAGCGTTGTTTCACTTCAAG 654
 QY 625 GAGCTGAATGTTGAGGACCTCTCCATTCAGACTAATTTATTTGAGCAAGAGCC 684
 DB 653 GAGCTGAATGTTGAGGACCTCTCCATTCAGACTAATTTATTTGAGCAAGAGCC 594
 QY 685 CTGAATGAAATTCACAAATTAATTCATGCACTTCTTTGAGAAAGACTTTGGAAG 744
 DB 593 CTGAATGAAATTCACAAATTAATTCATGCACTTCTTTGAGAAAGACTTTGGAAG 534
 QY 745 GAATTTGGTGTGATAGTGAATGTTGCTATCGGGTGGCACTGTTGAGTTACCCAA 804
 DB 533 GAATTTGGTGTGATAGTGAATGTTGCTATCGGGTGGCACTGTTGAGTTACCCAA 474
 QY 805 AAGGAGATGCTTCTAATGATGAGATTCAGTTTCTCGCATCATTTATTTGAGAACTACCA 864
 DB 473 AAGGAGATGCTTCTAATGATGAGATTCAGTTTCTCGCATCATTTATTTGAGAACTACCA 414
 QY 865 AATTAATGCTTAATTTTCAATTTGCTATCTTTTATTAATGCTTGAATGCTTCAAC 924
 DB 413 AATTAATGCTTAATTTTCAATTTGCTATCTTTTATTAATGCTTGAATGCTTCAAC 354
 QY 925 TTAATGAGACTTTAATATAGTTATGATACATCGAATGAAGAAAGCAAGCTAATATAG 984
 DB 353 TTAATGAGACTTTAATATAGTTATGATACATCGAATGAAGAAAGCAAGCTAATATAG 294
 QY 985 TTTACAGACCAAGGTGATTCACACTGTTTATTAATCTAGCATTAATTCATTTGCTTC 1044
 DB 293 TTTACAGACCAAGGTGATTCACACTGTTTATTAATCTAGCATTAATTCATTTGCTTC 234

QY 1045 AATCAAGTGTTCATATTTTGTAGTGAATACTTCTCATAGTCACAT 1104
 DB 233 AATCAAGTGTTCATATTTTGTAGTGAATACTTCTCATAGTCACAT 174
 QY 1105 TCTCTCAACCTAATTTGGAATATTTGCTGCTTTTGTCTTCTTATGATAGCA 1164
 DB 173 TCTCTCAACCTAATTTGGAATATTTGCTGCTTTTGTCTTCTTATGATAGCA 114
 QY 1165 TTTTAAATTAATTAATTAAGCTACCAATCTTTGTACATTTGTAATGTAGAAATTTT 1224
 DB 113 TTTTAAATTAATTAATTAAGCTACCAATCTTTGTACATTTGTAATGTAGAAATTTT 54
 QY 1225 TTTATATCTGTTAAATTAATTAATTTTCCACAA 1257
 DB 53 TTTATATCTGTTAAATTAATTAATTTTCCACAA 21

RESULT 8
 BQ008675/c
 LOCUS BQ008675
 DEFINITION UI-H-E10-ay1-c-24-0-UI.s1 NCI_CGAP_E10 Homo Sapiens cDNA clone
 IMAGE:5840207 3', mRNA sequence.
 ACCESSION BQ008675
 VERSION BQ008675.1 GI:19733576
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 796)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT Email: cgaabs-r@mail.nih.gov
 Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Dr. Jose Mercuende
 CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LMD at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 24-57, >AT rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1. 796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5840207"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_E10"
 /note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI_CGAP_E10 is a cDNA library containing the following
 tissue(s): Chondrosarcoma. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into p773-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is AACTTGCAC.
 TAG_TISSUE=chondrosarcoma
 TAG_LIB=UI-H-E10
 TAG_SEQ=AACTTGCAC"

ORIGIN

Query Match 55.1%; Score 693; DB 5; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 565 GCTCAGTGGCTAAATGAGAAATGATGCTGTCAGCGTGGATTTTCACTTCATG 624
DB 710 GCTCAGTGGCTAAATGAGAAATGATGCTGTCAGCGTGGATTTTCACTTCATG 651
OY 625 GAGCTAAATGTTAGAGACCTCTTCCATGGAAGCTATATTTATTTGACCAAGAGCC 684
DB 650 GAGCTAAATGTTAGAGACCTCTTCCATGGAAGCTATATTTATTTGACCAAGAGCC 591
OY 685 CTGAATGATTAATCAACATTAATTCATGCACTCTTCTGAGGAGCACTTGGAG 744
DB 590 CTGAATGATTAATCAACATTAATTCATGCACTCTTCTGAGGAGCACTTGGAG 531
OY 745 GAATGCTGCTGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGTCAATTAACCA 804
DB 530 GAATGCTGCTGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGTCAATTAACCA 471
OY 805 AAGGAGTCTCTACTGATGATGGAATTCAGTTCTGCAATCATTAATTTGAAGACTCCAA 864
DB 470 AAGGAGTCTCTACTGATGATGGAATTCAGTTCTGCAATCATTAATTTGAAGACTCCAA 411
OY 865 AATAAATGCTTAATTTGATTTGCTACCTCTTTTATTAATGCTTGAATGTTGAC 924
DB 410 AATAAATGCTTAATTTGATTTGCTACCTCTTTTATTAATGCTTGAATGTTGAC 351
OY 925 TTAATGATTTTAAATTAAGTTTATGATATCATCTGAAATGAAGCAAAAGCTAATATG 984
DB 350 TTAATGATTTTAAATTAAGTTTATGATATCATCTGAAATGAAGCAAAAGCTAATATG 291
OY 985 TTACAGACCAAGTGTGATTCACAGCTGTTTAAATGATTAATGATTAATTCATTTGCTTC 1044
DB 290 TTACAGACCAAGTGTGATTCACAGCTGTTTAAATGATTAATGATTAATTCATTTGCTTC 231
OY 1045 AATCAAAAGTGTTCATATTTTAAATGTTGATTAATGATTAATTCATTTGCTTCATG 1104
DB 230 AATCAAAAGTGTTCATATTTTAAATGTTGATTAATGATTAATTCATTTGCTTCATG 171
OY 1105 TCTCAACCTTAATTTGGAATATGTTGCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1164
DB 170 TCTCAACCTTAATTTGGAATATGTTGCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTT 111
OY 1165 TTTTAAAAAATATTAATAAGTACCAATCTTGTGACAAATTTGTAATGTTAAGAAATTTT 1224
DB 110 TTTTAAAAAATATTAATAAGTACCAATCTTGTGACAAATTTGTAATGTTAAGAAATTTT 51
OY 1225 TTTATATCTGTTAAATTAATTAATTTTCCACA 1257
DB 50 TTTATATCTGTTAAATTAATTAATTTTCCACA 18

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RESULT 9 AL575307 1102 bp mRNA linear EST 06-APR-2004
 LOCUS AL575307 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION Clone CS0D1061YA20 3-PRIME, mRNA sequence.

ACCESSION AL575307
 VERSION AL575307.3 GI:46248266
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31313615.
 Contact: Genoscope

FEATURES

source

Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnas-CS0D1061BA10NP1fc=4941.f.
 Location/Qualifiers
 1..1102
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1061YA20"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 55.0%; Score 691; DB 1; Length 1102;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 841; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 357 ATTCGGGTACACCTGGGATCCAGTGGGATGATTCAAAGAGAAAGGGGAGATGT 416
DB 879 ATTCGGGTACACCTGGGATCCAGTGGGATGATTCAAAGAGAAAGGGGAGATGT 820
OY 417 CTGAGGAAACCTTTGAGAGTCTGACACCCAACTCAAGAGTGTTCAGACTTCA 476
DB 819 CTGAGGAAACCTTTGAGAGTCTGACACCCAACTCAAGAGTGTTCAGACTTCA 760
OY 477 TTGAATTAATGATTAATTTGGAATATGCGGAGTGTTCATTTCAAAAGATGCTTCA 536
DB 759 TTGAATTAATGATTAATTTGGAATATGCGGAGTGTTCATTTCAAAAGATGCTTCA 700
OY 537 AATAGTCTTAAGATTTTGTTCAGTGGCTCATCTTGGCTAAATGCAAAATGATGTC 596
DB 699 AATAGTCTTAAGATTTTGTTCAGTGGCTCATCTTGGCTAAATGCAAAATGATGTC 640
OY 597 TGTGAGGTGTATTTCAATTCATTAAGAGCTGAATGTTTCAGACTCTTCCATTTGA 656
DB 639 TGTGAGGTGTATTTCAATTCATTAAGAGCTGAATGTTTCAGACTCTTCCATTTGA 580
OY 657 GCTATTAATTAATTTGACCAAGAGCCCTGAATGATTAATTAATTAATTTTCATGTC 716
DB 579 GCTATTAATTAATTTGACCAAGAGCCCTGAATGATTAATTAATTAATTTTCATGTC 520
OY 717 ACTTCTTCTGTGAAGAGCTTTGTGAAGATGTTGCTGATTAATGATTTGCTATC 776
DB 519 ACTTCTTCTGTGAAGAGCTTTGTGAAGATGTTGCTGATTAATGATTTGCTATC 460
OY 777 TGGGTGGCACTGTTCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 836
DB 459 TGGGTGGCACTGTTCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 400
OY 837 TCTGCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 896
DB 399 TCTGCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 340
OY 897 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 956
DB 339 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 280
OY 957 ATCTGAATGAAGCAAGCTAAATATGTTTACAGCAAGAGTGTTCACACTGTTT 1016
DB 279 ATCTGAATGAAGCAAGCTAAATATGTTTACAGCAAGAGTGTTCACACTGTTT 220

```

QY 1017 TTAATCTAGCATTAATTCATTTGCTTCATCAACAAAGGCTTCAATATTTTTCAGTT 1076
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 QY 1077 GGTAGAAATACCTTCTTCATAGTCACATTCCTCAACCTATTAATTTGGAATATGTTGG 1136
 DB 159 GGTAGAAATACCTTCTTCATAGTCACATTCCTCAACCTATTAATTTGGAATATGTTGG 100
 QY 1137 GCTCTTTGTTTTCTCTAGTATAGCATTTTAAATAAATATTAAGCTACCAATCTTT 1196
 DB 99 GCTCTTTGTTTTCTCTAGTATAGCATTTTAAATAAATATTAAGCTACCAATCTTT 40
 QY 1197 GTAC 1200
 DB 39 GTAC 36
 RESULT 10
 LOCUS BQ010155/c 702 bp mRNA linear EST 26-MAR-2002
 DEFINITION UI-H-ED0-axz-f-23-0-UI-81_NCI_CGAP_ED0 Homo sapiens cDNA clone
 IMAGE:5835670 3', mRNA sequence.
 ACCESSION BQ010155
 VERSION BQ010155
 KEYWORDS BQ010155.1 GI:19735056
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 702)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/BLNI, at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 27-60, >AT rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLA=yes.
 FEATURES
 source Location/Qualifiers
 1..702
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5835670"
 /issue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_11b="NCI_CGAP ED0"
 /note="Organ: Left Pubic Bone; Vector: pTT73-Pac
 (Pharmacia) with a modified polylinker; Site 1: Ecor I;
 Site 2: Not I; NCI_CGAP ED0 is a cDNA library containing
 the following tissue(s): Chondrosarcoma cell line C5. The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an Ecor I adaptor, digested with Not I, and cloned
 directionally into pTT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GCTCAAGGCT.
 TAG_TISSUE=chondrosarcoma
 TAG_LIB=UI-H-ED0
 TAG_SEQ=CCTCAAGGCT"

ORIGIN
 Query Match 54.3%; Score 682; DB 5; Length 702;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
 Matches 682; Conservative 0; Indels 0; Gaps 0;
 QY 576 CTAAATGAGAAATGATGCTGTCAGCGTTGATTTTCATATGATGAGCTGATGT 635
 DB 702 CTAAATGAGAAATGATGCTGTCAGCGTTGATTTTCATATGATGAGCTGATGT 643
 QY 636 TGAAGACCTCTCCATGGAAGCTATATTATTTTGAGCAAGAAAGCCCTGAATGAT 695
 DB 642 TGAAGACCTCTCCATGGAAGCTATATTATTTTGAGCAAGAAAGCCCTGAATGAT 583
 QY 696 TCAACAAATTAATATTCATGCACTCTCTGGAAGGAGCTTTGGAAGGAATGGTGT 755
 DB 582 TCAACAAATTAATATTCATGCACTCTCTGGAAGGAGCTTTGGAAGGAATGGTGT 523
 QY 756 GGATTTAGTAGAGTTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGAGATGCT 815
 DB 522 GGATTTAGTAGAGTTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGAGATGCT 463
 QY 816 TCTACTGATGAGAAATTCAGTTTCTGCAATCATTTATGAAAGAACTAACAAATPAATGCTT 875
 DB 462 TCTACTGATGAGAAATTCAGTTTCTGCAATCATTTATGAAAGAACTAACAAATPAATGCTT 403
 QY 876 TAATTTTCATTTGCTACCTCTTTTATTTATGCGCTTGAATGCTTCAATTAATGACAT 935
 DB 402 TAATTTTCATTTGCTACCTCTTTTATTTATGCGCTTGAATGCTTCAATTAATGACAT 343
 QY 936 TTTAAATTAAGTTATGATATACATGTAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA 995
 DB 342 TTTAAATTAAGTTATGATATACATGTAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA 283
 QY 996 AAGTGATTTTCAACCTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTG 1055
 DB 282 AAGTGATTTTCAACCTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTG 223
 QY 1056 GTTTCAATTTTATTTTATGTTGTTAGAAATCTTTCTTATAGTCAATCTCTCAACT 1115
 DB 222 GTTTCAATTTTATTTTATGTTGTTAGAAATCTTTCTTATAGTCAATCTCTCAACT 163
 QY 1116 ATTAATTTGGAATATTTGTTGCTTTTATTTTCTTTAGTATGACATTTTAAATAA 1175
 DB 162 ATTAATTTGGAATATTTGTTGCTTTTATTTTCTTTAGTATGACATTTTAAATAA 103
 QY 1176 ATATAAAGCTACCAATCTTTGTACATTTGTAAATGTTAAGAAATTTTATATCTGT 1235
 DB 102 ATATAAAGCTACCAATCTTTGTACATTTGTAAATGTTAAGAAATTTTATATCTGT 43
 QY 1236 TAAATTAATAATTTTCCACA 1257
 DB 42 TAAATTAATAATTTTCCACA 21
 RESULT 11
 AL551834 1100 bp mRNA linear EST 30-MAR-2004
 LOCUS AL551834 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS001061YA20 5-PRIME, mRNA sequence.
 ACCESSION AL551834
 VERSION AL551834 GI:45856624
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1100)
 REFERENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:11273650.
 Contact: Genoscope

ORIGIN TAG_SEQ=CGGTCACTC"

Query Match 50.9%; Score 640; DB 6; Length 723;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

567 TCACCTCGGCTAAATGAGAAATGAGATGCTGACAGCTGTGATTTCAATTCATGAGA 626
 708 TCACTTCGGCTAAATGAGAAATGAGATGCTGACAGCTGTGATTTCAATTCATGAGA 649
 627 GCTGAAATGTCAGAGACCTCTCCCATGAACTAATTAATTTGAGCAAGAGACCTT 686
 648 GCTGAAATGTCAGAGACCTCTCCCATGAACTAATTAATTTGAGCAAGAGACCTT 589
 687 GAAATGAATTCACAACTTAATTAATTCATGCACTTCTCTGAGAGAGACTTTGTGAGA 746
 588 GAAATGAATTCACAACTTAATTAATTCATGCACTTCTCTGAGAGAGACTTTGTGAGA 529
 747 ATTGCTGCTGATTAATGAGATGCTGATCTGGGTTGGACCTGTCAGATTACCAAAA 806
 528 ATTGCTGCTGATTAATGAGATGCTGATCTGGGTTGGACCTGTCAGATTACCAAAA 469
 807 GGAGATGCTTCTACTGATGAGATTCAGTTCTCGCATCATTAATGAGAACTACCAAAA 866
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 LOCUS BE607413
 DEFINITION colon carcinoma tissue cDNA library Homo sapiens
 ACCESSION BE607413
 VERSION BE607413.1 GI:13123454
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 683)
 Huang, Y.M., Wang, K., Zhang, J.Zh., Li, X.Y., Li, Y., Huang, D.Q.,
 Xie, Y., Mao, Y.M., Bao, L. and Sun, Z.R.
 Identification of genes differentially over-expressed in human
 colon carcinoma using combination of SSH and cDNA microarray

JOURNAL analysis
 Unpublished (2000)
 CONTACT Contact: Huang Y.M.
 COMMENT Department of Experimental Medicine
 Beijing 306 Hospital, Beijing
 No.9, Anxiang Beilei Road, Beijing, 100101, P.R.China
 Tel: 8610-66356111
 Fax: +86-10-66356111
 Email: hyboy@sina.com.

FEATURES
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1..683
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 /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION BQ425266.1 GI:21120581
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 1 (bases 1 to 851)
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCPD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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 ACCESSION BE607414
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 ORGANISM Homo sapiens
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 1 (bases 1 to 683)
 REFERENCE Huang, Y.W., Wang, K., Zhang, J.Zh., Li, X.Y., Li, Y., Huang, D.Q., Xie, Y., Mao, Y.W., Bao, L. and Sun, Zh.R.
 Identification of genes differentially over-expressed in human colon carcinoma using combination of SSH and CDNA microarray analysis
 Unpublished (2000)
 CONTACT: Huang Y.W.
 Department of Experimental Medicine
 Beijing 306 hospital, Beijing
 No.9, Anxiang Beilei Road, Beijing, 100101, P.R.China
 Tel: 8610-66356111
 Fax: +86-10-66356111
 Email: hywboy@sina.com.
 Location/Qualifiers
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ORIGIN

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 Best Local Similarity 99.9%; Pred. No. 0;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1036	82.4	1342	4 US-09-489-847-89	Sequence 89, Appl
2	992	78.9	1220	4 US-09-692-081-3	Sequence 3, Appl
3	966	77.0	1286	4 US-09-489-847-124	Sequence 124, App
4	803	63.9	837	4 US-09-834-759-512	Sequence 512, App
5	803	63.9	837	4 US-09-834-759-513	Sequence 513, App
6	732	58.2	732	4 US-09-834-759-510	Sequence 510, App
7	729	58.0	729	4 US-09-834-759-511	Sequence 511, App
8	662	52.7	1288	4 US-09-205-258-125	Sequence 125, App
9	530	42.2	683	3 US-09-232-575-63	Sequence 63, Appl
10	530	42.2	683	4 US-09-389-681-63	Sequence 63, Appl
11	530	42.2	683	4 US-09-620-405B-63	Sequence 63, Appl
12	530	42.2	683	4 US-09-339-338-63	Sequence 63, Appl
13	530	42.2	683	4 US-09-433-826B-63	Sequence 63, Appl
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17	530	42.2	683	4 US-09-590-751A-63	Sequence 63, Appl
18	41	3.3	403	4 US-09-692-081-6	Sequence 63, Appl
19	41	3.3	734	4 US-09-692-081-9	Sequence 9, Appl
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21	23	1.8	3546	1 US-08-162-809-9	Sequence 9, Appl
22	23	1.8	3591	1 US-08-162-809-13	Sequence 13, Appl
23	22	1.8	16550	4 US-08-916-421B-3	Sequence 3, Appl
24	22	1.8	16550	4 US-09-692-570-3	Sequence 3, Appl
25	20	1.6	855	4 US-09-252-991A-3095	Sequence 3095, Ap
26	20	1.6	858	4 US-09-252-991A-2762	Sequence 2762, Ap
27	20	1.6	861	4 US-09-252-991A-2874	Sequence 2874, Ap

C	28	20	1.6	4853	2	US-08-832-883-1	Sequence 1, Appl
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C	34	19	1.5	438	4	US-09-513-999C-129	Sequence 129, App
C	35	19	1.5	533	6	5482709-5	Patent No. 5482709
C	36	19	1.5	543	6	5273901-6	Patent No. 5273901
C	37	19	1.5	595	3	US-09-385-982-142	Sequence 142, App
C	38	19	1.5	912	4	US-09-328-352-3371	Sequence 3371, Ap
C	39	19	1.5	1108	4	US-09-800-729-42	Sequence 42, Appl
C	40	19	1.5	1141	4	US-09-800-729-78	Sequence 78, Appl
C	41	19	1.5	1297	4	US-09-800-729-80	Sequence 80, Appl
C	42	19	1.5	1459	4	US-09-569-611C-4	Sequence 4, Appl
C	43	19	1.5	1520	4	US-09-866-028-23	Sequence 23, Appl
C	44	19	1.5	1520	4	US-10-140-002-333	Sequence 333, App
C	45	19	1.5	1520	4	US-09-944-457-23	Sequence 23, Appl

ALIGNMENTS

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; Sequence 89, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
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; EARLIER FILING DATE: 1998-08-06
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Best Local Similarity 99.7%; Pred. No. 0;
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; Sequence 3, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert F.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
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FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-081-3

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1212; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 43 GCGGCGCTCGAGAGCGGCGGAGCCAGACGCTGACCAAGTTCCTCTCGGTCTCTCC 102
DB 6 GCGGCGCTCGAGAGCGGCGGAGCCAGACGCTGACCAAGTTCCTCTCGGTCTCTCC 65
QY 103 GCTTCAGCTCCGCGCTCCGCGAGCCGCGAGGCTATGCGACCCGAGGCGCCGCGCT 162
DB 66 GCTTCAGCTCCGCGCTCCGCGAGCCGCGAGGCTATGCGACCCGAGGCGCCGCGCT 125
QY 163 CCCCGCAGCGGCTCCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 222
DB 126 CCCCGCAGCGGCTCCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
QY 223 GCGGCTCTGAGATCCCAAGGAGAGCAAAAGCGCAGCTCCGAGAGGAGAGGTGTG 282
DB 186 GCGGCTCTGAGATCCCAAGGAGAGCAAAAGCGCAGCTCCGAGAGGAGAGGTGTG 245
QY 283 ACCTGATATATGGAATGCTTACAGAGGCGCAGAGAGTCTGCTGAGAGAGGAGGCC 342
DB 246 ACCTGATATATGGAATGCTTACAGAGGCGCAGAGAGTCTGCTGAGAGAGGAGGCC 305
QY 343 CTGGGCGCAATGTTATTCGCGGTACACCTGGGATCCAGGTCCGGATGATTCAGAGAG 402
DB 306 CTGGGCGCAATGCGCATTCGCGGTACACCTGGGATCCAGGTCCGGATGATTCAGAGAG 365
QY 403 AAAAGGGGGAATGCTGAGGAGAAAGCTTTGAGAGTCTGAGACACCACTACAGAGAT 462
DB 366 AAAAGGGGGAATGCTGAGGAGAAAGCTTTGAGAGTCTGAGACACCACTACAGAGAT 425
QY 463 GTTCATGAGTTCATTTAATATGAGATCTTGAAGAAATTTGCGAGATGATTA 522
DB 426 GTTCATGAGTTCATTTAATATGAGATCTTGAAGAAATTTGCGAGATGATTA 485
QY 523 CAAGATCGTTCAATATGCTCTAAGAGTTCATGAGTTCATGAGTTCATGAGTTCAT 582
DB 486 CAAGATCGTTCAATATGCTCTAAGAGTTCATGAGTTCATGAGTTCATGAGTTCAT 545
QY 583 GCGAAGATGCAATGCTGCGAGGCTGATTCATCAATGAGTTCATGAGTTCATGAGTTC 642
DB 546 GCGAAGATGCAATGCTGCGAGGCTGATTCATCAATGAGTTCATGAGTTCATGAGTTC 605
QY 643 CTCTCCCATGAGACTAATTAATTTGAGACCAAGAGCCCTGAATTAATTAATTA 702
DB 606 CTCTCCCATGAGACTAATTAATTTGAGACCAAGAGCCCTGAATTAATTAATTA 665
QY 703 TTAATATTCATGCACTTCTTCTGAGAGAGCTTTGAGAGAAATTTGCTGATTAAG 762
DB 666 TTAATATTCATGCACTTCTTCTGAGAGAGCTTTGAGAGAAATTTGCTGATTAAG 725
QY 763 TGAATGTTGATATGAGTGGGAGCTGCTCAAGATTAACCAAGAGAGATGCTTCAAG 822
DB 726 TGAATGTTGATATGAGTGGGAGCTGCTCAAGATTAACCAAGAGAGATGCTTCAAG 785
QY 823 GATGGAATTCAGTTCCTGATCATTAATTAAGAGATCAACCAAAATTAATGCTTAATTT 882
DB 786 GATGGAATTCAGTTCCTGATCATTAATTAAGAGATCAACCAAAATTAATGCTTAATTT 845
QY 883 CATTTGCTACTCTTTTATTAATGCTTGAAGTTCATTAATGATCAATTAAT 942
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Db 846 CATTGCTACCTCTTTTATATATGCTTGAGTGTTCATTAAATGACATTTTAAAT 905
Qy 943 AAGTTAT 1002
Db 906 AAGTTAT 965
Qy 1003 ATTTCACCTGTTTTTAAATCTGACATTTATTTTCTTCAATCAAAAAGTGTTCAA 1062
Db 966 ATTTCACCTGTTTTTAAATCTGACATTTATTTTCTTCAATCAAAAAGTGTTCAA 1025
Qy 1063 TATTTTTTATGTTGTTAGATATATCTTCTTCAATCAATTTCTTCAATCAATTT 1122
Db 1026 TA-TTTTTTATGTTGTTAGATATATCTTCTTCAATCAATTTCTTCAATCAATTT 1084
Qy 1123 GGAATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1182
Db 1085 GGAATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1144
Qy 1183 AGCTACCAATCTTGTACATTTGTAAATGTAAAGATTTTTTTTATCTGTTAAATA 1242
Db 1145 AGCTACCAATCTTGTACATTTGTAAATGTAAAGATTTTTTTTATCTGTTAAATA 1204
Qy 1243 AAATATTTTCCACA 1257
Db 1205 AAATATTTTCCACA 1219

RESULT 3
US-09-489-847-124
; Sequence 124, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,c,g, or c
US-09-489-847-124

Query Match 77.0%; Score 968; DB 4; Length 1286;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 67 CAGACGCTGACACGATCT 126
Db 60 CAGACGCTGACACGATCT 119
Qy 127 AGCCGGAGGACGATGCAAGCCCGAGGCGCGCGCTTCGCCGACGCGGCTCCGGGCGCTTC 186
Db 120 AGCCGGAGGACGATGCAAGCCCGAGGCGCGCGCTTCGCCGACGCGGCTCCGGGCGCTTC 179

Qy 187 TECTCTCTCTGCTGAGAGCTGCCCGCGCTCTGAGAGCGCTCTGAGATCCCAAGGGA 246
Db 180 TECTCTCTCTGCTGAGAGCTGCCCGCGCTCTGAGAGCGCTCTGAGATCCCAAGGGA 239
Qy 247 AGCAAAAGGCGAGCTCCGGGAGAGGAGTGTGACCTGTATATATGATATGTCTTAC 306
Db 240 AGCAAAAGGCGAG-CTCCGGGAGAGGAGTGTGACCTGTATATATGATATGTCTTAC 298
Qy 307 AAGGCGCAGAGAGATGCTGCTGAGACCGGAGGCTGCGGGCCAAATGTATTCGGGGA 366
Db 299 AAGGCGCAGAGAGATGCTGCTGAGACCGGAGGCTGCGGGCCAAATGTATTCGGGGA 358
Qy 367 CACTGGAGATCCAGGTCGGAGTGAATTCAAAGAGAAAGAGGAGATGTCTGAGGAAA 426
Db 359 CACTGGAGATCCAGGTCGGAGTGAATTCAAAGAGAAAGAGGAGATGTCTGAGGAAA 418
Qy 427 GCTTTGAGAGATCTGAGACCCAACTACAGACAGTTCATGAGATTGAATATATG 486
Db 419 GCTTTGAGAGATCTGAGACCCAACTACAGACAGTTCATGAGATTGAATATATG 478
Qy 487 GATATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGGTTCAATATAGTCTC 546
Db 479 GATATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGGTTCAATATAGTCTC 538
Qy 547 TAAGATTTTGTTCAGTGTCTCACTTCGGCTAAATGCAAGATGCAATGCTGACGCTT 606
Db 539 TAAGATTTTGTTCAGTGTCTCACTTCGGCTAAATGCAAGATGCAATGCTGACGCTT 598
Qy 607 GGTATTTCAATTCATGAGAGCTGAATGTTCAGACCTTCTCCATTTGAGCTATATTT 666
Db 599 GGTATTTCAATTCATGAGAGCTGAATGTTCAGACCTTCTCCATTTGAGCTATATTT 658
Qy 667 ATTTCAGCAAGAGAGCCCTGAAATGAAATGAAATGAAATGCAATGCTGCTTCG 726
Db 659 ATTTCAGCAAGAGAGCCCTGAAATGAAATGAAATGAAATGCAATGCTGCTTCG 718
Qy 727 TGAAGAGATTTGTGAGAGAAATTTGTGATGATTTGATGATTTGATGATTTGATG 786
Db 719 TGAAGAGATTTGTGAGAGAAATTTGTGATGATTTGATGATTTGATGATTTGATG 778
Qy 787 GTTGTTCAGATTTACCCAAAGAGATGCTTCTACATGATGAAATTCAGTTCTCGCATCA 846
Db 779 GTTGTTCAGATTTACCCAAAGAGATGCTTCTACATGATGAAATTCAGTTCTCGCATCA 838
Qy 847 TATATGAGAACTACCAAAATTAATGCTTAAATTTTCAATTTCCATCTCTTTTATTA 906
Db 839 TATATGAGAACTACCAAAATTAATGCTTAAATTTTCAATTTCCATCTCTTTTATTA 898
Qy 907 TGCCTTGAATGATTCATTTAATGACATTTTAAATGATTTATGATATCATCTGATGA 966
Db 899 TGCCTTGAATGATTCATTTAATGACATTTTAAATGATTTATGATATCATCTGATGA 958
Qy 967 AAAGCAAGCTAAATATATGTTTACAGACCAAGGTGATTTCACTGTTTTTAAATCTAG 1026
Db 959 AAAGCAAGCTAAATATATGTTTACAGACCAAGGTGATTTCACTGTTTTTAAATCTAG 1018
Qy 1027 CATATATCAATTTTGTCTTCAATCAAAAGGCTTCAATATTTTATGTTGTTGAAATA 1086
Db 1019 CATATATCAATTTTGTCTTCAATCAAAAGGCTTCAATATTTTATGTTGTTGAAATA 1078
Qy 1087 CTTTCTTCAATGATTCATTTCTCAACCTATATATTTGAAATTTGTGATCTTTTGT 1146
Db 1079 CTTTCTTCAATGATTCATTTCTCAACCTATATATTTGAAATTTGTGATCTTTTGT 1138
Qy 1147 TTTTCTTCAATGATTCATTTTAAATAAATAAAGCTACCAATCTTTGATCAATTTG 1206
Db 1139 TTTTCTTCAATGATTCATTTTAAATAAATAAAGCTACCAATCTTTGATCAATTTG 1198
Qy 1207 TAAATGTAAAGATTTTATATCTGTTAAATATATATTTTCCACA 1257
Db 1199 TAAATGTAAAGATTTTATATCTGTTAAATATATATTTTCCACA 1249

```

: RESULT 4
: US-09-834-759-512
: Sequence 512, Application US/09834759
: Patent No. 6660157
: GENERAL INFORMATION:
: APPLICANT: Jiang, Yugu
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
: FILE REFERENCE: 210121.470C9
: CURRENT APPLICATION NUMBER: US/09/834,759
: CURRENT FILING DATE: 2001-04-13
: NUMBER OF SEQ ID NOS: 547
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 512
: LENGTH: 837
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-834-759-512

```

```
Query Match      63.9%; Score 803; DB 4; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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QY	67	CAGAGCGTACACAGCTTCCCTCTCTCGAGTCTCCTCGGCTTCAGACTCCGGGCTGCCCGGC	126
Db	35	CAGAGCTTACCAACGTTCTCTCTCTCGAGTCTCCTCGGCTTCAGACTCCGGGCTGCCCGGC	94
QY	127	AGCCGGGAGCCATTCGACCCCGAGGGCCCGCGCTCCCGCGACGGGCTCCGGGCTCC	186
Db	95	AGCCGGGAGCCATTCGACCCCGAGGGCCCGCGCTCCCGCGACGGGCTCCGGGCTCC	154
QY	187	TGCTCTCTCTGCTGTCTGTGAGCTGCCCGCGCTGTGAGCGCTCTGAGATCCCAAGGGGA	246
Db	155	TGCTCTCTCTGCTGTCTGTGAGCTGCCCGCGCTGTGAGCGCTCTGAGATCCCAAGGGGA	214
QY	247	AGCAAAAGCGCAGCTCCGGCAGAGGGAGTGTGACCTGTATATGAAATGTGTTAC	306
Db	215	AGCAAAAGCGCAGCTCCGGCAGAGGGAGTGTGACCTGTATATGAAATGTGTTAC	274
QY	307	AAGGCGCAGCAGAGATGCTGTGTGAGACGGGAGCCCTTG3GGCAATGTATTCGGGATA	366
Db	275	AAGGCGCAGCAGAGATGCTGTGTGAGACGGGAGCCCTTG3GGCAATGTATTCGGGATA	334
QY	367	CACCTGGGATCCGAGGTCGGGATGGAATCAAGAGAAAGGGGGAAATGCTGAGGGAAA	426
Db	335	CACCTGGGATCCGAGGTCGGGATGGAATCAAGAGAAAGGGGGAAATGCTGAGGGAAA	394
QY	427	GCTTTGAGGAGTCCCTGAGACCCCACTAACAGCAGTTCATGAGTTCATTGAATTAATG	486
Db	395	GCTTTGAGGAGTCCCTGAGACCCCACTAACAGCAGTTCATGAGTTCATTGAATTAATG	454
QY	487	GCATGATCTTTGGGAAATTTGGGAGCTGTACATTTACAAAGATGCGTTCAATATGTCTC	546
Db	455	GCATGATCTTTGGGAAATTTGGGAGCTGTACATTTACAAAGATGCGTTCAATATGTCTC	514
QY	547	TAAGAGTTTGTTCAGTGCTCACTTCGGCTTAAATGACGAATGCATGCTGTACGCGTT	606
Db	515	TAAGAGTTTGTTCAGTGCTCACTTCGGCTTAAATGACGAATGCATGCTGTACGCGTT	574
QY	607	GGTATTTCAATTCATGAGCTGAATGTTCAAGACCTTCTCCATTGAAGCTATTAATTT	666
Db	575	GGTATTTCAATTCATGAGCTGAATGTTCAAGACCTTCTCCATTGAAGCTATTAATTT	634
QY	667	ATTGAGCAAGGAAGCCCTGAAATGAATTCAAAAATTAATTAATGCAACTTCTTCTG	726
Db	635	ATTGAGCAAGGAAGCCCTGAAATGAATTCAAAAATTAATTAATGCAACTTCTTCTG	694

Qy	727	TGAAAGACCTTGTGAAGAAATTGGGCTGCAATTAGTGAATGTTGCTATCTGGGTTGGCA	786
Db	695	TGGAAGACCTTTGTGAAGAAATTGGGCTGCAATTAGTGAATGTTGCTATCTGGGTTGGCA	754
Qy	787	CTTGTCAGATTACCCAAAAGAGATGCTTCTACTCGCA TGAATTCACTTCCTGCGATCA	846
Db	755	CTTGTCAGATTACCCAAAAGAGATGCTTCTACTCGCA TGAATTCACTTCCTGCGATCA	814
Qy	847	TTATGGAAGACCTACCCAAATTA	869
Db	815	TTATGGAAGACCTACCCAAATTA	837

RESULT 5
US-09-834-759-513
; Sequence 513, Application US/09834755
; Patent No. 6690107

```

1 GENERAL INFORMATION:
2 APPLICANT: Jiang, Yugu
3 APPLICANT: Dillon, Devin C.
4 APPLICANT: Mitcham, Jennifer L.
5 APPLICANT: Xu, Jiaqiong
6 APPLICANT: Harlocker, Susan L.
7 APPLICANT: Hepler, William T.
8 APPLICANT: Henderson, Robert A.
9 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
10 TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
11 FILE REFERENCE: 210121.470C9
12 CURRENT APPLICATION NUMBER: US/09/834,759
13 CURRENT FILING DATE: 2001-04-13
14 NUMBER OF SEQ ID NOS: 547
15 SOFTWARE: FastSeq for Windows Version 3.0
16 SEQ ID NO: 513
17 LENGTH: 837
18 TYPE: DNA
19 ORGANISM: Homo sapiens
20 US-09-834-759-513

```

Query Match	63.9%	Score 803;	DB 4;	Length 837;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 803; Conservative	0;	Mismatches	0;	Gaps 0;

OY	6	CAGACGGTACACAGTTTCCTCTCCGGTCTCTCCGCTCCAGCTCCGGCTGCCCCGC	12
Db	35	CAGACGCTGACACAGTTTCCTCTCTCGTCTCTCCGCTCCAGCTCCGGCTCCCGGC	94
OY	127	AGCCGGAGGCATGCGACCCACAGGCCCCCGCCCTCCCGCAGCGGCTCCGGGCTTC	186
Db	95	AGCCGGAGGCATGCGACCCACAGGCCCCCGCCCTCCCGAGAGGCTTCGGGGCTTC	15
OY	187	TGCTGCTCTCTGCTGCTGCACTGCTCCCGCCCTCGAGGCTCTGAGATCCCCAAAGGGA	248
Db	155	TGCTGCTCTCTGCTGCTGCACTGCTCCCGCCCTCGAGGCTCTGAGATCCCCAAAGGGA	214
OY	247	AGCAAAAGCGCAGCTCCCGCAGAGGAGGTGTGACCTGATPATATGAATGAGCTTAC	306
Db	215	AGCAAAAGCGCAGCTCCCGCAGAGGAGGTGTGACCTGATPATATGAGATGCTTAC	274
OY	307	AAAGGCCAGCAGGAGTGCTTGTCGAGACGGAGGCCCTTGAGGACCAATGTATTCGGGTA	366
Db	275	AAAGGCCAGCAGGAGTGCTTGTCAGACGGAGGCCCTTGAGGACCAATGTATTCGGGTA	334
OY	367	CACCTGGGATCCCAAGGTGGGGATGAGATTCAAAAGAGAAAGAGGGGAATGCTGAGGAAA	426
Db	335	CACCTGGGATCCCAAGGTGGGGATGAGATTCAAAAGAGAAAGAGGGGAATGCTGAGGAAA	394
OY	427	GCTTTGAGGAGTCTTGACACCCAACTAACAGAGTGTTCATGAGATTCAATTGAATATG	486
Db	395	GCTTTGAGGAGTCTTGACACCCAACTAACAGAGTGTTCATGAGATTCAATTGAATATG	454
OY	487	GCATATATCTTGGGAAAATTGCGAGGTGATATTACAAAGATCGTTCAATATGCTC	546
Db	455	GCATATATCTTGGGAAAATTGCGAGGTGATATTACAAAGATCGTTCAATATGCTC	514

Qy	547	TAAGAGTTTGTTCAGTGGCTACCTGGCTAAATGCAAGAAATGATGCTGCACGTT	606
Db	515	TAAGGTTTGTTCAGTGGCTACTCTGGCTAAATGCAAGAAATGATGCTGCACGTT	574
Qy	607	GSTATTTGCATTCATGAGCTGATGTTCAGSACCTCTTCCCATTTGAAGCTATATTT	666
Db	575	GSTATTTGCATTCATGAGCTGATGTTCAGSACCTCTTCCCATTTGAAGCTATATTT	634
Qy	667	ATTGGAACCAAGAAAGCCCTGAAATGATTCACAATTAATATTCATGCACTTCTTCTG	726
Db	635	ATTGGAACCAAGAAAGCCCTGAAATGATTCACAATTAATATTCATGCACTTCTTCTG	694
Qy	727	TGGAAGGACTTTGTGAGAGAAATTTGTGCTGAGATTAGTGATTTGTGCTATTTGGGTTGGCA	786
Db	695	TGGAAGGACTTTGTGAGAGAAATTTGTGCTGAGATTAGTGATTTGTGCTATTTGGGTTGGCA	754
Qy	787	CTGTGTCAGATTACCCAAAGAGATGCTTCACTGAGATGGAATTCAGTTTCTGCGATCA	846
Db	755	CTGTGTCAGATTACCCAAAGAGATGCTTCACTGAGATGGAATTCAGTTTCTGCGATCA	814
Qy	847	TTATTGAGAACTACCAATAATAA	869
Db	815	TTATTGAGAACTACCAATAATAA	837

```

RESULT 6
US-09-834-759-510
; Sequence 510 Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-510

Query Match      58.2%; Score 732; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      138 ATGCCAATCCCAAGGCGCCCGCCCTCCCGGCAGCGCGCTTCGCGGCTCTCTGCTGCTCTG 197
DB      1  ATGCCAATCCCAAGGCGCCCGCCCGCCCTCCCGGCAGCGCGCTTCGCGGCTCTCTGCTCTG 60
QY      198 CTGCTGCAGCTGCCCCGCGCCCTGCAGCGCGCTTGAGATCCCAAGGGAAGCAAAAGCG 257
DB      ~ 61 CTGCTGCAGCTGCCCCGCGCGCTGCAGCGCGCTTGAGATCCCAAGGGAAGCAAAAGCG 120
QY      258 CAGCTCCGGCAGAGGAGGTGTGTGACTGTATTAATGGAATGTGCTTACAGGGCCAGCA 317
DB      121 CAGCTCCGGCAGAGGAGGTGTGTGACTGTATTAATGGAATGTGCTTACAGGGCCAGCA 180
QY      318 GAGTGCCTGTGTGCAGAGCGGAGCCCTGGGGCCATNGTTAATCCGGGTACACTCTGGATC 377
DB      181 GAGTGCCTGTGTGCAGAGCGGAGCCCTGGGGCCATTTATTCCGGGTACACTCTGGATC 240
QY      378 CCAAGTCGGATGATTCAAGAGAAAGGGGAATGTCTGAGGAAAGCTTTGAGAG 437

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Db	241	CCAGGTGGGAGATTGAGTTCAAAGGAGAAAAAGGGGGAAAGTCTGAGGGAAAGCTTTGAGGAG	300
Oy	438	TCTCGAGACCCCACTACAGCAGTGTTCATGAGGTTCAATTGACATGATCTT	487
Db	301	TCTCGACACCCACACTACAGCAGTGTTCATGAGGTTCAATTGACATGATCTT	360
Oy	498	GGGAAATAATGCGAGAGTCACTTTTCAAAAGATGCGTCAAAATAGTGCTCAAGAGTTTG	557
Db	361	GGGAAATAATGCGAGAGTCACTTTTCAAAAGATGCGTCAAAATAGTGCTCAAGAGTTTG	420
Oy	558	TTCAATGAGCTCACTTGGGCTAAATGCAAAATGCAATGCTGTCAAGCTGGTATTTCACA	617
Db	421	TTCAATGAGCTCACTTGGGCTAAATGCAAAATGCAATGCTGTCAAGCTGGTATTTCACA	480
Oy	618	TTCAATGAGCTCAATGTTGTCAGAGCTCTTCCGCAATGAGCTAATAATTATTTGAGACCA	677
Db	481	TTCAATGAGCTCAATGTTGTCAGAGCTCTTCCGCAATGAGCTAATAATTATTTGAGACCA	540
Oy	678	GGAAGCCCTGGAATGGAATTCACAACTAATAATTCATGCACTTCTCTGTGGAGGACTT	737
Db	541	GGAAGCCCTGGAATGGAATTCACAACTAATAATTCATGCACTTCTCTGTGGAGGACTT	600
Oy	738	TGGAAGGAATGTGTCGCGATTAGTGATATGTGCTATCTGGGTGTGCACTGTTCGAT	797
Db	601	TGGAAGGAATGTGTCGCGATTAGTGATATGTGCTATCTGGGTGTGCACTGTTCGAT	660
Oy	798	TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCACTCAATTATTGAAGAA	857
Db	661	TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCACTCAATTATTGAAGAA	720
Oy	858	CTACCAAAATAA	869
Db	721	CTACCAAAATAA	732

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RESULT 7
US-09-834-759-511
; Sequence 511, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834.759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 511
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-511

Query Match          58.0%; Score 729; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      138  ATGCGACCCCGAGGCGCCGCGCTCCCGCAGCGGCGCTCGGCGGCTCTGCTGCTCTG 197
Db       1  ATGCGACCCCGAGGCGCCGCGCTCCCGCAGCGGCGGCGCTCTGCTGCTCTG 60

QY      198  CTGCTGCGAGCTGCGCGCGCGCGCTGAGAGCGCTCTGAGATCCCGCAAGGGGAGCAAAAGCG 257
Db       61  CTGCTGCGAGCTGCGCGCGCGCGCTGAGAGCGCTCTGAGATCCCGCAAGGGGAGCAAAAGCG 120

QY      258  CAGCTCCGCGCAGAGGAGGTGTGAGACTGTATATATGAATGTGCTTATCAAGGCGCAGCA 317

```

Db	121	CAGCTCCGAGAGGAGGTGTGTGACTGTATATATGAAATGTCTTACAAAGGCCACGA	188
QY	318	GGAGTGCCTGTGTGAGACGGGAGCCCTGGGGCCATGTATATCCGGGTACACTGGGATC	377
Db	181	GGAGTGCCTGTGTGAGACGGGAGCCCTGGGGCCATGTATATCCGGGTACACTGGGATC	248
QY	378	CCAGTTCGGGATGGAATTCAAAGGAAAGGGGGAATGTCTGAGGGAAGCTTTGAGAG	437
Db	241	CCAGTTCGGGATGGAATTCAAAGGAAAGGGGGAATGTCTGAGGGAAGCTTTGAGAG	300
QY	438	TCTGTGACACCCAACTCAAGCAGTGTTCATGAGTTCATTGAATTATGACATGATCTT	497
Db	301	TCTGTGACACCCAACTCAAGCAGTGTTCATGAGTTCATTGAATTATGACATGATCTT	366
QY	498	GGGAAATTTGGGAGTGTATCTTCAAGATGCTTCAAAATGATGCTCTTAAGATTTTG	557
Db	361	GGGAAATTTGGGAGTGTATCTTCAAGATGCTTCAAAATGATGCTCTTAAGATTTTG	420
QY	558	TTCAGTGCTCAGCTTGGCTTAAATGAGAAATGCATGCTGACAGCTTGGTATTTTACA	617
Db	421	TTCAGTGCTCAGCTTGGCTTAAATGAGAAATGCATGCTGACAGCTTGGTATTTTACA	480
QY	618	TTCAATGAGCTGAATGTTTACAGACCTCTTCCATTGAAGCTATTAATTTTGGACAA	677
Db	481	TTCAATGAGCTGAATGTTTACAGACCTCTTCCATTGAAGCTATTAATTTTGGACAA	540
QY	678	GGAGGCCCTGAATGAAATCAACAATTAATATCATGACACTCTTCTGGAAGACTT	737
Db	541	GGAGGCCCTGAATGAAATCAACAATTAATATCATGACACTCTTCTGGAAGACTT	600
QY	738	TGTGAAGGAATGTGTGTGTGATTAATGAGATGTTGTATCTGGGTGGCACTTGTCAAT	797
Db	601	TGTGAAGGAATGTGTGTGTGATTAATGAGATGTTGTATCTGGGTGGCACTTGTCAAT	660
QY	798	TACCCAAAAGAGATGCTTCTACTGTGATGGAATTCAGTTCTTCGCAATCATTATGAAGA	857
Db	661	TACCCAAAAGAGATGCTTCTACTGTGATGGAATTCAGTTCTTCGCAATCATTATGAAGA	720
QY	858	CTACCAAAA 866	
Db	721	CTACCAAAA 729	
RESULT 8			
US-09-205-258-125			
; Sequence 125, Application US/09205258			
; Patent No. 6525174			
; GENERAL INFORMATION:			
; APPLICANT: Young et al.			
; TITLE OF INVENTION: 207 Human Secreted Proteins			
; FILE REFERENCE: P2007P1			
; CURRENT APPLICATION NUMBER: US/09/205,258			
; EARLIER APPLICATION NUMBER: PCT/US98/11422			
; EARLIER FILING DATE: 1998-06-04			
; EARLIER APPLICATION NUMBER: 60/048,885			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,375			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,881			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,880			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,896			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,020			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,876			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,895			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,884			

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1 EARLIER FILING DATE: 1997-06-06
2 EARLIER APPLICATION NUMBER: 60/048,894
3 EARLIER FILING DATE: 1997-06-06
4 EARLIER APPLICATION NUMBER: 60/048,971
5 EARLIER FILING DATE: 1997-06-06
6 EARLIER APPLICATION NUMBER: 60/048,964
7 EARLIER FILING DATE: 1997-06-06
8 EARLIER APPLICATION NUMBER: 60/048,882
9 EARLIER FILING DATE: 1997-06-06
10 EARLIER APPLICATION NUMBER: 60/048,899
11 EARLIER FILING DATE: 1997-06-06
12 EARLIER APPLICATION NUMBER: 60/048,893
13 EARLIER FILING DATE: 1997-06-06
14 EARLIER APPLICATION NUMBER: 60/048,900
15 EARLIER FILING DATE: 1997-06-06
16 EARLIER APPLICATION NUMBER: 60/048,901
17 EARLIER FILING DATE: 1997-06-06
18 EARLIER APPLICATION NUMBER: 60/048,892
19 EARLIER FILING DATE: 1997-06-06
20 EARLIER APPLICATION NUMBER: 60/048,915
21 EARLIER FILING DATE: 1997-06-06
22 EARLIER APPLICATION NUMBER: 60/049,019
23 EARLIER FILING DATE: 1997-06-06
24 EARLIER APPLICATION NUMBER: 60/048,970
25 EARLIER FILING DATE: 1997-06-06
26 EARLIER APPLICATION NUMBER: 60/048,972
27 EARLIER FILING DATE: 1997-06-06
28 EARLIER APPLICATION NUMBER: 60/048,916
29 EARLIER FILING DATE: 1997-06-06
30 EARLIER APPLICATION NUMBER: 60/049,373
31 EARLIER FILING DATE: 1997-06-06
32 EARLIER APPLICATION NUMBER: 60/048,875
33 EARLIER FILING DATE: 1997-06-06
34 EARLIER APPLICATION NUMBER: 60/049,374
35 EARLIER FILING DATE: 1997-06-06
36 EARLIER APPLICATION NUMBER: 60/048,917
37 EARLIER FILING DATE: 1997-06-06
38 EARLIER APPLICATION NUMBER: 60/048,949
39 EARLIER FILING DATE: 1997-06-06
40 EARLIER APPLICATION NUMBER: 60/048,974
41 EARLIER FILING DATE: 1997-06-06
42 EARLIER APPLICATION NUMBER: 60/048,883
43 EARLIER FILING DATE: 1997-06-06
44 EARLIER APPLICATION NUMBER: 60/048,897
45 EARLIER FILING DATE: 1997-06-06
46 EARLIER APPLICATION NUMBER: 60/048,898
47 EARLIER FILING DATE: 1997-06-06
48 EARLIER APPLICATION NUMBER: 60/048,962
49 EARLIER FILING DATE: 1997-06-06
50 EARLIER APPLICATION NUMBER: 60/048,963
51 EARLIER FILING DATE: 1997-06-06
52 EARLIER APPLICATION NUMBER: 60/048,877
53 EARLIER FILING DATE: 1997-06-06
54 EARLIER APPLICATION NUMBER: 60/048,878
55 EARLIER FILING DATE: 1997-06-06
56 EARLIER APPLICATION NUMBER: 60/070,923
57 EARLIER FILING DATE: 1997-12-18
58 EARLIER APPLICATION NUMBER: 60/092,921
59 EARLIER FILING DATE: 1998-07-15
60 EARLIER APPLICATION NUMBER: 60/094,657
61 EARLIER FILING DATE: 1998-07-30
62 NUMBER OF SEQ ID NOS: 1227
63 SOFTWARE: PatentIn Ver. 2.0
64 SEQ ID NO 125
65 LENGTH: 1288
66 TYPE: DNA
67 ORGANISM: Homo sapiens
68 FEATURE:
69 NAME/KEY: SITE
70 LOCATION: (1286)
71 OTHER INFORMATION: n equals a,t,g, or c
72
73 US-09-205-258-125

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[illegible]

Db	Query Match	Best Local Similarity	Score	Size	Length	DB	Size	Length	DB
Db	1076	CTTCTTATAGTCACATCTCTCACTATTAATTGGGAATATTGTGTGTCTTTTCT	99.6%	680	683	Db	1135	1076	CTTCTTATAGTCACATCTCTCACTATTAATTGGGAATATTGTGTGTCTTTTCT
Qy	1146	TTTTTCTCTGTATAGATTTTAAAAAATATAAAGCTAACATCTTTGTACATTT	99.6%	680	683	Qy	1205	1146	TTTTTCTCTGTATAGATTTTAAAAAATATAAAGCTAACATCTTTGTACATTT
Db	1136	TTTTTCTCTGTATAGATTTTAAAAAATATAAAGCTAACATCTTTGTACATTT	99.6%	680	683	Db	1195	1136	TTTTTCTCTGTATAGATTTTAAAAAATATAAAGCTAACATCTTTGTACATTT
Qy	1206	GTAATGTAAAGATTTTATATCTGTTAAATATAATATTATTC	99.6%	680	683	Qy	1253	1206	GTAATGTAAAGATTTTATATCTGTTAAATATAATATTATTC
Db	1196	GTAATGTAAAGATTTTATATCTGTTAAATATAATATTATTC	99.6%	680	683	Db	1243	1196	GTAATGTAAAGATTTTATATCTGTTAAATATAATATTATTC
RESULT 9									
US-09-222-575-63/c									
Sequence 63, Application US/09222575									
Patent No. 6387697									
GENERAL INFORMATION:									
APPLICANT: Yugui, Jiang									
APPLICANT: Dillon, Devin C.									
APPLICANT: Mitchem, Jennifer L.									
APPLICANT: Xu, Jiansheng									
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer									
FILE REFERENCE: 210121.470									
CURRENT APPLICATION NUMBER: US/09/222.575									
CURRENT FILING DATE: 1998-12-28									
NUMBER OF SEQ ID NOS: 174									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 63									
LENGTH: 683									
TYPE: DNA									
ORGANISM: Human									
US-09-222-575-63									
Query Match									
Best Local Similarity 99.6%; Pred. No. 3.8e-253;									
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	516	ACATTTCAGAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG	99.6%	680	683	Qy	575	516	ACATTTCAGAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG
Db	683	ACATTTCAGAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG	99.6%	680	683	Db	624	683	ACATTTCAGAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG
Qy	576	CTAAATGCGAAATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGATGT	99.6%	680	683	Qy	635	576	CTAAATGCGAAATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGATGT
Db	623	CTAAATGCGAAATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGATGT	99.6%	680	683	Db	564	623	CTAAATGCGAAATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGATGT
Qy	636	TCAGAGCTCTTCCATG							

Query Match 42.2%; Score 530; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.8e-253;
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query 516 ACATTACAAAGATGCGTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 ACATTACAAAGATGCGTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624

Query 576 CTAATAATGCAAAATGATGCTGTGTCAGCGTGTGTAATTTTCAATTCATGAGCTGAATGT 635
Db 623 CTAATAATGCAAAATGATGCTGTGTCAGCGTGTGTAATTTTCAATTCATGAGCTGAATGT 564

Query 636 TCAGAACCTCTCCCATTTGAAGCTAATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 695
Db 563 TCAGAACCTCTCCCATTTGAAGCTAATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 504

Query 696 TCAACAATTAATATTCATGCACTTCTGTGGAAGCACTTGGAGGAATTTGATGT 755
Db 503 TCAACAATTAATATTCATGCACTTCTGTGGAAGCACTTGGAGGAATTTGATGT 444

Query 756 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTTCCAAAGAGATGCT 815
Db 443 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTTCCAAAGAGATGCT 384

Query 816 TCCTCTGATGGAATTCAGTTTCTGCGATCATTTTGAAGAACTACCAAAATTAATGCTT 875
Db 383 TCCTCTGATGGAATTCAGTTTCTGCGATCATTTTGAAGAACTACCAAAATTAATGCTT 324

Query 876 TAAATTTGATTTGCTACCTCTTTTATTAATGCTTGAATGTTTCACTTAAATGACAT 935
Db 323 TAAATTTGATTTGCTACCTCTTTTATTAATGCTTGAATGTTTCACTTAAATGACAT 264

Query 936 TTTAAATAGTTTATGTATACATCTGAATGAAGCAAGCTAAATATGTTTACAGACCA 995
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Query 996 AAGTGTGATTCACACGCTGTTTAAATCTAGCATTAATTTGCTTCAATCAAAAGTG 1055

RESULT 10
US-09-389-681-63/c
; Sequence 63, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqin, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-63

Query Match 42.2%; Score 530; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.8e-253;
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query 516 ACATTACAAAGATGCGTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 ACATTACAAAGATGCGTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624

Query 576 CTAATAATGCAAAATGATGCTGTGTCAGCGTGTGTAATTTTCAATTCATGAGCTGAATGT 635
Db 623 CTAATAATGCAAAATGATGCTGTGTCAGCGTGTGTAATTTTCAATTCATGAGCTGAATGT 564

Query 636 TCAGAACCTCTCCCATTTGAAGCTAATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 695
Db 563 TCAGAACCTCTCCCATTTGAAGCTAATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 504

Query 696 TCAACAATTAATATTCATGCACTTCTGTGGAAGCACTTGGAGGAATTTGATGT 755
Db 503 TCAACAATTAATATTCATGCACTTCTGTGGAAGCACTTGGAGGAATTTGATGT 444

Query 756 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTTCCAAAGAGATGCT 815
Db 443 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTTCCAAAGAGATGCT 384

Query 816 TCCTCTGATGGAATTCAGTTTCTGCGATCATTTTGAAGAACTACCAAAATTAATGCTT 875
Db 383 TCCTCTGATGGAATTCAGTTTCTGCGATCATTTTGAAGAACTACCAAAATTAATGCTT 324

Query 876 TAAATTTGATTTGCTACCTCTTTTATTAATGCTTGAATGTTTCACTTAAATGACAT 935
Db 323 TAAATTTGATTTGCTACCTCTTTTATTAATGCTTGAATGTTTCACTTAAATGACAT 264

Query 936 TTTAAATAGTTTATGTATACATCTGAATGAAGCAAGCTAAATATGTTTACAGACCA 995

RESULT 11
US-09-620-405B-63/c
; Sequence 63, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqin
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.47008
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-63

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Db 263 TTTAAATAGTTATGTATACATCTGAAGAAAAGCAAGCTAAATATGTTTACAGACCA 204
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Db 203 AAGTGTGATTTTACACGTGTTTAAATCTAGCATTTATCTATTTGCTTCAATCAAAAGTG 144
Qy 1056 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTCATAGTACATTTCTCAACCT 1115
Db 143 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTCATAGTACATTTCTCAACCT 84
Qy 1116 ATAAATTTGGAATATGTTGTGCTTTTGTGTTTCTCTAGTATAGCAATTTTAAAAA 1175
Db 83 ATAAATTTGGAATATGTTGTGCTTTTGTGTTTCTCTAGTATAGCAATTTTAAAAA 24
Qy 1176 ATATAAAGCTACCAATCTTTGT 1198
Db 23 ATATAAAGCTACCAATCTTTGT 1
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RESULT 12

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US-09-339-63/c
; Sequence 63, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47002
; CURRENT APPLICATION NUMBER: US/09/339,338A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-63
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Query Match 42.2%; Score 530; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.8e-253;
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 516 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624
Qy 576 CTAAATTCGAAAGATGATGCTGTGAGCGTTGGTATTTTCACTTCAATGAGCTGAATGT 635
Db 623 CTAAATTCGAAAGATGATGCTGTGAGCGTTGGTATTTTCACTTCAATGAGCTGAATGT 564
Qy 636 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 695
Db 563 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 504
Qy 696 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGAACTTTGTGAAGAAATGTTGCT 755
Db 503 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGAACTTTGTGAAGAAATGTTGCT 444
Qy 756 GGATTTAGTGTGCTATCTGGGTTGGCACTTTGTCAATTAACCAAAAGAGATGCT 815
Db 443 GGATTTAGTGTGCTATCTGGGTTGGCACTTTGTCAATTAACCAAAAGAGATGCT 384
Qy 816 TCTACTGATGGAATTCAGTTTCTCGCATCATTTATGGAAGAACTACCAAAATTAATGCTT 875
Db 383 TCTACTGATGGAATTCAGTTTCTCGCATCATTTATGGAAGAACTACCAAAATTAATGCTT 324
Qy 876 TAAATTTGATTTGCTACTCTTTTATTTATTTATGCTTGAATGTTCACTTAATGACAT 935
Db 323 TAAATTTGATTTGCTACTCTTTTATTTATTTATGCTTGAATGTTCACTTAATGACAT 264
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Qy 936 TTTAAATAGTTTANGTATACATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 995
Db 263 TTTAAATAGTTTANGTATACATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 204
Qy 996 AAGTGTGATTTTACACGTGTTTAAATCTAGCATTTATCTATTTGCTTCAATCAAAAGTG 1055
Db 203 AAGTGTGATTTTACACGTGTTTAAATCTAGCATTTATCTATTTGCTTCAATCAAAAGTG 144
Qy 1056 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTCATAGTACATTTCTCAACCT 1115
Db 143 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTCATAGTACATTTCTCAACCT 84
Qy 1116 ATAAATTTGGAATATGTTGTGCTTTTGTGTTTCTCTAGTATAGCAATTTTAAAAA 1175
Db 83 ATAAATTTGGAATATGTTGTGCTTTTGTGTTTCTCTAGTATAGCAATTTTAAAAA 24
Qy 1176 ATATAAAGCTACCAATCTTTGT 1198
Db 23 ATATAAAGCTACCAATCTTTGT 1
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RESULT 13

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US-09-433-826B-63/c
; Sequence 63, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47004
; CURRENT APPLICATION NUMBER: US/09/433,826B
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-63
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Query Match 42.2%; Score 530; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.8e-253;
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 516 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575
Db 683 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624
Qy 576 CTAAATTCGAAAGATGATGCTGTGAGCGTTGGTATTTTCACTTCAATGAGCTGAATGT 635
Db 623 CTAAATTCGAAAGATGATGCTGTGAGCGTTGGTATTTTCACTTCAATGAGCTGAATGT 564
Qy 636 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 695
Db 563 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 504
Qy 696 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGAACTTTGTGAAGAAATGTTGCT 755
Db 503 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGAACTTTGTGAAGAAATGTTGCT 444
Qy 756 GGATTTAGTGTGCTATCTGGGTTGGCACTTTGTCAATTAACCAAAAGAGATGCT 815
Db 443 GGATTTAGTGTGCTATCTGGGTTGGCACTTTGTCAATTAACCAAAAGAGATGCT 384
Qy 816 TCTACTGATGGAATTCAGTTTCTCGCATCATTTATGGAAGAACTACCAAAATTAATGCTT 875
Db 383 TCTACTGATGGAATTCAGTTTCTCGCATCATTTATGGAAGAACTACCAAAATTAATGCTT 324
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QY 876 TAATTTCATTGCTACCTCTTTTATATGCTTGAAGTTCACCTTAATGACAT 935
DB 323 TAATTTCATTGCTACCTCTTTTATATGCTTGAAGTTCACCTTAATGACAT 264
QY 936 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATGTTTACAGACA 995
DB 263 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATGTTTACAGACA 204
QY 996 AAGTGATTTTCACAGCTGTTTAAATCTAGCATTTATCTTGTTCATCAATCAAAAGT 1055
DB 203 AAGTGATTTTCACAGCTGTTTAAATCTAGCATTTATCTTGTTCATCAATCAAAAGT 144
QY 1056 GTTTCATATTTTTTTAGTTGTTAGAAATCTTCTTCATAGTCAATCTCTCAACCT 1115
DB 143 GTTTCATATTTTTTTAGTTGTTAGAAATCTTCTTCATAGTCAATCTCTCAACCT 84
QY 1116 ATAAATTTGGAATTTGTTGCTTTGTTTCTTTCTTCTAGTATGCAATTTTAAAAA 1175
DB 83 ATAAATTTGGAATTTGTTGCTTTGTTTCTTTCTTCTAGTATGCAATTTTAAAAA 24
QY 1176 ATATAAAGCTACCAATCTTTGT 1198
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 14
US-09-604-287A-63/C
Sequence 63, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 683
TYPE: DNA
ORGANISM: Homo sapien
US-09-604-287A-63

Query Match 42.2%; Score 530; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.8e-253;
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 516 ACATTTCAGAGATGCGTTCAATAGTGTCTTAAGATTTTGTGAGGCTCATTGGG 575
DB 683 ACATTTCAGAGATGCGTTCAATAGTGTCTTAAGATTTTGTGAGGCTCATTGGG 624
QY 576 CTTAAATGCAAGATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGAATG 635
DB 623 CTTAAATGCAAGATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGAATG 564
QY 636 TCAGAGCTCTTCCATTGAGCTTAAATTTTGGACCAAGAAAGCCCTGAATGAT 695
DB 563 TCAGAGCTCTTCCATTGAGCTTAAATTTTGGACCAAGAAAGCCCTGAATGAT 504
QY 696 TCAGAGCTCTTCCATTGAGCTTAAATTTTGGACCAAGAAAGCCCTGAATGAT 755
DB 503 TCAGAGCTCTTCCATTGAGCTTAAATTTTGGACCAAGAAAGCCCTGAATGAT 444
QY 756 GGATTTAGTATGTTGCTATCTGAGTGGCACTTGTTCAGATTAACCAAAAGAGATGCT 815
DB 443 GGATTTAGTATGTTGCTATCTGAGTGGCACTTGTTCAGATTAACCAAAAGAGATGCT 384

QY 816 TCTAGGATGGAATTCAGTTTCTGCGATCATTTATGGAAGTACCAAAATTAATGCTT 875
DB 383 TCTAGGATGGAATTCAGTTTCTGCGATCATTTATGGAAGTACCAAAATTAATGCTT 324
QY 876 TAATTTCATTGCTACCTCTTTTATATGCTTGAAGTTCACCTTAATGACAT 935
DB 323 TAATTTCATTGCTACCTCTTTTATATGCTTGAAGTTCACCTTAATGACAT 264
QY 936 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATGTTTACAGACA 995
DB 263 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATGTTTACAGACA 204
QY 996 AAGTGATTTTCACAGCTGTTTAAATCTAGCATTTATCTTGTTCATCAATCAAAAGT 1055
DB 203 AAGTGATTTTCACAGCTGTTTAAATCTAGCATTTATCTTGTTCATCAATCAAAAGT 144
QY 1056 GTTTCATATTTTTTTAGTTGTTAGAAATCTTCTTCATAGTCAATCTCTCAACCT 1115
DB 143 GTTTCATATTTTTTTAGTTGTTAGAAATCTTCTTCATAGTCAATCTCTCAACCT 84
QY 1116 ATAAATTTGGAATTTGTTGCTTTGTTTCTTTCTTCTAGTATGCAATTTTAAAAA 1175
DB 83 ATAAATTTGGAATTTGTTGCTTTGTTTCTTTCTTCTAGTATGCAATTTTAAAAA 24
QY 1176 ATATAAAGCTACCAATCTTTGT 1198
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 15
US-09-285-480-63/C
Sequence 63, Application US/09285480
Patent No. 6590076
GENERAL INFORMATION:
APPLICANT: Yugu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C1
CURRENT APPLICATION NUMBER: US/09/285,480
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 181
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 683
TYPE: DNA
ORGANISM: Homo sapien
US-09-285-480-63

Query Match 42.2%; Score 530; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.8e-253;
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 516 ACATTTCAGAGATGCGTTCAATAGTGTCTTAAGATTTTGTGAGGCTCATTGGG 575
DB 683 ACATTTCAGAGATGCGTTCAATAGTGTCTTAAGATTTTGTGAGGCTCATTGGG 624
QY 576 CTTAAATGCAAGATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGAATG 635
DB 623 CTTAAATGCAAGATGATGCTGTGAGGCTGTGATTTTCAATTCATGAGCTGAATG 564
QY 636 TCAGAGCTCTTCCATTGAGCTTAAATTTTGGACCAAGAAAGCCCTGAATGAT 695
DB 563 TCAGAGCTCTTCCATTGAGCTTAAATTTTGGACCAAGAAAGCCCTGAATGAT 504
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GenCore version 5.1.6
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SUMMARIES

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1	1257	100.0	1257	6	AX092390 Sequence
2	1257	100.0	1257	6	AX376298 Sequence
3	1257	100.0	1257	6	AX454660 Sequence
4	1257	100.0	1257	6	AX459648 Sequence
5	1257	100.0	1257	6	AX491138 Sequence
6	1257	100.0	1257	6	AX697362 Sequence
7	1257	100.0	1257	6	AY58914 Homo sapi
8	1155	91.9	1284	6	AX829144 Sequence
9	1117	88.9	1236	6	BC014245 Sequence
10	1089	86.6	1257	6	BD269636 Human sec
11	1036	82.4	1342	6	BD223153 98 human
12	1036	82.4	1342	6	AR243851 Sequence
13	992	78.9	1220	6	AY136825 Sequence
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ALIGNMENTS

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DEFINITION Sequence 121 from Patent WO0116318.
ACCESSION AX092390
VERSION AX092390.1 GI:13444509
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Eaton D.L., Filvaroff E., Gerritsen M.E., Goddard A., and Godowski P.J., Grimaldi C.J., Gurney A.L., Watanabe C.K. and Wood W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0116318-A 121 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
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Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS AX376298 1257 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 365 from Patent WO0168848.
ACCESSION AX376298
VERSION AX376298.1 GI:19170540
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 365 20-SEP-2001;
Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION	Sequence 245 from Patent WO0208284.
ACCESSION	AX454660
VERSION	AX454660.1 GI:21713954

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Eulaziotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 245 31-JAN-2002;

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gebler, Hanspeter (US) ; Gerlitsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurnee, Austin L. (US) ; Hillan, Kenneth J. (US) ; Margers, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

FEATURES	location/Qualifiers
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RESULT 4
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LOCUS Sequence 2 from Patent WO0216602.
DEFINITION AX459648
ACCESSION AX459648.1 GI:21725519
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Polakis, P.,
TITLE Williams, P.M., Wood, W.I., Wu, T.D. and Zhang, Z.
JOURNAL Compositions and methods for the diagnosis and treatment of tumor
PATENT: WO 0216602-A 2 28-FEB-2002;
GENENTECH, INC. (US)
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LOCUS Sequence 245 from Patent WO020690.
DEFINITION AX491138
ACCESSION AX491138.1 GI:22323906
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J.,
Patel, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
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TITLE and Ye, W.
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 245 03-JAN-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
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Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX697362
LOCUS Sequence 430 from Patent WO0078961.
DEFINITION AX697362
VERSION AX697362.1 GI:29498494
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L., Baton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A., Godowski, P.J., Gueney, A.L., Smith, V., Tunas, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K. Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0078961-A 430 28-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS 1257 bp mRNA linear p11 03-OCT-2003
DEFINITION Homo sapiens clone DNA76393 CTRC1 (UN0762) mRNA, complete cds.
ACCESSION AY358914
VERSION AY358914.1 GI:37182945
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bakayoceta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1257)
Clarke,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B.,
Dowd,P., Batton,D., Foster,J., Grimaldi,C., Gu,O., Haas,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C.,
Schonfeldt,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiandt,D., Woods,K.,
Xie,M.H., Yanaura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski, P.
The Secreted Protein discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 1257)
AUTHORS Clarke,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Db	181	GCCTCTGCTGCTCTCTGCTGCTGAGCTGCGCGCGCGCTGAGCGCTTCTGAGATCCCA					240
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LOCUS Sequence 37 from Patent WO02059377.
AX829144
VERSION AX829144.1 GI:39838921

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mack,D.H., Glah,K.C. and Afar,D.
TITLE Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
JOURNAL Patent: WO 02059377-A 37 01-AUG-2002;
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RESULT 9			
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LOCUS	BC014245	1236 bp	mRNA linear PRI 29-JUN-2004
DEFINITION	Homo sapiens collagen triple helix repeat containing 1, mRNA (cDNA clone MGC:20766 IMAGE:4586039), complete cds.		
ACCESSION	BC014245		
VERSION	BC014245.2	GI:33878497	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eubacteria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1236)		
	Straussberg, R.L., Collins, F.S., Wagner, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Ditchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stjepanec, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Ueda, T.B., Toshiyuki, S., Carminci, P., Prange, C., Rata, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McMan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wozniak, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.U., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M., Scherf, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1236)		
AUTHORS	Straussberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-SEP-2001) National Institutes of Health, Mammalian		

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Qy 607 GGAATTTTCACTTCAATGAGAGTGAATGTTGAGAGTCTTCCCATTTGAAGCTATATTT 666
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RESULT 11
LOCUS BD223153 1342 bp DNA linear PAT 17-JUL-2003
DEFINITION 98 human secretory proteins.
ACCESSION BD223153
VERSION BD223153.1 GI:33032923
KEYWORDS JP 2002521055-A/88.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1342)
AUTHORS Komatsu, S., Rosen, C.A., Ruben, S.M., Duan, R., Moore, P.A.,
Shi, Y., Lafleur, D., Wei, Y.F., Ni, J., Florence, R.A., Young, P.E.,
Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H.S. and
Mucenksi, M.
TITLE 98 human secretory proteins
JOURNAL Patent: JP 2002521055-A 88 16-JUL-2002;

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COMMENT HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002521055-A/88
PD 16-JUL-2002
PF 29-JUL-1998 JP 2000562480
PR 30-JUL-1998 US 60/094657, 05-AUG-1998 US 60/095486 PR
06-AUG-1998 US 60/095455, 06-AUG-1998 US 60/095454 PR
12-AUG-1998 US 60/096319
PI GEORGE A KOMATSU, CRAIG A ROSEN, STEVEN
PI RUBEN, ROXANNE DUAN,
PI PAUL A MOORE, YANGLU SHI, DAVID LAFLEUR, YING FEI WEI, JIAN NI, PI
KIMBERLY A FLORENCE, PAUL E YOUNG, LAURIE A BREWER, DANIEL R
SOPPET,
PI GREGORY A ENDRESS, REINHARD EBNER, HENRIK S OLSEN, MICHAEL PI
MUCENSKI
PC C12N15/09, A61K31/713, A61K38/00, A61K48/00, C07K14/47, C07K16/18,
PC C12N1/15,
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PC A61P11/06, A61P17/06, A61P19/02, A61P25/02, A61P25/14, A61P25/16,
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FH Key
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION AR405953
ACCESSION AR405953.1 GI:40155009
VERSION
KEYWORDS
ORGANISM Unknown.
SOURCE
REFERENCE 1 (bases 1 to 1220)
AUTHORS Lindner,V. and Friesel,R.E.
TITLE Compositions, methods and kits relating to remodel
JOURNAL Patent: US 6630325-A 3 07-OCT-2003;
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LOCUS AY136825
DEFINITION Homo sapiens collagen triple helix repeat-containing protein 1
(CTHRC1) mRNA, complete cds.
ACCESSION AY136825
VERSION AY136825.1 GI:25989620
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1221)
AUTHORS Lehnert,W., Moore,D.P., Harmon,K.J., Mancini,M.L. and Lindner,V.
TITLE Expression of the novel collagen triple helix repeat-containing
gene (Cthrc1) suggests functions in multiple organ systems
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1221)
AUTHORS Lindner,V.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2002) Center for Molecular Medicine, Maine
Medical Center Research Institute, 81 Research Drive, Scarborough,
ME 04074, USA
FEATURES Location/Qualifiers

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Query Match 78.8%; Score 991; DB 9; Length 1221;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1211; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 189 GCGCTCTGAGATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 248
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RESULT 15
BD223185
LOCUS BD223185 1286 bp DNA linear PART 17-JUL-2003
DEFINITION 98 human secretory proteins.
ACCESSION BD223185.
VERSION BD223185.1 GI:33032955
KEYWORDS JP 2002521055-A/120.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1286)
Komatsoulis,G.A., Rosen,C.A., Ruben,S.M., Duan,R., Moore,P.A.,
Shi,Y., Lafleur,D., Wei,Y.F., Ni,J., Florence,K.A., Young,P.B.,
Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H.S. and
Mucenski,M.
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Patent: JP 2002521055-A 120 16-JUL-2002;
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PN JP 2002521055-A/120
PD 16-JUL-2002
PF 29-JUL-1999 JP 2000562480
PR 30-JUL-1998 US 60/094657.05-AUG-1998 US 60/095486 PR
06-AUG-1998 US 60/095455.06-AUG-1998 US 60/095454 PR
12-AUG-1998 US 60/096319
PI GEORGE A KOMATSOUKIS, CRAIG A ROSEN, STEVEN
M RUBEN, ROXANNE DUAN,
PI PAUL A MOORE, YANGLU SHI, DAVID LAFLEUR, YING FEI WEI, JIAN NI, PI
KIMBERLY A FLORENCE, PAUL B YOUNG, LAURIE A BREWER, DANIEL R
SOPPET,
PI GREGORY A ENDRESS, REINHARD EBNER, HENRIK S OLSEN, MICHAEL PI
MUCENSKI
PC C12N15/09, A61K31/713, A61K38/00, A61K48/00, C07K4/47, C07K6/18,

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Run on: December 25, 2004, 05:33:57 ; Search time 94 Seconds

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Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPOGPASPORLRGLL...GDASTGMSVSRHIIIEELPX 243

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=humand40.cdi
-LIST=100 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	729	4	US-09-834-759-511 Sequence 511, App
2	1301	100.0	732	4	US-09-834-759-510 Sequence 510, App
3	1301	100.0	837	4	US-09-834-759-512 Sequence 512, App
4	1301	100.0	837	4	US-09-834-759-513 Sequence 513, App
5	1294	99.5	1220	4	US-09-692-081-3 Sequence 3, Appl
6	1291	99.2	1342	4	US-09-489-847-89 Sequence 124, App
7	1266	97.3	1286	4	US-09-489-847-124 Sequence 124, App
8	1258.5	96.7	1288	4	US-09-205-258-125 Sequence 125, App
9	1216	93.5	1192	4	US-09-692-081-1 Sequence 1, Appl
10	1211	93.1	734	4	US-09-692-081-9 Sequence 9, Appl
11	734	56.4	403	4	US-09-692-081-6 Sequence 6, Appl
12	626	48.1	683	3	US-09-222-575-63 Sequence 63, Appl

13	626	48.1	683	4	US-09-389-681-63 Sequence 63, Appl
14	626	48.1	683	4	US-09-620-405B-63 Sequence 63, Appl
15	626	48.1	683	4	US-09-339-338-63 Sequence 63, Appl
16	626	48.1	683	4	US-09-433-828B-63 Sequence 63, Appl
17	626	48.1	683	4	US-09-604-287A-63 Sequence 63, Appl
18	626	48.1	683	4	US-09-285-480-63 Sequence 63, Appl
19	626	48.1	683	4	US-09-834-759-63 Sequence 63, Appl
20	626	48.1	683	4	US-09-590-751A-63 Sequence 63, Appl
21	129.5	10.0	3170	4	US-09-169-768-15 Sequence 1, Appl
22	129.5	10.0	3171	4	US-09-169-768-15 Sequence 1, Appl
23	129.5	10.0	3181	1	US-08-655-086-1 Sequence 1, Appl
24	129.5	10.0	3349	4	US-09-169-768-13 Sequence 13, Appl
25	129.5	10.0	3531	4	US-09-169-768-7 Sequence 7, Appl
26	129.5	10.0	3541	4	US-09-169-768-9 Sequence 9, Appl
27	129.5	10.0	4167	4	US-09-169-768-12 Sequence 12, Appl
28	129.5	10.0	4409	4	US-09-331-347C-22 Sequence 22, Appl
29	120.5	9.3	1196	1	US-08-167-939A-5 Sequence 5, Appl
30	120.5	9.3	1196	1	US-08-567-538-5 Sequence 5, Appl
31	120	9.2	2543	1	US-08-555-669-11 Sequence 11, Appl
32	120	9.2	2543	3	US-09-073-663-11 Sequence 11, Appl
33	120	9.2	20966	4	US-09-776-976-7 Sequence 7, Appl
34	120	9.2	20966	4	US-09-909-547-7 Sequence 7, Appl
35	120	9.2	20966	4	US-09-569-852B-1 Sequence 1, Appl
36	118.5	9.1	1981	4	US-09-620-312D-870 Sequence 870, App
37	118.5	9.1	2823	4	US-09-919-497-7 Sequence 7, Appl
38	118.5	9.1	3171	4	US-09-169-768-19 Sequence 19, Appl
39	117.5	9.0	5102	4	US-08-494-168-1 Sequence 1, Appl
40	117.5	9.0	5102	1	US-08-227-357-51 Sequence 51, Appl
41	115.5	8.9	1333	3	US-09-227-357-51 Sequence 51, Appl
42	115.5	8.9	6674	4	US-09-620-312D-110 Sequence 110, App
43	115	8.8	695	4	US-09-404-879A-212 Sequence 212, App
44	115	8.8	695	4	US-09-338-933-212 Sequence 212, App
45	115	8.8	695	4	US-09-215-681-212 Sequence 212, App
46	115	8.8	695	4	US-09-216-002A-212 Sequence 212, App
47	115	8.8	695	4	US-09-667-857-212 Sequence 212, App
48	115	8.8	1881	3	US-09-029-348-20 Sequence 20, Appl
49	113	8.7	4707	3	US-09-181-706-1 Sequence 1, Appl
50	113	8.7	4707	3	US-09-458-791-1 Sequence 1, Appl
51	113	8.7	4707	3	US-09-459-066-1 Sequence 1, Appl
52	113	8.7	9164	4	US-09-814-912A-80 Sequence 80, Appl
53	112.5	8.6	366	4	US-09-569-852B-4 Sequence 4, Appl
54	112.5	8.6	1313	2	US-08-463-911-6 Sequence 6, Appl
55	112.5	8.6	4454	4	US-09-569-852B-5 Sequence 5, Appl
56	112	8.6	438	4	US-09-513-999C-129 Sequence 129, App
57	112	8.6	709	4	US-09-398-522-115 Sequence 115, App
58	112	8.6	1297	4	US-09-800-728-80 Sequence 80, Appl
59	111	8.5	4359	4	US-09-484-970B-4 Sequence 4, Appl
60	111	8.5	18609	3	US-08-943-731-1 Sequence 1, Appl
61	110.5	8.5	4517	3	US-09-140-804-9 Sequence 9, Appl
62	110.5	8.5	4517	4	US-09-686-838B-9 Sequence 9, Appl
63	110.5	8.5	4517	4	US-09-776-976-5 Sequence 5, Appl
64	110.5	8.5	4517	4	US-09-909-547-5 Sequence 5, Appl
65	110	8.5	1299	4	US-09-976-594-814 Sequence 814, App
66	110	8.5	2721	6	US-09-919-497-6 Sequence 6, Appl
67	110	8.5	6458	4	US-07-945-283-1 Sequence 1, Appl
68	110	8.5	8438	1	US-09-620-312D-1061 Sequence 1061, App
69	109	8.4	3389	4	US-09-297-269-39 Sequence 39, Appl
70	108.5	8.3	1572	4	US-08-463-911-1 Sequence 1, Appl
71	108	8.3	1276	2	US-09-776-976-3 Sequence 3, Appl
72	108	8.3	1276	4	US-09-909-547-3 Sequence 3, Appl
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75	107.5	8.3	1138	4	US-09-800-728-44 Sequence 44, Appl
76	107.5	8.3	1149	4	US-09-800-728-47 Sequence 47, Appl
77	107	8.2	2487	4	US-09-620-312D-160 Sequence 160, App
78	106.5	8.2	1050	4	US-09-800-729-46 Sequence 46, App
79	106.5	8.2	1588	6	US10466-1 Patent No. 5510466
80	106.5	8.2	1807	6	US10466-1 Patent No. 5510466
81	105.5	8.1	804	4	US-09-404-879A-213 Sequence 213, App
82	105.5	8.1	804	4	US-09-338-933-213 Sequence 213, App
83	105.5	8.1	804	4	US-09-215-681-213 Sequence 213, App
84	105.5	8.1	804	4	US-09-216-002A-213 Sequence 213, App
85	105.5	8.1	804	4	US-09-667-857-213 Sequence 213, App

86 105.5 8.1 1134 3 US-09-342-681C-15 Sequence 15, App1
87 105.5 8.1 1338 4 US-09-336-536-1 Sequence 1, App1
88 105.5 8.1 1347 3 US-09-140-804-1 Sequence 1, App1
89 105.5 8.1 1347 4 US-09-686-838B-1 Sequence 1, App1
90 105.5 8.1 1377 4 US-09-866-028-41 Sequence 41, App1
91 105.5 8.1 1377 4 US-10-140-002-361 Sequence 361, App1
92 105.5 8.1 1377 4 US-09-944-457-41 Sequence 41, App1
93 105.5 8.1 1661 3 US-09-342-681C-3 Sequence 3, App1
94 105 8.1 1868 1 US-08-893-467B-1 Sequence 1, App1
95 105 8.1 1868 3 US-08-893-467B-1 Sequence 1, App1
96 105 8.1 2230 4 US-09-620-312D-282 Sequence 282, App1
97 105 8.1 3120 4 US-09-169-768-29 Sequence 29, App1
98 104.5 8.0 1152 4 US-09-776-976-1 Sequence 1, App1
99 104.5 8.0 1152 4 US-09-909-547-1 Sequence 1, App1
100 104 8.0 444 4 US-09-397-787-161 Sequence 161, App1

ALIGNMENTS

RESULT 1
US-09-834-759-511
Sequence 511, Application US/09834759
Patent No. 6680197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugui
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Heppler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 511
LENGTH: 729
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-511

Alignment Scores:
Pred. No.: 1.07e-128 Length: 729
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-511 (1-729)

QY 1 MetArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 1 ATGGAGCCCGAGGGGCCCCCGCCCTCCCGCAGCGGCTCCGCGGCTCTGCTCTG 60
QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGlnIleProGlyGlyLeuGlnysAla 40
DB 61 CTGCTGCGAGCTGCGCCGCGCGCTCGAGCGCTCTGAGATCCCGAAGGGAGCAAGAGCG 120
QY 41 GlnLeuArgGlnArgGlnValValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
DB 121 CAGCTCCGCGAGAGGAGAGTGTGTGAGCTGTATATGAAATGTCTCAAGGGGCACACA 180
QY 61 G1yValProGlyArgAspGlySerProGlyValAlaValIleProGlyThrProGlyIle 80
DB 181 GAGATGCTGCTGCTCAAGACGAGAGCCCTGGGCGCAATGTTATTTCCGGGTACCTGGGATC 240
QY 81 ProGlyArgAspGlyPheLeuGlyGlnIulysGlyGlnCysLeuArgGlnSerPheGlnGln 100
DB 241 CCAAGTCGGAGTGTATCTCAAGAGAGAAAGGGGAAATGTCTGAGGAGAAAGCTTTGAGAG 300

QY 101 SerTrpThrProAsnTyrllyGlnCysSerTrpSerSerLeuAsnTyrllyLeuAspLeu 120
DB 301 TCTTGACACCCCACTACACAGACAGTTCATGAGTTCATGATATATGATGATGATCTT 360
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetArgSerArgSerAlaLeuArgValLeu 140
DB 361 GGGAAATTTGCGAGTGTACATTTTCAAGATGCGTTCAATATGCTCTTAAGAGTTTG 420
QY 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTrpTyrrPheThr 160
DB 421 TTCAGTGGCTACTCGGCTAAATGCAAGATGCAAGCTGTGACGCTTGATTTTCA 480
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlleAspGln 180
DB 481 TTCATGTAGAGCTGATGTTCAGACCTCTCCCATTAAGCTATTAATTTATTTGGACCA 540
QY 181 GlySerProGlnLeuMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 541 GGAAGCCCTGAATGATATTCACAAATTAATTTATGCACTTCTTCTGGAGAGACTT 600
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 601 TGTGAAGGAATGTGGTGTGATAGTGTGATGCTCTATCTGGGTGGCACTTGTTCAGAT 660
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGln 240
DB 661 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGATTCGATTCGCATATTATGAAGA 720
QY 241 LeuProLys 243
DB 721 CTACCAAAA 729

RESULT 2
US-09-834-759-510
Sequence 510, Application US/09834759
Patent No. 6680197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugui
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Heppler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 510
LENGTH: 732
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-510

Alignment Scores:
Pred. No.: 1.08e-128 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-510 (1-732)

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DB 1 ATGGAGCCCGAGGGGCCCCCGCCCTCCCGCAGCGGCTCCGCGGCTCTGCTCTG 60
QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGlnIleProGlyGlyLeuGlnysAla 40

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Db      61 CTGCTGACAGCTCCCGCCGCTCGAGCGCTCGAGATCCCAAGGGAAGCAAAAGGCG
Qy      41 GlnLeuArgGlnArgGluValAlaPheLeuTyrAenGlyMetCysLeuGlnInLProAla 60
Db      121 CAGCTCCGGCAGAGGAGGTGTGACCTGTATTAAGGATGTGCTTAAAGGCCACAGA 180
Qy      61 GlyValProGlyArgAspGlySerProGlyAlaAenValIleProGlyThrProGlyIle 80
Db      181 GGAGTCCCTGGTCCGAGACGGAGCCCTGGGCCAATGTTATTCGGGTACACTGGGATC 240
Qy      81 ProGlyArgAspGlyPheLeuGlyGlyGluCysLeuArgGlySerPheGlnGlu 100
Db      241 CCAGGTCCGGATGATTCAGAGAGAAAGGGGGAATGCTGAGGGAAAGCTTTGAGAG 300
Qy      101 SerTPHrProAenTyrIleGlnCysSerTPSerserLeuAenTyrGlyIleAenPleu 120
Db      301 TCCTGACACCCACATCAAGACAGTGTTCATGAGATTCATTAATATGACATAGATCTT 360
Qy      121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIleu 140
Db      361 GGGAATATTCGGAGTGTACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 420
Qy      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db      421 TTCAGTGGCTCATCTCGGCTAAATGCAAAATGCAATGCTGTCAGCGTTGATTTTACA 480
Qy      161 PheAenGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAenPleu 180
Db      481 TTCATATGGATCGAATGTTGAGAGCTCTCCATTAAGCATATATTAATTTGAGCCAA 540
Qy      181 GlySerProGluMetAsnSerThrIleAenIleHisArgThrSerSerValGluGlyLeu 200
Db      541 GGAGGCTTGAATGATTCACAAATTAATTCATCGACCTTCTGTGGAAGGACTT 600
Qy      201 CysGluGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAap 220
Db      601 TGTGAAGGATTTGCTGCTGATTAAGTGATGTTGCTATCTGGGTTCGCACTTGTAGAT 660
Qy      221 TyrProLysGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGluGlu 240
Db      661 TACCCAAAAGGAGATGCTTCTACTGATGGAATTCAGTTTCGCACTTATTTGAAGA 720
Qy      241 LeuProLys 243
Db      721 CTACCAAAA 729

RESULT 3
US-09-834-759-512
; Sequence 512, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS OF METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121, 470C9
; CURRENT APPLICATION NUMBER: US/09/834, 759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 512
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-512
Alignment Scores:

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Pred. No.: 1,326-128
Score: 1301.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-512 (1-837)

Qy      1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db      106 ATGCAACCCCAAGAGGCGCCGCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCCG 165
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnLysAla 40
Db      166 CTGCTGACAGTCCCGCCCGCTCGAGCCCTCTGAGATCCCAAGGGAAGCAAAAGGCG 225
Qy      41 GlnLeuArgGlnArgGluValAlaPheLeuTyrAenGlyMetCysLeuGlnInLProAla 60
Db      226 CAGTCCCGCAGAGGAGGTGTGACCTGTATTAAGGATGTGCTTAAAGGCCACAGA 285
Qy      61 GlyValProGlyArgAspGlySerProGlyAlaAenValIleProGlyThrProGlyIle 80
Db      286 GGAGTCCCTGGTCCGAGACGGAGCCCTGGGCCAATGTTATTCGGGTACACTGGGATC 345
Qy      81 ProGlyArgAspGlyPheLeuGlyGlyGluCysLeuArgGlySerPheGlnGlu 100
Db      346 CCAGGTCCGGATGATTCAGAGAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGAG 405
Qy      101 SerTPHrProAenTyrIleGlnCysSerTPSerserLeuAenTyrGlyIleAenPleu 120
Db      406 TCCTGAGACCCACATCAAGACAGTGTTCATGAGATTCATTAATATGAGATGATCTT 465
Qy      121 GlyValIleAlaGluCysThrPheThrIleMetArgSerSerAlaLeuArgValIleu 140
Db      466 GGGAATATTCGGAGTGTACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 525
Qy      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db      526 TTCAGTGGCTCATCTCGGCTAAATGCAAAATGCAATGCTGTCAGCGTTGATTTTACA 585
Qy      161 PheAenGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAenPleu 180
Db      586 TTCATATGGATCGAATGTTGAGAGCTCTCCATTAAGCATATATTAATTTGAGCCAA 645
Qy      181 GlySerProGluMetAsnSerThrIleAenIleHisArgThrSerSerValGluGlyLeu 200
Db      646 GGAGGCTTGAATGATTCACAAATTAATTCATCGACCTTCTGTGGAAGGACTT 705
Qy      201 CysGluGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAap 220
Db      706 TGTGAAGGATTTGCTGCTGATTAAGTGATGTTGCTATCTGGGTTCGCACTTGTAGAT 765
Qy      221 TyrProLysGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGluGlu 240
Db      766 TACCCAAAAGGAGATGCTTCTACTGATGGAATTCAGTTTCGCACTTATTTGAAGA 825
Qy      241 LeuProLys 243
Db      826 CTACCAAAA 834

RESULT 4
US-09-834-759-513
; Sequence 513, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.

```

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 513
LENGTH: 837
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-513

Alignment Scores:
Pred. No.: 1,32e-128 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-513 (1-837)

Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db ATGGACCCCGAGGCGCCCGCCCTCCCGACGCGCTCCGCGCTCTGCTCTG 165

Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnYsAla 40
Db CTGCTGACAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 225

Qy 41 GlnLeuArgGlnArgGlnValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
Db CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGATGTCTTACAAAGGCGACGA 285

Qy 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db GGAATGCTGTGTGAGACGAGGAGCCCTGGGCAATGTATTCGAGTACACCTGGATC 345

Qy 81 ProGlyArgAspGlyPheLeuGlyGlyGlnGlyGlnCysLeuArgGlnSerPheGlnGln 100
Db CCAAGTCCGAGATGATCAAGAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGAG 405

Qy 101 SerTrpThrProAsnTrpTyrGlnCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu 120
Db TCTTGACACCACTACCAAGACAGTTCATGAGATTCATTAATTAATGAGATGATCTT 465

Qy 121 GlyIleIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db GGGAAATTCGGAGATGATCACTTACAAAGATGCTCAAAATGAGTCTTAAGAGTTTG 525

Qy 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db TTCAAGTGGCTCACTTCGGCTAAATGAGAAATGATCTGTGAGATTTGACA 585

Qy 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db TTCAATGAGATGATGATTTCAAGACCTCTCCCATTAAGCTATTAATTAATTTGAGCAA 645

Qy 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db GGAAGCCCTGAAATGAATTCACAAATTAATTAATTCACACTTCTTCTGTGAAAGGACTT 705

Qy 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db TGTGAAGAAATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 765

Qy 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGln 240
Db TACCAAAAGAGATGCTTCTTACATGATGATGATGATGATGATGATGATGATGATGAT 825

Qy 241 LeuProIys 243
|||||

Db 826 CTACCAAA 834

RESULT 5
US-09-692-081-3
Sequence 3, Application US/09692081
Patent No. 6630325
GENERAL INFORMATION:
APPLICANT: LINDNER, Volkhard
APPLICANT: PRIESEL, Robert F.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
CURRENT APPLICATION NUMBER: US/09/692,081
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1220
TYPE: DNA
ORGANISM: Homo sapiens
US-09-692-081-3

Alignment Scores:
Pred. No.: 1,28e-127 Length: 1220
Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-692-081-3 (1-1220)

Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db ATGGACCCCGAGGCGCCCGCCCTCCCGACGCGCTCCGCGCTCTGCTCTG 160

Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnYsAla 40
Db CTGCTGACAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 220

Qy 41 GlnLeuArgGlnArgGlnValAlaLeuLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
Db CAGCTCCGCGAGGAGGAGGTGTGACCTGTATTAATGATGTCTTACAAAGGCGACGA 280

Qy 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db GGAATGCTGTGTGAGACGAGGAGCCCTGGGCAATGTATTCGAGTACACCTGGATC 340

Qy 81 ProGlyArgAspGlyPheLeuGlyGlyGlnGlyGlnCysLeuArgGlnSerPheGlnGln 100
Db CCAAGTCCGAGATGATCAAGAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGAG 400

Qy 101 SerTrpThrProAsnTrpTyrGlnCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu 120
Db TCTTGACACCACTACCAAGACAGTTCATGAGATTCATTAATTAATTAATGAGATGATCTT 460

Qy 121 GlyIleIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db GGGAAATTCGGAGATGATCACTTACAAAGATGCTCAAAATGAGTCTTAAGAGTTTG 520

Qy 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db TTCAAGTGGCTCACTTCGGCTAAATGAGAAATGATCTGTGAGATTTGACA 580

Qy 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db TTCAATGAGATGATGATTTCAAGACCTCTCCCATTAAGCTATTAATTAATTTGAGCAA 640

Qy 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db GGAAGCCCTGAAATGAATTCACAAATTAATTAATTCACACTTCTTCTGTGAAAGGACTT 700

Qy 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
|||||

Db	701	IGTGAAGAAATTGGGCTGGATTAGTGCATGTTGCATCGGTTGGCACTGTTGCAGT	760
Oy	221	TyrProLysGlyAspAlaSerThrGlyTyrPaaSerValSerArgIleIleIleGluGln	240
Db	761	TACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAAGTTCTCGCATCATTTATGAAGA	820
Oy	241	LeuProLys 243	
Db	821	CTACCAAAA 829	
RESULT 6			
US-09-489-847-89			
: Sequence 89, Application US/09489847			
: Patent No. 6476195			
: GENERAL INFORMATION:			
: APPLICANT: Rosen et al			
: TITLE OF INVENTION: 98 Human Secreted Proteins			
: FILE REFERENCE: P2031P1			
: CURRENT APPLICATION NUMBER: US/09/489,847			
: CURRENT FILING DATE: 2000-01-24			
: EARLIER APPLICATION NUMBER: PCT/US99/17130			
: EARLIER FILING DATE: 1999-07-29			
: EARLIER APPLICATION NUMBER: 60/094,657			
: EARLIER FILING DATE: 1998-07-30			
: EARLIER APPLICATION NUMBER: 60/095,486			
: EARLIER FILING DATE: 1998-08-05			
: EARLIER APPLICATION NUMBER: 60/096,319			
: EARLIER FILING DATE: 1998-08-12			
: EARLIER APPLICATION NUMBER: 60/095,454			
: EARLIER FILING DATE: 1998-08-06			
: EARLIER APPLICATION NUMBER: 60/095,455			
: EARLIER FILING DATE: 1998-08-06			
: NUMBER OF SEQ ID NOS: 376			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 89			
: LENGTH: 1342			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-09-489-847-89			
Alignment Scores:			
Pred. No.: 3,086-127			
Score: 1291.00			
Percent Similarity: 99.59%			
Best Local Similarity: 99.18%			
Query Match: 99.23%			
DB: 4 Gaps: 0			
US-10-063-734-122 (1-243) x US-09-489-847-89 (1-1342)			
Oy	1	MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu	20
Db	141	ATGCAACCCCAAGGCGCCGCCGCTCCCGCAGCGGCTCCGGGCTCTCGCTGCTCCTG	200
Oy	21	LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyGlyGlnVala	40
Db	201	CTGCTGCAAGCTGCCCGCGCTCTGAGCGCTCTGACATCCCAAGGCGAAGCAAGGCGC	260
Oy	41	GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla	60
Db	261	CAGCTCCCGCAAGGAGGAGTGGTGGACCTGTATTAATGGAATGGCTTACAAAGGCCAGCA	320
Oy	61	GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle	80
Db	321	GGAAGTCTGGTGGTCAAGACGGGAGCCCTGGGGCCAAATTCGCAATTCGGGTACACTGGGATC	380
Oy	81	ProGlyArgAspGlyPheLysGlyGlyGlyGlyCysLeuArgGlnSerPheGluGln	100
Db	381	CCAGGTCCGGATGGAATTCAAAAGCAAAAGGGGGAATGTCTGAGGAGAAAGCTTTGAGAG	440
Oy	101	SerTyrThrProAsnTyrLysGlnCysSerTyrPserSerLeuAsnTyrGlyIleAspLeu	120
Db	441	TCTTGACACCCCACTACAGCAAGTGTTCATGGAGTTCAATGAATATATGGCATAGATCTT	500

QY	12	GLYLSVSLLEALAGLUCVSTThPhethrlysmwEArGSeRanSeRAlaleuArGVallau	140
Db	501	GGGAAATATGGCGAGCTGACATTTCACAAAGATCGCTTCAAAATAGTCCTTAAGAGTTTG	560
QY	141	PheserGISeRleuArGVLeuLysCysArGVaanaIaCy8CysGVlnArGVTPYrPhethr	160
Db	561	TTCAGTGGCTCACTTCGGCTTAATAATGCAGAAATGCATGCTGTGAGCGTTGATTTACCA	620
QY	161	PhesangIYAlaGLUCVSeSeGIYProLeuProlleGIuAlaIleIeYrleuApgIn	180
Db	621	TTCAATGAGCTGATGTTCACGAGACCTCTCCCATTAAGCATATATTAATTTGGACCA	680
QY	181	GIYSeRProGIuMeArSeRThrIleAaniIeHIsArGVThSeSeRValGIuGIYLeu	200
Db	681	GGAGACCTGAAATGAAATTCACAACTTAATATTCATCGCACTTCTTGTGAGAGACTT	740
QY	201	CysGIuGIYIleGIYAlaGIYLeuValaApValaIaIeITrPVaGIYThCysSeRaP	220
Db	741	TGTGAAGAAATGGTGGCTGATTAATGATGTGTGATCTGGGTTGGCACTTGTCAGAT	800
QY	221	TyrProLySGIYAspAlaSerThrGIYTrpAnsSerValSeArGIleIleIleGIuGIu	240
Db	801	TACCCAAAGAGAGATCTTCACTGATGAGATTCAGATTTCGACATATTAATGAAGA	860
QY	241	LeuProLyS 243	
Db	861	CTACCAAAA 869	
RESULT 7			
US-09-489-847-124			
; Sequence 124, Application US/09489847			
; Patent No. 6476195			
GENERAL INFORMATION:			
; APPLICANT: Rosen et al			
; TITLE OF INVENTION: 98 Human Secreted Proteins			
; FILE REFERENCE: P2031P1			
; CURRENT APPLICATION NUMBER: US/09/489,847			
; EARLIER FILING DATE: 2000-01-24			
; EARLIER APPLICATION NUMBER: PCT/US99/11130			
; EARLIER FILING DATE: 1999-07-29			
; EARLIER APPLICATION NUMBER: 60/094,657			
; EARLIER FILING DATE: 1998-07-30			
; EARLIER APPLICATION NUMBER: 60/095,486			
; EARLIER FILING DATE: 1998-08-05			
; EARLIER APPLICATION NUMBER: 60/096,319			
; EARLIER FILING DATE: 1998-08-12			
; EARLIER APPLICATION NUMBER: 60/095,454			
; EARLIER FILING DATE: 1998-08-06			
; EARLIER APPLICATION NUMBER: 60/095,455			
; EARLIER FILING DATE: 1998-08-06			
; NUMBER OF SEQ ID NOS: 376			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 124			
; LENGTH: 1286			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: SITE			
; LOCATION: (1284)			
; OTHER INFORMATION: n equals a,t,g, or c			
US-09-489-847-124			
Alignment Scores:			
Pred. No.: 1,29e-124 Length: 1286			
Score: 1266.00 Matches: 241			
Percent Similarity: 99.18% Conservative: 2			
Best Local Similarity: 99.18% Mismatches: 0			
Query Match: 97.31% Indels: 1			
DB: 4 Gaps: 0			
US-10-063-734-122 (1-243) x US-09-489-847-124 (1-1286)			

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 131 ATCGACCCCAAGGGCCCCGCGCTCCCGCAGGGGCTCCGGCCCTCCGCTGCTG 190
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnAla 40
Db 191 CTGCTCAAGTGGCCCGCGCGCTGAGCGCTGAGATCCCAAGGGGAAAGGCG 250
QY 41 GlnLeuArgGlnArgGlnValValAlaPheLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 251 CA-CTCCGCGAGGGAGGTGGAGGTGGAGCTGTATATGATGATGCTTACAGGGCCAGCA 309
QY 61 GlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
Db 310 GGAGTCCCTGCTGAGAGCGGAGCCCTGGGGCCAAATGCCATTCCGGTACACTGGGATC 369
QY 81 ProGlyValArgAspGlyValArgGlyGlyGlnValGlyGlnCysLeuArgGlnSerPheGlnGln 100
Db 370 CCGAGTGGAGTGAATTCAAAGAGAAAGAGGAGAAATGCTGAGGGAAAGCTTTGAGGAG 429
QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
Db 430 TCTGGACACCCCACTACAGAGCTGTTCATGAGATTCATTGATTAATGCAAGATCTT 489
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIleu 140
Db 490 GGGAAATTCGCGAGGTGATCATTTACAAAGATCGTTCAAAATGCTCTCTAAGAGTTTG 549
QY 141 PheSerGlySerLeuArgLeuGlnCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 550 TTCAGTGGCTCACTTGGCTTAATACAGAAATGCAATGCTGAGGTTGGAATTTCAACA 609
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db 610 TTCATGAGGTGAATGTTCAAGACTCTTCCATTGAAGCTATATTATTGACCA 669
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db 670 GGAAGCCCTGAATGATTAATCAATTAATTCATCGCATCTTCTGCAAGAGACTT 729
QY 201 CysGlnGlyIleGlyValAlaGlyLeuValAlaIleTyrValGlyThrCysSerAsp 220
Db 730 TGTGAAGGATTTGGTGTGATTTAGTGATTTGCTGATGCTGGGTTGGCACTTGTCAGAT 789
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGln 240
Db 790 TACCCAAAGAGATGCTTCTACTGATGATGATTCAGTTTCTCGCATTTATTGAAGA 849
QY 241 LeuProGly 243
Db 850 CTACCAAAA 858

RESULT 8
US-09-205-258-125
Sequence 125, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 1288

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1286)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-125

Alignment Scores:
Pred. No.:      8,09e-124      Length:      1288
Score:          1258.50       Matches:      240
Percent Similarity: 99.18%    Conservative: 1
Best Local Similarity: 98.77%  Mismatches:     2
Query Match:    96.73%       Indels:       1
DB:             Gaps:        0

US-10-063-734-122 (1-243) x US-09-205-258-125 (1-1288)
QY      1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
      |||
Db      130 ATGCCAGCCCAAGGCCCCCGCCCTCCCGCAGCGGCTCCGCGCTCTCTGCTCTCTG 189
QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlu11eProlysglylysglnysala 40
      |||
Db      190 CTGCTGCACTGCGCGCGCGCTGAGCGGCTTGAGATCCCAAGGGGAAGCAAGGGCG 249
QY      41 GlnLeuArgGlnArgGluValValAlaPleuTyraArgGlyMetCysLeuGlnGlyProAla 60
      |||
Db      250 C--ATCCGCGAGGGAGGAGGTGTGAGACTGTATATATGGAATGTCTTACAGGGCCAGCA 307
QY      61 GlyValProGlyYArgAAspGlySerProGlyYAlaAsnVal11eProGlyThrProGlyIle 80
      |||
Db      308 GAGATCTCTGTGTGACACGGAGACCTTGCGGCAATGCGATTCCGGGTACACCTGGGATC 367
QY      81 ProGlyYArgAAspGlyPheLeuysglylylysglylyCysLeuArgGlySerPheGlnGlu 100
      |||
Db      368 CAGGCTCGGAGATGATTCAAGAGAGAAAGGGGAATGTCTGAGGAAAGCTTGAAGAG 427
QY      101 SerTyrThrProAsnTyrllysglnCysSerTyrSerSerLeuAsnTyrllyleuPleu 120
      |||
Db      428 TCCTGACACACCAACTACAGAGGTGTATGAGATTCATTTGAATATGCAATAGATCTT 487
QY      121 GlyLyIleAlaGluCysThrPheThrlyMetArgSerAsnSerAlaLeuArgValLeu 140
      |||
Db      488 GGGAAATATTCGAGATGATACATTACAGATCGTTCAATATGCTCTTAAGAGTTTG 547
QY      141 PheSerGlySerLeuArgLeuysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
      |||
Db      548 TTCAAGTGGCTCACTTGGGCTAAATACAGAAATGCATGCTGTCAGGTTGATTTCA 607
QY      161 PheArgGlyAlaGluCysSerGlyProLeuPro11eGluAla11eIleTyrlleuAspGln 180
      |||
Db      608 TTCAATGGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTAATTTATTTGGACAA 667
QY      181 GlySerProGlnMetArgSerThr11eAsn11eHisArgThrSerSerVal11eGluTyru 200
      |||
Db      668 GGAAGGCTCGAATTAATTAACAATTAATTAATTCATTCGACTTCTTGAGAGGACTT 727
QY      201 CysGlnGly11eGlyAlaGlyLeuValAlaPleuVal11eIleTyrllyGlyThrCysSerAsp 220
      |||
Db      728 TGTGAAGGAATGTGTCTGTGATTAAGTGTGATGTTGCTATCTGGGTTGGCACTTGTCA 787
QY      221 TyrProLysglyAspAlaSerThrGlyTyrPAsnSerValSerArg11eIle11eGluGlu 240
      |||
Db      788 TACCCCAAAAGAGATCTTCTACTGATGGAATTCAGTTTCTGCACTATTAATGAAGAA 847
QY      241 LeuProLyse 243
      |||
Db      848 CTACCAAAA 856

RESULT 9
US-09-692-081-1
; Sequence 1, Application US/09692081
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; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhart
; APPLICANT: FRIESEL, Robert F.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-692-081-1

Alignment Scores:
Pred. No.:      2.31e-119      Length:      1192
Score:          1216.00       Matches:      231
Percent Similarity: 95.51%    Conservative: 3
Best Local Similarity: 94.29%  Mismatches:     9
Query Match:    93.47%       Indels:       2
DB:             Gaps:        1

US-10-063-734-122 (1-243) x US-09-692-081-1 (1-1192)
QY      1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGly-----LeuLeuLeu 18
      |||
Db      97 ATGACACCCCAAGGCGCGCCCTCCCAAGCTGCTGCTGCTCTCTCTGTGTGCTA 156
QY      19 LeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGlu11eProlysglylysgln 38
      |||
Db      157 CTGCTCTCTGTGAGCTGTCCCGCGCTTCAAGCGCTTGTGAATATCCAAAGTGAAGCAA 216
QY      39 LyAlaGlnLeuArgGlnArgGluValValAlaPleuTyraArgGlyMetCysLeuGlnGly 58
      |||
Db      217 AAAGCGCTATCCGAGAGGGAAGTGTAGACTGTATATATGGAATGTGCTTACAAAGGA 276
QY      59 ProAlaGlyValProGlyYArgAAspGlySerProGlyYAlaAsnVal11eProGlyThrPro 78
      |||
Db      277 CAGAGGAGATTCGTGTGTGATGAGATGAGACCTGGGGCAATGCGCAATTCGACACCG 336
QY      79 GlyIleProGlyYArgAAspGlyPheLeuysglylylysglylyCysLeuArgGlySerPhe 98
      |||
Db      337 GGAATCCAGCTGCGGATGATTAACAAGAGAGAAAGGGAATGCTTAAGGAAAGCTTT 396
QY      99 GlnGluSerTyrThrProAsnTyrllysglnCysSerTyrSerSerLeuAsnTyrllyle 118
      |||
Db      397 GAGGAATCCCTGGAGCCCAACTACAGAGGTGTATGAGATTCATTAATATATGCAATA 456
QY      119 AspLeuGlyLyse11eAlaGluCysThrPheThrlyMetArgSerAsnSerAlaLeuArg 138
      |||
Db      457 GATCTTGGGAAATATTCGGAATGTATCATTAACAAGATCGATCCAAAGCGCTTTCGA 516
QY      139 Val11eLeuPheSerGlySerLeuArgLeuysCysArgAsnAlaCysCysGlnArgTyrPhe 158
      |||
Db      517 GTTCTGTAGTGGCTCGCTTGGCTCAATATGAGAAATGCTTGTGTAAGCGCTGTAT 576
QY      159 PheThrPheAsnGlyValaGluCysSerGlyProLeuPro11eGluAla11eIleTyrlleu 178
      |||
Db      577 TTTAACCTTTAATGAGACTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATCATCTAT 636
QY      179 AspGlnGlySerProGlnMetArgSerThr11eAsn11eHisArgThrSerSerVal11eGlu 198
      |||
Db      637 GACCAAGGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 696
QY      199 GlyLeuCysGlnGly11eGlyAlaGlyLeuValAlaPleuVal11eIleTyrllyGlyThrCys 218
      |||
Db      697 GGACTGTGAAGGATGTGTGTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 756
QY      219 SerAspTyrllyProLyse11eAspAlaSerThrGlyTyrPAsnSerValSerArg11eIle 238
      |||
Db      757 TCAGATTAACCCCAAGAGAGACGCTTCTACTGAGTGAATTTGTGTGTCCGCAATCATCAT 816
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DB 42 ACCTGTCAGATTACCCCAAGAGACGCTTCACTGCGTGG 1
RESULT 12
US-09-222-575-63/C
; Sequence 63, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-63
Alignment Scores:
Pred. No.: 3,586-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 3 Gaps: 0
US-10-063-734-122 (1-243) x US-09-222-575-63 (1-683)
QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGCGTTCAATAGCTCTAAGAGTTTGTTCAGTGGCTCATTCCG 624
QY 147 LeuLysCyArgAsnAlaCySCysGlnArgTyrPheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACAGAAATGATGCTGTCAGCGTGTATTCATTCAATGAGAGCTGATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCACTGATGAAGTAAATTAATTGACCAAGAAAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCySGluGlyIleGlyAla 206
DB 503 TCACAAATTAAATTCATGCGACTTCTCTGTGGAAGACTTTGTGAAGAAATGGTCT 444
QY 207 GlyLeuValAspValAlaIleTyrPValGlyThrCysSerAspTyrProLysGlyAspAla 226
DB 443 GGATTAAGTGAATGTTCTATCTCGGTGGVACTTGTTCAGATTACCCAAAGAGATGCT 384
QY 227 SerThrGlyTTPAsnSerValSerArgIleIleIleGluGluLeuProLys 243
DB 383 TCTACTGATGAGAAATTCAGTTCTCGVATCATTATTAAGAAACTACCAAAA 333
RESULT 13
US-09-389-681-63/C
; Sequence 63, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
```

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; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-63
Alignment Scores:
Pred. No.: 3,586-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0
US-10-063-734-122 (1-243) x US-09-389-681-63 (1-683)
QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGCGTTCAATAGCTCTAAGAGTTTGTTCAGTGGCTCATTCCG 624
QY 147 LeuLysCyArgAsnAlaCySCysGlnArgTyrPheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACAGAAATGATGCTGTCAGCGTGTATTCATTCAATGAGAGCTGATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCACTGATGAAGTAAATTAATTGACCAAGAAAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCySGluGlyIleGlyAla 206
DB 503 TCACAAATTAAATTCATGCGACTTCTCTGTGGAAGACTTTGTGAAGAAATGGTCT 444
QY 207 GlyLeuValAspValAlaIleTyrPValGlyThrCysSerAspTyrProLysGlyAspAla 226
DB 443 GGATTAAGTGAATGTTCTATCTCGGTGGVACTTGTTCAGATTACCCAAAGAGATGCT 384
QY 227 SerThrGlyTTPAsnSerValSerArgIleIleIleGluGluLeuProLys 243
DB 383 TCTACTGATGAGAAATTCAGTTCTCGVATCATTATTAAGAAACTACCAAAA 333
RESULT 14
US-09-620-405B-63/C
; Sequence 63, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.47008
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-63
Alignment Scores:
Pred. No.: 3,586-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0
```

US-10-063-734-122 (1-243) x US-09-620-405B-63 (1-683)

QY 127 ThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGGCTTAAATAGTCTTAAGAGTTTGTTCATGTGCTCACTTCGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACGAATCATGCTCTCAGCGTTGGATTTCATTCATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCATTTGAAGCTAAATATTATTGACCAAGAAAGCCCTGAATGAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuProlGlyVala 206
DB 503 TCACACATTATATATTCATGCACTTCTTCGTGGAAGAGCTTGTGAAGAAATGGTGT 444

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCysSerAspTyProLysGlyAspAla 226
DB 443 GGATTAGTGATGTCTATCTGTGGTGGYACTTGTTCAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlGly 243
DB 383 TCTACGTGATGGAATTCAGTTCTCTGATCATTTATTGAAGAACTACCAAA 333

RESULT 15
US-09-339-338-63/c
; Sequence 63, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yungui, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-63

Alignment Scores:
Pred. No.: 3.58e-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-339-338-63 (1-683)

QY 127 ThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGGCTTAAATAGTCTTAAGAGTTTGTTCATGTGCTCACTTCGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACGAATCATGCTCTCAGCGTTGGATTTCATTCATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCATTTGAAGCTAAATATTATTGACCAAGAAAGCCCTGAATGAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuProlGlyVala 206
DB 503 TCACACATTATATATTCATGCACTTCTTCGTGGAAGAGCTTGTGAAGAAATGGTGT 444

DB 503 TCACACATTATATTCATGCACTTCTTCGTGGAAGAGCTTGTGAAGAAATGGTGT 444

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCysSerAspTyProLysGlyAspAla 226
DB 443 GGATTAGTGATGTCTATCTGGTGGYACTTGTTCAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlGly 243
DB 383 TCTACGTGATGGAATTCAGTTCTCTGATCATTTATTGAAGAACTACCAAA 333

RESULT 16
US-09-433-826B-63/c
; Sequence 63, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-63

Alignment Scores:
Pred. No.: 3.58e-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-433-826B-63 (1-683)

QY 127 ThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGGCTTAAATAGTCTTAAGAGTTTGTTCATGTGCTCACTTCGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACGAATCATGCTCTCAGCGTTGGATTTCATTCATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCATTTGAAGCTAAATATTATTGACCAAGAAAGCCCTGAATGAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuProlGlyVala 206
DB 503 TCACACATTATATTCATGCACTTCTTCGTGGAAGAGCTTGTGAAGAAATGGTGT 444

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCysSerAspTyProLysGlyAspAla 226
DB 443 GGATTAGTGATGTCTATCTGGTGGYACTTGTTCAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlGly 243
DB 383 TCTACGTGATGGAATTCAGTTCTCTGATCATTTATTGAAGAACTACCAAA 333

RESULT 17
US-09-604-287A-63/c
; Sequence 63, Application US/09604287A
; Patent No. 6585572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu

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; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-63

Alignment Scores:
Pred. No.: 3,58e-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-604-287A-63 (1-683)
QY 127 ThrPheThrLywMeArGSeArSeArSeArAlaLeuArGValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGGCTCAATATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 147 LeuLySvCyArGAsnAlaCySvGlnArGTPTrPheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGCGAAGATGATGCTGCTGAGCCGTGGTATTTCCATTCATGAGCTGATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyrrLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTTCCATTCAGCTATTAATTTATTTGACCAAGAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCySvGlnGlyIleGlyAla 206
DB 503 TCACATTAATTAATTCATGCACTTCTCTGCGAAGACTTTGTGAAGAAATGGTGCT 444
QY 207 GlyLeuValAspValAlaIleTPValGlyThrCySvSerAspTyrrProLySGlyAspAla 226
DB 443 GGATTAGTGATGCTGCTATCTGCGTGGTGGYACTTGTCAGATTACCAAAAGAGATGCT 384
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProLyS 243
DB 383 TCTACTGATGAGATTCAGATTCTCGATCATTAATGAGAACTACCAAAA 333

RESULT 18
US-09-285-480-63/C
; Sequence 63, Application US/09285480
; GENERAL INFORMATION:
; APPLICANT: Yuqin, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.47001
; CURRENT APPLICATION NUMBER: US/09/285,480
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-285-480-63
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; Alignment Scores:
Pred. No.: 3,58e-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-285-480-63 (1-683)
QY 127 ThrPheThrLywMeArGSeArSeArSeArAlaLeuArGValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGGCTCAATATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 147 LeuLySvCyArGAsnAlaCySvGlnArGTPTrPheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGCGAAGATGATGCTGCTGAGCCGTGGTATTTCCATTCATGAGCTGATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyrrLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTTCCATTCAGCTATTAATTTATTTGACCAAGAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCySvGlnGlyIleGlyAla 206
DB 503 TCACATTAATTAATTCATGCACTTCTCTGCGAAGACTTTGTGAAGAAATGGTGCT 444
QY 207 GlyLeuValAspValAlaIleTPValGlyThrCySvSerAspTyrrProLySGlyAspAla 226
DB 443 GGATTAGTGATGCTGCTATCTGCGTGGTGGYACTTGTCAGATTACCAAAAGAGATGCT 384
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProLyS 243
DB 383 TCTACTGATGAGATTCAGATTCTCGATCATTAATGAGAACTACCAAAA 333

RESULT 19
US-09-834-759-63/C
; Sequence 63, Application US/09834759
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqin
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-834-759-63

Alignment Scores:
Pred. No.: 3,58e-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-63 (1-683)
QY 127 ThrPheThrLywMeArGSeArSeArSeArAlaLeuArGValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGGCTCAATATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
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Db 623 CCCAGGCTGTGCTGTGAGCTGAGCCCTGCGCCCTGCTGTGCT-GGCCCTGC 681
QY 60 aGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 682 TGGAAACCTGCTGTGATGACAGCCTGTGCTTAAAGGCCAATGCTCTCTGTAT 741
QY 80 eProGlyArgAspGlyPheIysGlyGluCysLeuArgGluSerPheGluG1 100
Db 742 TGTGTGCTCTCCGCTGCTCTCCCTGTGCTGCGAGGC-----CC 777
QY 100 uSerThrProAsnThrIysGlyGlnCysSerThrSer 112
Db 778 CTC-TGACCCCAAGGCCCGCGGCTCTCTGTCTC 813
RESULT 24
US-09-169-768-13
; Sequence 13, Application US/09169768
; Patent No. 6492508
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
; APPLICANT: BROCHTER, DOUGLAS
; APPLICANT: BROKAW, JANE
; APPLICANT: ZHANG, GUANGHUI
; APPLICANT: PAOLELLA, DAVID
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILMORTH & BARRESE
; STREET: 333 EARLE OVINGTON BOULEVARD
; CITY: UNIONDALE
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 11553
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/169,768
; APPLICATION NUMBER: US/09/169,768
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEN, JEFFREY S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 228-8484
; TELEFAX: (516) 228-8516
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-09-169-768-13
Alignment Scores:
Pred. No.: 0.00173 Length: 3349
Score: 129.50 Matches: 43
Percent Similarity: 49.56% Conservative: 13
Best Local Similarity: 38.05% Mismatches: 36
Query Match: 9.95% Indels: 23
Gaps: 4
US-10-063-734-122 (1-243) x US-09-169-768-13 (1-3349)
QY 3 ProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeu-LeuLeuLeuLeuLeu 22
Db 542 CCCACCGGCCCCGCTGTCTCTCT-----GGCTTCCCTGTGCTGTGTGTCT 589
QY 22 uGlnLeuProAlaProSerSerAlaSerGluIleProIysGlyIysGlnIleAlaGlnLe 42
Db 590 AAGGCTGAAGCTG-----GTCCCAAGGCGCCCGAGGCTCTGAAGCT 631

QY 42 uArgGlnArgGluValValAlaPheLeu-----TyrAsnGlyMetCysLeuGlnGlyProAl 60
Db 632 CCCAGGCTGTGCTGTGAGCCTTGCCCCCTGCGCCCTGCTGTGCTGTCT-GGCCCTGC 690
QY 60 aGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 691 TGGAAACCTGCTGTGATGACAGCCTGTGCTTAAAGGCCAATGCTCTCTGTAT 750
QY 80 eProGlyArgAspGlyPheIysGlyGluCysLeuArgGluSerPheGluG1 100
Db 751 TGTGTGCTCTCCGCTGCTCTCCCTGTGCTGCGAGGC-----CC 786
QY 100 uSerThrProAsnThrIysGlyGlnCysSerThrSer 112
Db 787 CTC-TGACCCCAAGGCCCGCGGCTCTCTGTCTC 822
RESULT 25
US-09-169-768-7
; Sequence 7, Application US/09169768
; Patent No. 6492508
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
; APPLICANT: BROCHTER, DOUGLAS
; APPLICANT: BROKAW, JANE
; APPLICANT: ZHANG, GUANGHUI
; APPLICANT: PAOLELLA, DAVID
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILMORTH & BARRESE
; STREET: 333 EARLE OVINGTON BOULEVARD
; CITY: UNIONDALE
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 11553
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/169,768
; APPLICATION NUMBER: US/09/169,768
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEN, JEFFREY S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 228-8484
; TELEFAX: (516) 228-8516
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-09-169-768-7
Alignment Scores:
Pred. No.: 0.00187 Length: 3531
Score: 129.50 Matches: 43
Percent Similarity: 49.56% Conservative: 13
Best Local Similarity: 38.05% Mismatches: 36
Query Match: 9.95% Indels: 23
Gaps: 4
US-10-063-734-122 (1-243) x US-09-169-768-7 (1-3531)
QY 3 ProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeu-LeuLeuLeuLeuLeu 22
Db 542 CCCACCGGCCCCGCTGTCTCTCT-----GGCTTCCCTGTGCTGTGTGTCT 589

QY 226 aSerThrglyTPaNsErValSerArgIlelleIleGlulnleuPro 242
DB 601 GAGCTCCGGGTGACCTCGTGAAGGCAACACAGTTTGGCA 649
RESULT 31
US-08-555-669-11
Sequence 11, Application US/08555669
Patent No. 5773248
GENERAL INFORMATION:
APPLICANT: Brewton, Richard G.
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,669
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3694
TELEFAX: 415-854-3660
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 47..2098
US-08-555-669-11
Alignment Scores:
Pred. No.: 0.0116 Length: 2543
Score: 120.00 Matches: 43
Percent Similarity: 38.40% Conservative: 5
Best Local Similarity: 34.40% Mismatches: 33
Query Match: 9.22% Indels: 45
DB: 1 Gaps: 5
US-10-063-734-122 (1-243) x US-08-555-669-11 (1-2543)
QY 6 ProAla1aSerProGln---ArgLeuArgGly----- 15
DB 11 CCCGCCCGGAGCGGCGGCTCAGGCAATGCGGCGCGCGCGCGCGCG 70
QY 16 -----LeuLeuLeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluIle 33
DB 71 CCGCTCTGCTCTCTCTCTCTCTCTCGGCGGCACTTCTGGCGCGCGCGGCGGCGGAGAGATG 130
QY 34 ProlysglyLysGlnLysAlaGlnLeuArgGlnArgGlnValAlaPleuTyraGly 53
DB 131 GGA----- 133
QY 54 MetCysLeuGlnGlyProAlaGlyValProGlyLysArgPleuTyraGlyValAlaSerVal 73

DB 134 -----CTCCCCGGCCCCCGGCCCCCGGCGGCGCTTGGAAAGCCCGGCGAGAGCC 187
QY 74 Ile-----ProGlyThrProGlyIleProGlyLysArgPleuTyraGly 87
DB 188 ATTGAACGAGAGAGCTGTCTCTCAGCTCGTCCCGGAGACCAAGGGGGCCCA 247
QY 88 GlyGlyLysGlyGlnCysLeuArgGlnSerIleGluGlnSerTyrPheArgIleTyLys 107
DB 248 GGAAGGCC-GGGGAAACAGAGGA-----GGCTGGCTCGCGGAGACTGCC 291
QY 108 GlnCysSerTyrSer 112
DB 292 GGGTGTGATGTCT 306
RESULT 32
US-09-073-663-11
Sequence 11, Application US/09073663
Patent No. 6127523
GENERAL INFORMATION:
APPLICANT: Brewton, Richard G.
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 8.1
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,663
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5913D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 47..2098
US-09-073-663-11
Alignment Scores:
Pred. No.: 0.0116 Length: 2543
Score: 120.00 Matches: 43
Percent Similarity: 38.40% Conservative: 5
Best Local Similarity: 34.40% Mismatches: 33
Query Match: 9.22% Indels: 45
DB: 3 Gaps: 5
US-10-063-734-122 (1-243) x US-09-073-663-11 (1-2543)
QY 6 ProAla1aSerProGln---ArgLeuArgGly----- 15
DB 11 CCCGCCCGGAGCGGCGGCTCAGGCAATGCGGCGCGCGCGCGCGCG 70
QY 16 -----LeuLeuLeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluIle 33


```
OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer bind
LOCATION: 3788..3806
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer bind
LOCATION: 11099..11117
OTHER INFORMATION: 99-14387-129.mis
NAME/KEY: primer bind
LOCATION: 11119..11137
OTHER INFORMATION: 99-14387-129.mis complement
NAME/KEY: primer bind
LOCATION: 15101..15119
OTHER INFORMATION: 9-12-48.mis
NAME/KEY: primer bind
LOCATION: 15121..15139
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer bind
LOCATION: 15177..15195
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer bind
LOCATION: 15197..15215
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer bind
LOCATION: 15428..15446
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer bind
LOCATION: 15481..15499
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer bind
LOCATION: 15501..15519
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: 15844..15862
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer bind
LOCATION: 15864..15882
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer bind
LOCATION: 17151..17169
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer bind
LOCATION: 17171..17189
OTHER INFORMATION: 9-16-189.mis complement
US-09-776-976-7

Alignment Scores:
Pred. No.: 0.279 Length: 20966
Score: 120.00 Matches: 61
Percent Similarity: 39.41% Conservative: 19
Best Local Similarity: 30.05% Mismatches: 66
Query Match: 9.22% Indels: 59
DB: 4 Gaps: 11

US-10-063-734-122 (1-243) x US-09-776-976-7 (1-20966)
QY 13 LeuArgGlyLeuLeu-----LeuLeuLeuGlnLeuPro----- 25
Db 15146 CTCGAGTGTCTGTGGGAGCTGTTCTACTGCTATTAGCTCCCGGKATGACGAG 15205
QY 26 -----AlaProSerSerLaserGlnLleProLysGlyLysGlnLysAla 40
Db 15206 GAAACCAAGACTCAAGGCGCGAGTCTGCTCTCCCTGCCAAG----- 15250
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 15251 -----GGGCGCTGCACAGCGTTGGATGCG 15274
QY 61 GlnValProGlyValArgAspGlySerProGlyValAsnValLleProGlyThrProGlyTle 80
Db 15275 GGCATCCACAGGCGAT-----CCGGGCGCATTAAT-----GGGCGCCACAGGCGCGT 15316
```

```
QY 81 ProGlyArgAspGlyPheLysGlyGlnLysGlyGlnLysGlyGlnLysGlyGlnLysGlyGln 100
Db 15317 GATGCGAAGATGGGACCCCTGTGGAGAGGGTAAAGAA-AGGAGATCCAGTAAGATATG 15375
QY 101 SerTPTrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyr----- 116
Db 15376 TTCTGG-----CTCTTTTATCAAGACTCTTCACTGATTTAACTTAAAGAAKCAATTC 15432
QY 117 -----GlyLleAspLeuGlyLysLleAlaGlnLysGlySerThrLysMetArg 132
Db 15433 ATTATTAACTAAGGCGCTGACACAGGAGAAA-GCAAGCTTTTATTATGTT----- 15482
QY 133 SerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuTyrCysAlaGlnAla 152
Db 15483 AACCATTAAGCAACTGARGTATTGGGGTGGCTTCCACAGATGAGTGTAGA---TGG 15539
QY 153 CysCysGlnArgTyrPheThrPheAsnGlyValaGlnCysSerGlyProLeuProIle 172
Db 15540 TGCCCTATTAACCAAGACTTGGCTTTCGATCGACCTCTTTCATTCCTCCTTTC 15599
QY 173 GluAlaIleTyrLeuAspGlnGlySerProGlnLysSerThrIleAsnLleHis 192
Db 15600 CCATCT-----TCACCC-----TCATCCCTATTCCAGTACAT 15632
QY 193 ArgThrSer 195
Db 15633 TCATATTCT 15641

RESULT 34
US-09-909-547-7
Sequence 7, Application US/09909547
Patent No. 6579852
GENERAL INFORMATION:
APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Binafin, Bernard
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76 Use, CIP
CURRENT FILING DATE: US/09/909,547
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/176,228
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent .pm
SEQ ID NO 7
LENGTH: 20966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..4811
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 4812..4851
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 15144..15365
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 16277..20559
OTHER INFORMATION: exon 3
NAME/KEY: misc feature
LOCATION: 20560..20966
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OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 3787
OTHER INFORMATION: 9-27-261 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 11118
OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 15120
OTHER INFORMATION: 9-12-48 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15196
OTHER INFORMATION: 9-12-124 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15427
OTHER INFORMATION: 9-12-355 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15500
OTHER INFORMATION: 9-12-428 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 15863
OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17170
OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
NAME/KEY: primer bind
LOCATION: 3528..3545
OTHER INFORMATION: 9-27.pu
NAME/KEY: primer bind
LOCATION: 3928..3946
OTHER INFORMATION: 9-27.rp complement
NAME/KEY: primer bind
LOCATION: 10990..11008
OTHER INFORMATION: 99-14387.pu
NAME/KEY: primer bind
LOCATION: 11423..11442
OTHER INFORMATION: 99-14387.rp complement
NAME/KEY: primer bind
LOCATION: 15073..15092
OTHER INFORMATION: 9-12.pu
NAME/KEY: primer bind
LOCATION: 15503..15520
OTHER INFORMATION: 9-12.rp complement
NAME/KEY: primer bind
LOCATION: 15759..15776
OTHER INFORMATION: 99-14405.pu
NAME/KEY: primer bind
LOCATION: 16191..16211
OTHER INFORMATION: 99-14405.rp complement
NAME/KEY: primer bind
LOCATION: 16982..17001
OTHER INFORMATION: 9-16.pu
NAME/KEY: primer bind
LOCATION: 17384..17402
OTHER INFORMATION: 9-16.rp complement
NAME/KEY: misc binding
LOCATION: 3775..3799
OTHER INFORMATION: 9-27-261.probe
NAME/KEY: misc binding
LOCATION: 15184..15208
OTHER INFORMATION: 9-12-124.probe
NAME/KEY: misc binding
LOCATION: 15415..15439
OTHER INFORMATION: 9-12-355.probe
NAME/KEY: misc binding
LOCATION: 15488..15512
OTHER INFORMATION: 9-12-428.probe

NAME/KEY: misc binding
LOCATION: 15851..15875
OTHER INFORMATION: 99-14405-105.probe
NAME/KEY: misc binding
LOCATION: 17158..17182
OTHER INFORMATION: 9-16-189.probe
NAME/KEY: primer bind
LOCATION: 3768..3786
OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer bind
LOCATION: 3788..3806
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer bind
LOCATION: 11099..11117
OTHER INFORMATION: 99-14387-129.mis
NAME/KEY: primer bind
LOCATION: 11119..11137
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: 15101..15119
OTHER INFORMATION: 9-12-48.mis
NAME/KEY: primer bind
LOCATION: 15121..15139
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer bind
LOCATION: 15177..15195
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer bind
LOCATION: 15197..15215
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer bind
LOCATION: 15408..15426
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer bind
LOCATION: 15428..15446
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer bind
LOCATION: 15481..15499
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer bind
LOCATION: 15501..15519
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: 15844..15862
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer bind
LOCATION: 15864..15882
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer bind
LOCATION: 17151..17169
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer bind
LOCATION: 17171..17189
OTHER INFORMATION: 9-16-189.mis complement

US-09-909-547-7

Alignment Scores:

	Pred. No.:	Length:	Score:
DB:	4	20966	120.00
		Matches:	61
		Conservative:	19
		Mismatches:	66
		Indels:	59
		Gaps:	11

US-10-063-734-122 (1-243) x US-09-909-547-7 (1-20966)

QY 13 leuATGgLyLeuLeu-----leuLeuLeuGlnLeuPro----- 25
DB 15146 CTCAGAGTCTGTGCTGGAGCTGTTCTACTGCTATTGACTCTGCGCCGKATGACG 15205
QY 26 -----AlaProSerSerAlaSerGlnIleProLyGlyLysGlnYala 40
DB 15206 GAAACAGACGTCAGAGCGCCGAGTCTGCTTCCCTGCCAAG----- 15250

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OY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 15251 -----GGGGCCCTGGCACAGTTGGATGGCG 15274
OY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 15275 GGCATCCCGAGGCAT-----CCGGGCCATATAT-----GGGGCCCGACGGCCCGT 15316
OY 81 ProGlyArgAspGlyPheLeuGlyGlyGluGluCysLeuArgGluSerPheGluGlu 100
Db 15317 GATGGCAGATGGCACCCCTGGTGGAGAGGTGAGAA-AGCAGATCCAGTAAAGATGT 15375
OY 101 SerThrProAsnTyrGlyGlyGlySerThrSerSerLeuAsnTyr----- 116
Db 15376 TTCTGG---CCTCTTTCATCAGACGACCTCTACATGATATATATGAAAGKATTC 15432
OY 117 -----GlyLeuAspLeuGlyGlyGluGluCysThrPheThrIleMetArg 132
Db 15433 ATTATTAATAAGGCTTACACAGGAGGAGAA-GCAAACTTTTATATTT----- 15482
OY 133 SerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuGlyCysArgAsnAla 152
Db 15483 AACCATAGCAACCTGATGATTTGGGCTTCTTCCAGAGATGAGTGA---TGG 15539
OY 153 CysCysGlnArgTyrPheThrPheAsnGlyAlaGluCysSerGlyProLeuProIle 172
Db 15540 TGCCCTATTAACCAAGACTTGGCTTGTGCATCTGCAGATCCCTTTCCATCCCTTTC 15599
OY 173 GluAlaIleIleTyrLeuAspGlnGlySerProGluMetAsnSerThrIleAsnIleHis 192
Db 15600 CCATCT-----TACCC-----TCATCCTATATCCAGTACAT 15632
OY 193 ArgThrSer 195
Db 15633 TCATATCT 15641

RESULT 35
US-09-569-852B-1
: Sequence 1, Application US/09569852B
: Patent No. 6582909
: GENERAL INFORMATION:
: APPLICANT: Bouquelere, Lydie
: APPLICANT: Demoin, Blake
: APPLICANT: Bihaïn, Bernard
: APPLICANT: Yen-Pocin, Frances
: TITLE OF INVENTION: APM1 Biallelic Markers and Uses Thereof
: FILE REFERENCE: GEN-T113XC2
: CURRENT APPLICATION NUMBER: US/09/569,852B
: CURRENT FILING DATE: 2002-03-12
: PRIOR APPLICATION NUMBER: PCT/IB99/01858
: PRIOR FILING DATE: 1999-11-04
: PRIOR APPLICATION NUMBER: US 09/434,848
: PRIOR FILING DATE: 1999-11-04
: PRIOR APPLICATION NUMBER: US 60/119,593
: PRIOR FILING DATE: 1999-02-10
: PRIOR APPLICATION NUMBER: US 60/107,113
: PRIOR FILING DATE: 1998-11-04
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 20966
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)..(4811)
: OTHER INFORMATION: 5' regulatory region
: NAME/KEY: primer bind
: LOCATION: (14683)..(14701)
: OTHER INFORMATION: 17-34-860.mis
: NAME/KEY: primer bind
: LOCATION: (14703)..(14721)

OTHER INFORMATION: 17-34-860.mis complement
NAME/KEY: primer bind
LOCATION: (14728)..(14756)
OTHER INFORMATION: 17-34-915.mis
NAME/KEY: primer bind
LOCATION: (14758)..(14776)
OTHER INFORMATION: 17-34-915.mis complement
NAME/KEY: primer bind
LOCATION: (14796)..(14814)
OTHER INFORMATION: 17-35-71.mis
NAME/KEY: primer bind
LOCATION: (14816)..(14834)
OTHER INFORMATION: 17-35-71.mis complement
NAME/KEY: primer bind
LOCATION: (15031)..(15049)
OTHER INFORMATION: 17-35-306.mis
NAME/KEY: primer bind
LOCATION: (15051)..(15069)
OTHER INFORMATION: 17-35-306.mis complement
NAME/KEY: primer bind
LOCATION: (15101)..(15119)
OTHER INFORMATION: 9-12-48.mis
NAME/KEY: primer bind
LOCATION: (15121)..(15139)
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer bind
LOCATION: (15177)..(15195)
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer bind
LOCATION: (15197)..(15215)
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer bind
LOCATION: (15408)..(15426)
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer bind
LOCATION: (15428)..(15446)
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer bind
LOCATION: (15481)..(15499)
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer bind
LOCATION: (15501)..(15519)
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: (15661)..(15679)
OTHER INFORMATION: 17-36-47.mis
NAME/KEY: primer bind
LOCATION: (15681)..(15699)
OTHER INFORMATION: 17-36-47.mis complement
NAME/KEY: primer bind
LOCATION: (15771)..(15789)
OTHER INFORMATION: 17-36-120.mis
NAME/KEY: primer bind
LOCATION: (15791)..(15809)
OTHER INFORMATION: 17-36-120.mis complement
NAME/KEY: primer bind
LOCATION: (15844)..(15862)
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer bind
LOCATION: (15864)..(15882)
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer bind
LOCATION: (17151)..(17169)
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer bind
LOCATION: (17171)..(17189)
OTHER INFORMATION: 9-16-189.mis complement
NAME/KEY: primer bind
LOCATION: (17810)..(17828)
OTHER INFORMATION: 17-37-629.mis
NAME/KEY: primer bind
LOCATION: (17830)..(17848)
OTHER INFORMATION: 17-37-629.mis complement
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NAME/KEY: primer_bind
LOCATION: (17992)..(18010)
OTHER INFORMATION: 17-37-811.mis
NAME/KEY: primer_bind
LOCATION: (18012)..(18030)
OTHER INFORMATION: 17-37-811.mis complement
NAME/KEY: primer_bind
LOCATION: (18470)..(18488)
OTHER INFORMATION: 17-38-349.mis
NAME/KEY: primer_bind
LOCATION: (18490)..(18508)
OTHER INFORMATION: 17-38-349.mis complement
NAME/KEY: primer_bind
LOCATION: (926)..(944)
OTHER INFORMATION: 17-30-216.mis
NAME/KEY: primer_bind
LOCATION: (946)..(964)
OTHER INFORMATION: 17-30-216.mis complement
NAME/KEY: primer_bind
LOCATION: (3719)..(3737)
OTHER INFORMATION: 9-27-211.mis
NAME/KEY: primer_bind
LOCATION: (3739)..(3757)
OTHER INFORMATION: 9-27-211.mis complement
NAME/KEY: primer_bind
LOCATION: (3754)..(3772)
OTHER INFORMATION: 9-27-246.mis
NAME/KEY: primer_bind
LOCATION: (3774)..(3792)
OTHER INFORMATION: 9-27-246.mis complement
NAME/KEY: primer_bind
LOCATION: (3768)..(3786)
OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer_bind
LOCATION: (3788)..(3806)
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer_bind
LOCATION: (5076)..(5094)
OTHER INFORMATION: 17-31-298.mis
NAME/KEY: primer_bind
LOCATION: (5096)..(5114)
OTHER INFORMATION: 17-31-298.mis complement
NAME/KEY: primer_bind
LOCATION: (5191)..(5209)
OTHER INFORMATION: 17-31-413.mis
NAME/KEY: primer_bind
LOCATION: (5211)..(5229)
OTHER INFORMATION: 17-31-413.mis complement
NAME/KEY: primer_bind
LOCATION: (5364)..(5382)
OTHER INFORMATION: 17-31-413.mis complement
NAME/KEY: primer_bind
LOCATION: (10618)..(10636)
OTHER INFORMATION: 17-32-24.mis
NAME/KEY: primer_bind
LOCATION: (10638)..(10656)
OTHER INFORMATION: 17-32-24.mis complement
NAME/KEY: primer_bind
LOCATION: (11020)..(11038)
OTHER INFORMATION: 99-14387-50.mis
NAME/KEY: primer_bind
LOCATION: (11040)..(11058)
OTHER INFORMATION: 99-14387-50.mis complement
NAME/KEY: primer_bind
LOCATION: (11099)..(11117)
OTHER INFORMATION: 99-14387-129.mis
NAME/KEY: primer_bind
LOCATION: (11199)..(11217)
OTHER INFORMATION: 99-14387-129.mis complement
NAME/KEY: primer_bind
LOCATION: (11169)..(11187)
OTHER INFORMATION: 99-14387-199.mis
NAME/KEY: primer_bind

LOCATION: (11189)..(11207)
OTHER INFORMATION: 99-14387-199.mis complement
NAME/KEY: primer_bind
LOCATION: (13954)..(13972)
OTHER INFORMATION: 17-33-TGAGACT.mis
NAME/KEY: primer_bind
LOCATION: (13974)..(13992)
OTHER INFORMATION: 17-33-TGAGACT.mis complement
NAME/KEY: exon
LOCATION: (4812)..(4851)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (15144)..(15365)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (16277)..(20559)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (20560)..(20966)
OTHER INFORMATION: 3' regulatory region

Alignment Scores:
Pred. No.: 0.279 Length: 20966
Score: 120.00 Matches: 61
Percent Similarity: 39.41% Conservative: 19
Best Local Similarity: 30.05% Mismatches: 66
Query Match: 9.22% Indels: 59
Gaps: 11

US-10-063-734-122 (1-243) x US-09-569-852B-1 (1-20966)

QY 13 LeuArgGlyLeuLeu-----LeuLeuLeuGlnLeuPro----- 25
DB 15146 CTCAGAGCTGTGTGTGAGAGCTGTTCTACGTCTTACTGCTGCGGKATGACCG 15205
QY 26 -----AlaProSerSerAlaSerGluLeProLyseGlyGlnysAla 40
DB 15206 GAACACGACGTCACAGGCGCGAGTCGCTCCCTGCCAG----- 15250
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
DB 15251 -----GGGCGCTGCACAGCTTGATGCGG 15274
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 15275 GGCATCCAGGCGAT-----CCGGCCATTAAT-----GGGCCCCAGGCGGT 15316
QY 81 ProGlyArgAspGlyPheLyseGlyGlnGlyGlyGlyCysLeuArgGluSerPheGluGlu 100
DB 15317 GATGCGAGAGTGGCACCCCTGTGAGAGGCTGAGAA-AGGAGATCCAGGTAGATGT 15375
QY 101 SerTyrThrProAsnTyrlsGlnCysSerTyrPheSerSerLeuAsnTy----- 116
DB 15376 TTCCTG---CCTCTTTCATCAGACCTCCCTACACTGATATTAACATATGAAGCATTC 15432
QY 117 -----GlyLeaSpLeuGlyValIleAlaGluCysThrPheThrIleMetArg 132
DB 15433 ATTATTAAGTAAGGCTGACACAGGAGAAA-GCAAAAGCTTTTATATT----- 15482
QY 133 SerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgGluSerCysArgAsnAla 152
DB 15483 AACCATACCAACCTGATGTGATTTGGTGTGCTTCACAGATGACGTGAC---TGG 15539
QY 153 CysCysGlnArgTyrPheThrPheAsnGlyAlaGluCysSerGlyProLeuPheIle 172
DB 15540 TGCCTATTAACCAAGACTTGGCTTGTGCTGATGACAGCTCCCTTTCATCCCTTTC 15599
QY 173 GluAlaIleIleTyrlsLeuAspGlnGlySerProGluMetAsnSerThrIleAsnIleHis 192
DB 15600 CCATCT-----TCACCC-----TCATCCCTATTTCCAGTACAT 15632
QY 193 ArgThrSer 195
|||

STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3171 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-169-768-19

Alignment Scores:
Pred. No.: 0.0233 Length: 3171
Score: 118.50 Matches: 33
Percent Similarity: 38.46% Conservative: 23
Best Local Similarity: 36.26% Mismatches: 23
Query Match: 9.11% Indels: 33
DB: 4 Gaps: 4

US-10-063-734-122 (1-243) x US-09-169-768-19 (1-3171)
QY 3 ProGlnGlyProAlaAlaSer-----ProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 586 CCGAGGCGGCGCGGAGCGAGGCTCCAGGCGGCTCGTGT----- 630
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnVala 40
DB 631 -----GAACCGGCGCGCGCGGCG-----CCGCGCGGT----- 657
QY 41 GlnLeuArgGlnArgGlnValaValaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 658 -----GCGGCGGCGCGCGGCT-----GCGGCGGCGCGGCT 672
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 673 GGTACCTCTGCGCGGAGCGGTGAGCGAGTCCAGAAAGTGCACAGCGCGCGCGGTATT 732
QY 81 ProGlyArgAspGlyPheLeuGlyGlnValaValaValaValaValaValaValaVala 91
DB 733 GCAGGTGCACCGGCGCTTCCCGGATGCCCGCGCG 765

RESULT 39
US-08-494-168-1
Sequence 1, Application US/08494168
Patent No. 5731192
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
NUMBER OF INVENTIONS: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40397/104/BAER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(2..82, 86..97, 101..4399, 4403..4420, 4424
LOCATION: ..4465, 4469..4876, 4880..5101)
US-08-494-168-1

Alignment Scores:
Pred. No.: 0.061 Length: 5102
Score: 117.50 Matches: 42
Percent Similarity: 44.26% Conservative: 12
Best Local Similarity: 34.43% Mismatches: 27
Query Match: 9.03% Indels: 42
DB: 1 Gaps: 8

US-10-063-734-122 (1-243) x US-08-494-168-1 (1-5102)
QY 4 GlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeuGln 23
DB 1679 CAGGCGCCAGCAGGCGCTCA-----GGCTTAGTGGCGCTCTG----- 1717
QY 24 LeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnValaValaValaVala 43
DB 1718 -----GCTCTTCAAGA-----CCCAAGGAAG-----AAG 1744
QY 44 GlnArgGlnValaValaAspLeuTyrAsnGlyMet----- 54
DB 1745 GGGGAACCAATTCTAGTCAATCCAAAGATGCGAGATCGGGGTGATTCTGCTCC 1804
QY 55 ---CysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnVal 73
DB 1805 CAGGCGCTTCCGTGTATTAAGAGAACCAAGAGAGAGATACAGT----- 1855
QY 74 IleProGlyThrProGlyIleProGlyAlaAspGlyPheLeuGlyGlnValaValaVala 91
DB 1856 TTACACAGTCTGCGAGGCTTCCGGGTATGTGACAGGCTTCCCAAGTCAAAAGGGG 1915
QY 92 GluCysLeuArgGlnSerPheGlnGlnSerTyrProAsnTyrIleGlnCysSerTyr 111
DB 1916 TT-----ACCTGACTTCTGTGTAAGAAAGGCATCTCG 1950
QY 112 SerSer 113
DB 1951 TCCACC 1956
RESULT 40
US-09-227-357-51

Sequence 51, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661

EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 1333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (485)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (493)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (486)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (496)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (587)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (633)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1330)
OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-51
Alignment Scores:
Pred. No.: 0.0131 Length: 1333
Score: 115.50 Matches: 31
Percent Similarity: 53.73% Conservative: 5
Best Local Similarity: 46.27% Mismatches: 22
Query Match: 8.88% Indels: 9
DB: 3 Gaps: 3
US-10-063-734-122 (1-243) x US-09-227-357-51 (1-1333)
QY 30 AlasegtulileProlysglylysglnLysAlaGlnLeuArgGlnArgGlnValAlaasp 49
Db 146 GCCAGTGCACAAACCCCGGGTAAAT-----CAGTTGAAGAGAGAACTACTCCCC 196
QY 50 LeuTyraanglyMetCys-----LeuGlnGlyProAlaGlyValProGlyArg 65
Db 197 AGGTAT-----ACTCCAGCACTTCTGCTGCTGAGACTTCCAGGAGCCCTGGAGCA 250
QY 66 AspGlySerProGlyAlaAsnValIleProGlyThrProGlyTyrIleProGlyArgAspGly 85
Db 251 AATGTTCCCTCGGCCCCCATGTCGCGAGCGCTTCCAGAGAGATGTAGACGCGC 310
QY 86 PheTyrglyGlnTyrglyGln 92
Db 311 AGGAAAGAGAGAAAGGTGAA 331
RESULT 41
US-09-620-312D-110
Sequence 110, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan

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Best Local Similarity: 36.11% Mismatches: 47

Query Match: 8.84% Indels: 14
DB: 4 Gaps: 5
US-10-063-734-122 (1-243) x US-09-216-003A-212 (1-695)
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProLyseGlyLyseGlnLyseAlaGln 41
DB 335 TTAGACTGCCCAACCA-----GAAATTCATTGGAGAAATGTTGTGCAGTT 288
QY 42 LeuArgGlnArgGluValValAlaPleuTyR-----AsnGlyMetCysLeuGlnGlyPro 59
DB 287 TGCCCAAGCTCCCAACTGCTCTACTGCGCTCTTAATGTCAGAGACTCAAGCCCC 228
QY 60 AlaGlyValProGlyValArgAspGlySerProGlyValAlaSerValIleProGlyThrProGly 79
DB 227 AAGGGAGATCCAGGCCCTCTGATATTCCTGGAGAAATGTGACCTGTGATTCAGGA 168
QY 80 IleProGlyValArgAspGlyPheLyseGlyGlyValCysLeuArgGlnSerPhe--- 98
DB 167 CAACCAAGGATCCCTGTTCTCTGCGCCCCCTGGAATCTG-----GAATCATGCCCT 114
QY 99 -----GluGlnSerTrpThrProAsnTyRlyseGlnCysSerTrpSerSerLeuAsnTyR 116
DB 113 ACTGATCTCAGAACTATCTCTCCCAATGATTCATATGATGTCAGTCT----- 63
QY 117 GlyIleAspLeuGlyLyseIleAla 124
DB 62 GGAGTAGCAGTAGAGAGACTCGCA 39
RESULT 46
US-09-667-857-212/c
; Sequence 212, Application US/09667857
; Patent No. 669664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Piling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.46205
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 212
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(695)
; OTHER INFORMATION: n = A,T,C or G
US-09-667-857-212
Alignment Scores:
Pred. No.: 0.00555 Length: 695
Score: 115.00 Matches: 39
Percent Similarity: 43.52% Conservative: 8
Best Local Similarity: 36.11% Mismatches: 47
Query Match: 8.84% Indels: 14
DB: 4 Gaps: 5
US-10-063-734-122 (1-243) x US-09-667-857-212 (1-695)
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProLyseGlyLyseGlnLyseAlaGln 41
DB 335 TTAGACTGCCCAACCA-----GAAATTCATTGGAGAAATGTTGTGCAGTT 288

QY 42 LeuArgGlnArgGluValValAlaPleuTyR-----AsnGlyMetCysLeuGlnGlyPro 59
DB 287 TGCCCAAGCTCCCAACTGCTCTACTGCGCTCTTAATGTCAGAGACTCAAGCCCC 228
QY 60 AlaGlyValProGlyValArgAspGlySerProGlyValAlaSerValIleProGlyThrProGly 79
DB 227 AAGGGAGATCCAGGCCCTCTGATATTCCTGGAGAAATGTGACCTGTGATTCAGGA 168
QY 80 IleProGlyValArgAspGlyPheLyseGlyGlyValCysLeuArgGlnSerPhe--- 98
DB 167 CAACCAAGGATCCCTGTTCTCTGCGCCCCCTGGAATCTG-----GAATCATGCCCT 114
QY 99 -----GluGlnSerTrpThrProAsnTyRlyseGlnCysSerTrpSerSerLeuAsnTyR 116
DB 113 ACTGATCTCAGAACTATCTCTCCCAATGATTCATATGATGTCAGTCT----- 63
QY 117 GlyIleAspLeuGlyLyseIleAla 124
DB 62 GGAGTAGCAGTAGAGAGACTCGCA 39
RESULT 47
US-09-029-348-20
; Sequence 20, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: 0087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-20
Alignment Scores:
Pred. No.: 0.0249 Length: 1881
Score: 115.00 Matches: 39
Percent Similarity: 43.52% Conservative: 8
Best Local Similarity: 36.11% Mismatches: 47
Query Match: 8.84% Indels: 14
DB: 3 Gaps: 5
US-10-063-734-122 (1-243) x US-09-029-348-20 (1-1881)
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProLyseGlyLyseGlnLyseAlaGln 41
DB 214 TTAGACTGCCCAACCA-----GAAATTCATTGGAGAAATGTTGTGCAGTT 261
QY 42 LeuArgGlnArgGluValValAlaPleuTyR-----AsnGlyMetCysLeuGlnGlyPro 59
DB 262 TGCCCAAGCTCCCAACTGCTCTACTGCGCTCTTAATGTCAGAGACTCAAGCCCC 321
QY 60 AlaGlyValProGlyValArgAspGlySerProGlyValAlaSerValIleProGlyThrProGly 79
DB 322 AAGGGAGATCCAGGCCCTCTGATATTCCTGGAGAAATGTGACCTGTGATTCAGGA 381
QY 80 IleProGlyValArgAspGlyPheLyseGlyGlyValCysLeuArgGlnSerPhe--- 98
DB 382 CAACCAAGGATCCCTGTTCTCTGCGCCCCCTGGAATCTG-----GAATCATGCCCT 435
QY 99 -----GluGlnSerTrpThrProAsnTyRlyseGlnCysSerTrpSerSerLeuAsnTyR 116
DB 436 ACTGATCTCAGAACTATCTCTCCCAATGATTCATATGATGTCAGTCT----- 486
QY 117 GlyIleAspLeuGlyLyseIleAla 124

DB 487 GGAGTAGCAGTAGAGGACTCGCA 510
RESULT 48
US-09-181-706-1
Sequence 1, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. Dubose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a
APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
APPLICATION NUMBER: --to be assigned-- (USN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4707
US-09-181-706-1
Alignment Scores:
Pred. No.: 0.162 Length: 4707
Score: 113.00 Matches: 77
Percent Similarity: 34.54% Conservative: 28
Best Local Similarity: 25.33% Mismatches: 84
Query Match: 8.69% Indels: 116
DB: 3 Gaps: 18
US-10-063-734-122 (1-243) x US-09-181-706-1 (1-4707)
QY 2 ArgProGlnGlyProAlaIleSerProGlnArgLeuArgGlyLeuLeuLeuLeu 21
DB 31 CGCCCGCCCGCCCGCCGAGCGCCCACTGCC-----CTGCTGCGCTATCTG 75

QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuAlaGln 41
DB 76 CTGGCACTGGCGGCTCCCGCGCGCGCGAGCGCCCTGTGCGGTGCGAGCAAGCC 135
QY 42 Leu-----ArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeu 56
DB 136 ATCGAAGCATCGCGCGGAGCGAGAGAGACCGCTGTTGTGGGAGCGGCACTGCTT- 194
QY 57 GlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGly 76
DB 195 ---GGACCACTGGACTA-----CAGCTGAGACACAGCTCTCGGCGCT 236
QY 77 ThrProGlyIleProGly-----ArgAspGlyPheLeuGly---GluGlyGlyGlu 92
DB 237 GATCCGGAGCAAGCGGAGCACTGCACAGACCGGCTCTCGTGGCGCCCGCGCGGCC 296
QY 93 CysLeuArgGlu-SerPheGluGlu----- 100
DB 297 CGGCGCCGAGAGCAAGCTTCAGCAAGCTGCTGCTCCCTACCGGAGGCGCGCGCCCT 356
QY 101 -----SerTrpThrProAsnTyrIleGlnCys----- 109
DB 357 CGGCGGCTGCTGCTCACCGGCTGACCTTCAGACCGGCGCGCTGCGAGGTGCGCCCT 416
QY 110 -----SerTrpSerLeuAsnTyrGlyIleAspLeu----- 120
DB 417 GGGCAACTGAGCGCGCACTCTCGCGCAACGAGCAGAGGTGTGTCGCCACCGCGCA 476
QY 121 -GlyLeuIleAlaGluCysThrPheThrIleValMetArgSerAsnSerAlaLeuArgVal 140
DB 477 GGGCTCGAGCGCGCGCTGTGTGTACCGCGCGCGCGGACCAAC----- 519
QY 140 uPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpThrPhe 160
DB 520 -----CGCTGCTAC----- 528
QY 160 rPheAsnGlyValaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspG 180
DB 529 -----CTGGCGGTGCGCGCCACCTACGTGCTGCTCA 560
QY 180 nGlySerProGluMetAsnSerThrIleAsn-----IleHisArgThrSer-- 195
DB 561 G-----CCGAGAGCGCGAGCGCTGCAACCCCGCGCATCCGACACGACAGCGCAT 614
QY 196 -----SerValGluGly-----Le 200
DB 615 CGGCTCAAGAGCACGAGGAGGCGGAGCGCTGCGCACGAGAGCTGGGCGCTCAAGCT 674
QY 200 uCysGlnGlyIleGlyAla---GlyLeuValaAspValaIleTyrValaGlyThrCys-- 218
DB 675 GTGCGAGGGCGCGGCGGAGCTGCACCTCGTGAAGCGCTTCTCTGGAAGCGAGCATCA 734
QY 219 -----SerAspTyrProGlyGlyAspAlaSerThrGlyTyrAsnSerVa 233
DB 735 CTTCCTCACTACCTCACTCACTATACAGCGGC---GCTGCACCGGCTGGCCAGCAT 791
QY 233 lSerArgIle 236
DB 792 GGCGCGCATC 801
RESULT 49
US-09-458-791-1
Sequence 1, Application US/09458791
Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.

```

CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4707
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-458-791-1
Alignment Scores:
Pred. No.: 0.162 Length: 4707
Score: 113.00 Matches: 77
Percent Similarity: 34.54% Conservative: 28
Best Local Similarity: 25.33% Mismatches: 84
Query Match: 8.69% Indels: 116
DB: 3 Gaps: 18
US-10-063-734-122 (1-243) x US-09-458-791-1 (1-4707)
QY 2 ArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 21
DB 31 GGGCCCCGGGCCCCGGAGCCAGCTGCCC-----CTGGCTCGCTATCTG 75
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnGlnGln 41
DB 76 CTGGCACTGGCGGCTCCCGGCGGGGCGGAGCGCGTGTGGGCGTGGAGCAAGCC 135
QY 42 Leu-----ArgGlnArgGlnValAlaAspLeuTyraGlnGlyMetCysLeu 56
DB 136 ATCGAGGCAATCGCGGCGAGCCGAGGAGCGCGGTGTGTGGCGGCGGCACTGCTC- 194
QY 57 GlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnAlaIleProGly 76
DB 195 ---GGACGAGCTGAGCTA-----CAGCTGGAGCAAGCTCTCGGGCCT 236
QY 77 ThrProGlyIleProGly-----ArgAspGlyPheLeuGly---GlnGlyGln 92
DB 237 GATACGGGAGCAAGCGGGAATGCAAGAGCGGCTGTGCTGGCGCCCGCGGGGGCC 296
QY 93 CysLeuArgGln-SerPheGlnGln----- 100
DB 297 CCGGCGCGGAGAGCACTTCAAGCAAGCTGTCTGCTACCGGAGGAGGCGGCGGCT 356
QY 101 -----SerTrpThrProAsnTyrlValGlnCys----- 109

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DB 357 CCGGGGGCTGTCTGCTACCGGCTGGACCTTCGACCGGGGCGGCTGGAGGTGGCCCT 416
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QY 121 -GlyLysIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgVal 140
DB 477 GGGCTGACGGCGGGGTGTGTACCGCGGGGCGGAACAC----- 519
QY 140 uphSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTyPhe 160
DB 520 -----CGCTGGTAC----- 528
QY 160 rPheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlLeuAsp 180
DB 529 -----CTGGCGGTGGCGGCACTTACGTCCTGCTGA 560
QY 180 nGlySerProGlnMetAsnSerThrIleAsn-----IleHisArgThrSer-- 195
DB 561 G-----CCGAGAGCGGCGAGCGGCTGCAACCCCGGCGCATCCGACACGAC 614
QY 196 -----SerValGlnGly----- 200
DB 615 CCGGCTCAAGACAGAGGAGGCGGAGCGCTGGCCAGCAGAGCTGGGGCGCTCAAGCT 674
QY 200 uCysGlnGlyIleGlyAla--GlyLeuValAspValAlaIleTrpValGlyThrCys-- 218
DB 675 GTGCGAGGGCGGCGGCGAGCTGCACTTGTGAGCCCTTCTGTGAGGAGGACATCTA 734
QY 219 -----SerAspTyrlProGlySerGlyAspAlaSerThrGlyTrpAsnSerVa 233
DB 735 CTTCCTCACTACCCCTCACTAATAAGAGCGGC---GCTGCACCGGCTGCGCCAGAT 791
QY 233 lSerArgIle 236
DB 792 GCGGCGGATC 801
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US-09-459-066-1
; Sequence 1, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SENAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189

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TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4707
US-09-459-066-1

Alignment Scores:

Pred. No.:	0.162	Length:	4707
Score:	113.00	Matches:	77
Percent Similarity:	34.54%	Conservative:	28
Best Local Similarity:	25.33%	Mismatches:	84
Query Match:	8.69%	Indels:	116
DB:	3	Gaps:	18

US-10-063-734-122 (1-243) x US-09-459-066-1 (1-4707)

QY 2 ArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeuLeu 21
DB 31 CGCCCCCGCGCGCCGCGAGCCGACCTGCCCC-----CTGCTCGCTATCTG 75
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLysGlnLysAlaGln 41
DB 76 CTGGCAGTGGCGCTCCGCGCGGCGGAGCGAGCCGCTGTGGCGCTGGAGCAAGCC 135
QY 42 Leu-----ArgGlnArgGluValAlaAspLeuTyraAsnGlyMetCysLeu 56
DB 136 ATCGAGGCCATCGCGCGAGCAAGAGAGCGCGCTGTGTGGCGAGCGAGCTGCTT- 194
QY 57 GlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGly 76
DB 195 ---GGACCAAGCTGAGCTA-----CAGCTGGAAGCAAGCTCTCGCGCT 236
QY 77 ThrProGlyIleProGly-----ArgAspGlyPheLysGly---GluLysGlyGlu 92
DB 237 GTACCGGAGCAAGCGGCGCACTGCAAGAGCGGCTGTCTGTGGCGCCCCCGCGGCGC 296
QY 93 CysLeuArgGlu-SerPheGluGlu-----100
DB 297 CCGGCGCGGAGCACTTCAGCAAGCTGCTGCCCTACCGGAGGCGGCGCGCT 356
QY 101 -----SerTyrProAsnTyrLysGlnCys-----109
DB 357 CGGCGGCTGCTGCTCACCGGCTTGACCTTCAGCGGCGGCGCTGTGAGAGTGGCGCT 416
QY 110 -----SerTyrSerSerLeuAsnTyrGlyIleAspLeu-----120
DB 417 GGGCAACTGTAGCCGCACTCCCTGCGCAACCGGAGCGGTGTCTGTGCCACCGCA 476
QY 121 -GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLe 140
DB 477 GGGCTCGAGCGCGCGGTGTGTACCGCGGCGCGAACAAC-----519
QY 140 uPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPhePhe 160
DB 520 -----CGCTGGTAC-----528
QY 160 rPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleLysTyrLeuAspG 180
DB 529 -----CTGGCGGTGGCGCCACCTACCTACCTGTGCTGCTGA 560
QY 180 nGlySerProGluMetAsnSerThrIleAsn-----IleHisArgThrSer-- 195
DB 561 G-----CCGGAGAGCGGAGCGGCTGCAACCCCGGCGCATCCGACCAAGACAGACGCGCAT 614

QY 196 -----SerValGlnGly-----Le 200
DB 615 CGCGCTCAAGAGCAACGAGGCGGCGAGCTGCGCACGAGAGCTGGGCGCTCAAGCT 674
QY 200 uCysGlnGlyIleGlyAla---GlyLeuValAspValAlaIleTyrPValGlyThrCys-- 218
DB 675 GTGCGAGGCGCGGCGAGCTGCACTTGTGTGAGCGCTTCTCTGTGAACGCGAGCATCTA 734
QY 219 -----SerAspTyrProLysGlyAspAlaSerThrGlyTyrPheAsnSerVa 233
DB 735 CTTCCTACTACCTACCTCAACTATACGAGCGGC---CTTCACCGGCTGGCCAGCAT 791
QY 233 lSerArgIle 236
DB 792 GCGCGCATC 801

Search completed: December 25, 2004, 07:50:50
Job time: 117 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 25, 2004, 05:35:17 ; Search time 551 Seconds

(without alignments)
2455.663 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-THR MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEARSIZE=500 -MITLEN=0
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Database : Published Applications NA.*

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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1301	100.0	729	US-10-007-805-511	Sequence 511, App
3	1301	100.0	729	US-10-076-622-511	Sequence 511, App
4	1301	100.0	729	US-10-124-805-511	Sequence 511, App
5	1301	100.0	732	US-09-834-759-510	Sequence 510, App
6	1301	100.0	732	US-10-007-805-510	Sequence 510, App
7	1301	100.0	732	US-10-076-622-510	Sequence 510, App
8	1301	100.0	732	US-10-060-036-4556	Sequence 4556, App
9	1301	100.0	732	US-10-124-805-510	Sequence 510, App
10	1301	100.0	837	US-09-834-759-512	Sequence 512, App
11	1301	100.0	837	US-09-834-759-513	Sequence 513, App
12	1301	100.0	837	US-10-007-805-512	Sequence 512, App
13	1301	100.0	837	US-10-007-805-513	Sequence 513, App
14	1301	100.0	837	US-10-076-622-512	Sequence 512, App
15	1301	100.0	837	US-10-076-622-513	Sequence 513, App
16	1301	100.0	837	US-10-060-036-4557	Sequence 4557, App
17	1301	100.0	837	US-10-124-805-512	Sequence 512, App
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19	1301	100.0	1257	US-09-938-418-2	Sequence 2, Appl
20	1301	100.0	1257	US-09-946-374-430	Sequence 430, App
21	1301	100.0	1257	US-10-006-867-121	Sequence 121, App
22	1301	100.0	1257	US-10-052-586-365	Sequence 365, App
23	1301	100.0	1257	US-10-063-547-121	Sequence 121, App
24	1301	100.0	1257	US-10-063-547-121	Sequence 121, App
25	1301	100.0	1257	US-10-174-580-365	Sequence 365, App
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27	1301	100.0	1257	US-10-175-727-365	Sequence 365, App
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ALIGNMENTS

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; Sequence 511, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: JIANG, YUQIU
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 511
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-511
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Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-10-063-734-122 (1-243) x US-09-834-759-511 (1-729)

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DB 1 ATGCGACCCCGAGGCGCCGCGCTCTCCCGACGCGGCTCCGCGGCTCTGCTCTG 60
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DB 361 GGGAAATTTGGGAGTGTACATTACAAAGATGGCTCAATATGCTCTAAGAGTTTGG 420
QY 141 PheSerGlySerLeuArgLeuLeuCysArgAsnAlaCysGlnGlnArgTyrPheThr 160
DB 421 TTCACTGCTCACTTCCTGCTTAAATTCAGAAATCAGTCTGCGCTGTGATTTTCACA 480
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 481 TTCATGAGCTGATGATGTTTCAGACCTCTTCCCATTTAGCTATTAATTTTGGACCA 540
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 541 GGAAGCCTCGAAATGAATTCACAAATTAATATTCATGCACTTCTCTGGAGAGACTT 600
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
DB 601 TGTGAGGAATTTGCTGCTGATTTAGTGTGATGCTTCTGCTGCTGCTGCTGCTGCTG 660
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGln 240
DB 661 TACCCAAAGAGATGCTTCTACGATGATGATTCAGTTCTCGCATCATTTATGAAGA 720
QY 241 LeuProLys 243
DB 721 CTACCAAAA 729
```

RESULT 2

```
US-10-007-805-511
; Sequence 511, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
```

```
; APPLICANT: JIANG, YUQIU
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 511
; LENGTH: 729
```

[illegible]

	APPLICANT	Perkins, David H.
;	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE THERAPY
;	TITLE OF INVENTION:	AND DIAGNOSTICS OF BREAST CANCER
;	FILE REFERENCE:	210121.470C11
;	CURRENT APPLICATION NUMBER:	US/10/076,622
;	CURRENT FILING DATE:	2002-02-13
;	NUMBER OF SEQ. ID NOS:	627
;	SOFTWARE:	FastSeq for Windows Version 4.0
;	SEQ ID NO 511	
;	LENGTH:	729
;	TYPE:	DNA
;	ORGANISM:	Homo sapiens
;	US-10-076-622-511	
Alignment Scores:		
Prod. No.:	1.07e-144	Length: 729
Score:	1301.00	Matches: 243
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	14	Gaps: 0
US-10-063-734-122 (1-243) x US-10-076-622-511 (1-729)		
QY	1	MetArgProGlnGlyProAlaIaIaSerProGlnIaIaGlyLeuLeuLeuLeuLeu 20
DB	1	ATGCGACCCGAGGCGCCCGCCCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
QY	21	LeuLeuGlnLeuProAlaIaProSerSerIaIaSerGluIleProGlyGlyLeuLeuAla 40
DB	61	CTGCTGAGCTGCGCGCGCCGCTGAGCGCTCTGAGATCCCGAGGGGAGCAGAAAGCG 120
QY	41	GlnLeuArgGlnArgGluValaIaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
DB	121	CAGCTCCGGGAGGAGGAGGTGTGAGCCTGTATATGAAATGTGCTTACAGGGCCAGCA 180
QY	61	GlyValaIaProGlyIaArgAspGlySerProGlyAlaAsnValaIleProGlyIaIle 80
DB	181	GGAATGCTGTGTGTCAGACCGGAGCCCTGGGGCCAAATGTATATCCGGGATCACTGGGATC 240
QY	81	ProGlyIaArgAspGlyPheIaGlyGluIaGlyGlyCysLeuArgGlySerPheGluGlu 100
DB	241	CGAGGTGGGATGTGATTCAAGAGAGAAAGGGGAGATCTCGAGGGAAAGCTTGGAGAG 300
QY	101	SetTrpThrProAsnTyrlaGlyGlnCysSerTrpSerSerLeuAsnTyrlaGlyIleAspLeu 120
DB	301	TCTCGACACCCACACACACAGAGTTCATGAGATTCATTGAATTAATGCGATAGATCTT 360
QY	121	GlyValaIleAlaGluCysThrPheThrIaIaMetIaArgSerAsnSerAlaLeuArgValaLeu 140
DB	361	GGGAAATAATGGCGAGTGTACATTTCAAAAGATGCTCAATAATAGTCTCAAGAGTTTGG 420
QY	141	PheSerGlySerLeuArgLeuIaCysPheArgAsnAlaCysCysGlnaArgTrpIaPheThr 160
DB	421	TTGAGTGGCTCACTTGGCTAAAGACAAATGATCTGTACAGCTGTGATTTCACA 480
QY	161	PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIaIleTyrlaLeuAspGln 180
DB	481	TTCAATGGAGCTGAAATGTTCAAGACTCTCTCCCATGAGCTATATATTAATTATTTGACCAA 540
QY	181	GlySerProGluIaIaSerIaIaSerThrIleAsnIleIaIaIaIaIaIaIaIaIaIaIaIaIa 200
DB	541	GGAGCCCTGGAATGAATCAACAACTTAATTCACCATCTTCTTGTTGAGAGGACTT 600
QY	201	CysGluGlyIaIleGlyAlaGlyLeuValaAspValaAlaIleTrpValaGlyIaIaIaIaIaIa 220
DB	601	TGTGAAGAAATGTGTCTGATTAAGATGTGTCTATCTGGGTGGCATTTGTTCAGAT 660
QY	221	TyrProGlyGlyIaAspAlaSerThrGlyTyrlaAsnSerValaSerArgIleIleIleGluGlu 240
DB	661	TACCCAAAAGAGATGCTCTTACTAGATGAAATTCAGTTTCTCCGATCATATTGAAAGAA 720
QY	241	LeuProIaIa 243

```
Db      721 CTACCAAAA 729
|||||
RESULT 4
US-10-124-805-511
; Sequence 511, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 511
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-511

Alignment Scores:
Pred. No.:      1.07e-144      Length:      729
Score:          1301.00        Matches:      243
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             15           Gaps:         0

US-10-063-734-122 (1-243) x US-10-124-805-511 (1-729)
Qy      1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
Db      1 ATGCAACCCAGAGGCGCCGCCCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 60
Qy      21 LeuLeuGInLeuProAlaProSerSerAlaSerGInIleProGlyGlyGInIleVala 40
Db      61 CTGCTGCAAGTCCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGAGAAAGGCG 120
Qy      41 GInLeuArgGInArgGInValaValaLeuLeuTyraAngIyMetCysLeuGInIyProAla 60
Db      121 CAGCTCCGCGAGAGGAGGAGTGTGATGACCTGTATATGATGATGCTTACAAAGGCCAGCA 180
Qy      61 G1yValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAAGTCTGTGTCAGACGAGGAGCCCTGGGCGCAATGTATTCGAGTACACTGGATC 240
Qy      81 ProGlyArgAspGlyPheIyGlyGInIyGlyGInCysLeuArgGInSerPheGInGIn 100
Db      241 CCAGGTCCGAGATGATTCAAAGAGAGAAAGGGGAGATGCTGAGGAGAAAGCTTTGAGAG 300
Qy      101 SerTrpThrProAsnTyrlYsgInCysSerTrpSerSerLeuAsnTyrlYleAspLeu 120
Db      301 TCCGAGAACCACTACAGAGAGTTCATGAGATTCATGAATTAATGAGCATAGATCTT 360
Qy      121 G1yIleIleAlaGInCysThrPheThrIyMetArgSerAsnSerAlaLeuArgValIleu 140
Db      361 GGGAGAAATTCGGAGGTGACATTTCACAPAGATGCTTCAAAATAGGCTCAAGATTG 420
Qy      141 PheSerGlySerLeuArgLeuIyGlyCysArgAsnAlaCysGInArgTrpIyPheThr 160
Db      421 TTCAGTGGCTCACTTCGGCTAAATGCAAGAAATGATCTGTGACGCTTGATTTCA 480
Qy      161 PheAsnGlyAlaGInCysSerGlyProLeuProIleGInAlaIleIleTyrlYleAspGIn 180
Db      481 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATGGAAGCTATTAATTAATTTGAGCAA 540
Qy      181 G1ySerProGInMetAsnSerThrIleAsnIleHisArgThrSerSerValGInGlyIleu 200
Db      541 GGAAGCCTGAAATGAATTCACAACTTAATTAATTCACACTTCTTGTGGAAGGACTT 600
```

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Qy      201 CysGInGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      601 TGTGAAGAAATGTGGTGGATGTAGATGTGTCTATCTGGGTGGCACTTGTTCAGAT 660
Qy      221 TyrProIyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGInGIn 240
Db      661 TACCAAAAGAGAGATGCTTCTACTGATGATGAATTCAGTTTCTGCATCATTAATGAAGA 720
Qy      241 LeuProIyG 243
Db      721 CTACCAAAA 729
|||||
RESULT 5
US-09-834-759-510
; Sequence 510, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-510

Alignment Scores:
Pred. No.:      1.07e-144      Length:      732
Score:          1301.00        Matches:      243
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             9           Gaps:         0

US-10-063-734-122 (1-243) x US-09-834-759-510 (1-732)
Qy      1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
Db      1 ATGGAACCCAGAGGCGCCGCCCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 60
Qy      21 LeuLeuGInLeuProAlaProSerSerAlaSerGInIleProIyGlyGInIyVala 40
Db      61 CTGCTGAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGAGAAAGGCG 120
Qy      41 GInLeuArgGInArgGInValaValaLeuLeuTyraAngIyMetCysLeuGInIyProAla 60
Db      121 CAGCTCCGCGAGGAGGAGTGTGACCTGTATTAATGAATGCTTTCACAAAGGCCAGCA 180
Qy      61 G1yValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAAGTCTGTGTCAGACGAGGAGCCCTGGGCGCAATGTATTCGAGTACACTGGATC 240
Qy      81 ProGlyArgAspGlyPheIyGlyGInIyGlyGInCysLeuArgGInSerPheGInGIn 100
Db      241 CCAGGTCCGAGATGATTCAAAGAGAGAAAGGGGAGATGCTGAGGAGAAAGCTTTGAGAG 300
Qy      101 SerTrpThrProAsnTyrlYsgInCysSerTrpSerSerLeuAsnTyrlYleAspLeu 120
Db      301 TCCGAGAACCACTACAGAGAGTTCATGAGATTCATGAATTAATGAGCATAGATCTT 360
Qy      121 G1yIleIleAlaGInCysThrPheThrIyMetArgSerAsnSerAlaLeuArgValIleu 140
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Db 361 GGGAAATTGGCGAGTGTACATTTCACAAAGATCCGTTCAATATAGCTCTTAAGATTGG 420
Qy 141 PheSerGlySerLeuArgLeuLysCySarGAsnAlaCyGcGlnArgTrpTyRheThr 160
Db 421 TTCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGCAGCGGTGGATTTCACA 480
Qy 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyRleuAspGln 180
Db 481 TTCAAATGGAGCTGAATGTTTCAGAGACTCTCCCATTTGAAGCTATTAATTTATTTGACCA 540
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 541 GGAAGCCCTGGAATGATTCACAAATTAATTCATCGACACTTCTTCGTGGAAGACTT 600
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 601 TGTGAAGGATTCGCTCGATTAGTGATGTTGCTATCGGTGGCACTTGTTCAGAT 660
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 661 TACCCAAAAGAGATCTTCTACTGATGAGATTCAGTTCTCGCATCATTAATTGAAGA 720
Qy 241 LeuProLys 243
Db 721 CTACCAAAA 729
RESULT 6
US-10-007-805-510
; Sequence 510, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-510
Alignment Scores:
Pred. No.: 1,07e-144 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-063-734-122 (1-243) x US-10-007-805-510 (1-732)
Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 1 ATGCGACCCCGAGGCCCCCGCCCTCCCGCAGCGGCTCGCGCCCTCCGTGCTCTCG 60
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyGlnValAla 40
Db 61 CTGCTCAGCTGCTCCCGCGCCCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 120

Qy 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 121 CAGCTCCGGCAGAGGAGAGGTGGTGGACCTGTTATTAATGAAATGTCTTACAGGGCCAGCA 180
Qy 61 GlyAlaProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 181 GGAAGTCCCTGGTGCAGAGCGGAGCCCTGGGGCAATGTATTATCCGGGTACACTGGGATC 240
Qy 81 ProGlyArgAspGlyPheLysGlyGluLysGlyValCysLeuArgGlnSerPheGluGlu 100
Db 241 CCAGTCCGGAGATTCAGAAAGAGAAAAGGGGAAATGTCTGAGGGAAGCTTTGAGAG 300
Qy 101 SerTrpTrpProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db 301 TCTTGACACCCCACTTACAGCAGTCTTCATGAGATTCATTGAATTAATGACATATCTT 360
Qy 121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 361 GGGAAATTGGCGAGTGTACATTTCACAAAGATGCGTTCAAAATAGCTCTTAAGAGTTTG 420
Qy 141 PheSerGlySerLeuArgLeuLysCySarGAsnAlaCyGcGlnArgTrpTyRheThr 160
Db 421 TTCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTCAAGCTTGTATTTCACA 480
Qy 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyRleuAspGln 180
Db 481 TTCAAATGGAGCTGAATGTTTCAGAGACTCTCCCATTTGAAGCTATTAATTTATTTGACCA 540
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 541 GGAAGCCCTGGAATGATTCACAAATTAATTCATCGACACTTCTTCGTGGAAGACTT 600
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 601 TGTGAAGGATTCGCTCGATTAGTGATGTTGCTATCGGTGGCACTTGTTCAGAT 660
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 661 TACCCAAAAGAGATCTTCTACTGATGAGATTCAGTTCTCGCATCATTAATTGAAGA 720
Qy 241 LeuProLys 243
Db 721 CTACCAAAA 729
RESULT 7
US-10-076-622-510
; Sequence 510, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-510
Alignment Scores:
Pred. No.: 1,07e-144 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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US-10-063-734-122 (1-243) x US-10-076-622-510 (1-732)
QY      1 MetArpProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db      1 ATGCGACCCCAAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCCGCTGCTGCTG 60
QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProArgGlyLeuGlnAla 40
Db      61 CTGCTGACAGCTGCCCCGCTGCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGGG 120
QY      41 GlnLeuArgGlnArgGlnValValAlaPleuTyTAsnGlyMetCysLeuGlnGlyProAla 60
Db      121 CAGCTCCGCGACAGGAGGAGGTGTGACCTGTATTAAGATGCTTACAAAGGCGCAGCA 180
QY      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAGAGCTCGTGTGAGACGGAGACCTGGGGCCCAATGTTATTCGGGATCACCTGGGATC 240
QY      81 ProGlyArgAspGlyPheLeuGlyGlyValGlyCysLeuArgGlyLeuSerPheGlnGly 100
Db      241 CCAGCTCGGAGATGATTCAAAGAGAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAG 300
QY      101 SerTrpThrProAsnTyTylsGlnCysSerTrpSerSerLeuAsnTyTylIleAspLeu 120
Db      301 TCTGTGACACCCCACTACAGCAAGGTGTATGATGAGTTCATTAATTAATGCAATGATCTT 360
QY      121 GlyIysIleAlaGlyCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
Db      361 GGGAATAATGGCGAGGTATCATTTTCAAAAGATGCGTTCAAAATAGTCTTAAAGATTTTG 420
QY      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpThrPheThr 160
Db      421 TTCAATGCTCACTTCGCTGCTAAATGCAAAATGATGCTGTGAGGTGTGATTTTCA 480
QY      161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyTLeuAspGln 180
Db      481 TTCATGAGCTGATGATGTTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGACCA 540
QY      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db      541 GGAAGCCTGAATGATTAATTCACATTAATTCATTCGACCTCTTCTGTGAAAGACTT 600
QY      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      601 TGTGAAGAAATTTGGTGTGATTAAGTATGATGATGCTATCTGGGTGGCACTTGTCAGAT 660
QY      221 TyrProLysGlyAspAlaSerThrGlyTTPAsnSerValSerArgIleIleIleGlnGly 240
Db      661 TACCAAAAGAGAGATGCTTCTACTGATGAGATTCAGATTTCTCGCATCTTAATTAAGAA 720
QY      241 LeuProLys 243
Db      721 CTACCAAAA 729
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RESULT 8

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US-10-060-036-4556
; Sequence 4556, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121 566
; CURRENT APPLICATION NUMBER: US/10/060, 036
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
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```
; SEQ ID NO 4556
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4556
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Alignment Scores:

Pred. No.:	1,07e-144	Length:	732
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatch:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-063-734-122 (1-243) x US-10-060-036-4556 (1-732)

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QY      1 MetArpProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db      1 ATGCGACCCCAAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCCGCTGCTGCTG 60
QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProArgGlyLeuGlnAla 40
Db      61 CTGCTGACAGCTGCCCCGCTGCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGGG 120
QY      41 GlnLeuArgGlnArgGlnValValAlaPleuTyTAsnGlyMetCysLeuGlnGlyProAla 60
Db      121 CAGCTCCGCGACAGGAGGAGGTGTGACCTGTATTAAGATGCTTACAAAGGCGCAGCA 180
QY      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAGAGCTCGTGTGAGACGGAGACCTGGGGCCCAATGTTATTCGGGATCACCTGGGATC 240
QY      81 ProGlyArgAspGlyPheLeuGlyGlyValGlyCysLeuArgGlyLeuSerPheGlnGly 100
Db      241 CCAGCTCGGAGATGATTCAAAGAGAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAG 300
QY      101 SerTrpThrProAsnTyTylsGlnCysSerTrpSerSerLeuAsnTyTylIleAspLeu 120
Db      301 TCTGTGACACCCCACTACAGCAAGGTGTATGATGAGTTCATTAATTAATGCAATGATCTT 360
QY      121 GlyIysIleAlaGlyCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
Db      361 GGGAATAATGGCGAGGTATCATTTTCAAAAGATGCGTTCAAAATAGTCTTAAAGATTTTG 420
QY      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpThrPheThr 160
Db      421 TTCAATGCTCACTTCGCTGCTAAATGCAAAATGATGCTGTGAGGTGTGATTTTCA 480
QY      161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyTLeuAspGln 180
Db      481 TTCATGAGCTGATGATGTTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGACCA 540
QY      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db      541 GGAAGCCTGAATGATTAATTCACATTAATTCATTCGACCTCTTCTGTGAAAGACTT 600
QY      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      601 TGTGAAGAAATTTGGTGTGATTAAGTATGATGATGCTATCTGGGTGGCACTTGTCAGAT 660
QY      221 TyrProLysGlyAspAlaSerThrGlyTTPAsnSerValSerArgIleIleIleGlnGly 240
Db      661 TACCAAAAGAGAGATGCTTCTACTGATGAGATTCAGATTTCTCGCATCTTAATTAAGAA 720
QY      241 LeuProLys 243
Db      721 CTACCAAAA 729
```

RESULT 9

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US-10-124-805-510
; Sequence 510, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
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```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleach, Paul R.
; APPLICANT: Pereg, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124, 805
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-510

Alignment Scores:
Pred. No.: 1,07e-144 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x US-10-124-805-510 (1-732)

QY 1 MetATGProGInGlyProAlaIaSerProGInARgLeuARgLyLeuLeuLeuLeu 20
DB 1 ATGCGACCCCGAGGGCCCCCGCCCTCCGCGAGCGCTCCGCGCTCTGCTGCTCG 60

21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProLyGInLySAla 40
DB 61 CTGCTGCACTGCCCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGAAAGAGGCG 120

41 GInLeuARgInARgGInValAlaAspLeuTyraSngLyMetCysLeuGInGlyProAla 60
DB 121 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 180

61 G1yValProG1yARgARgLySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 181 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 240

81 ProG1yARgARgLyPheLySgLyGInLySgLyCysLeuARgLySerPheGInGIn 100
DB 241 CCGAGTCCGGATGATTTCAAGAGAAAGAGGAAATGTTGAGGAAAGCTTTGAGGAG 300

101 SerTrpThrProAsnTyrlYsGInCysSerTrpSerSerLeuAsnTyrgIyIleAspLeu 120
DB 301 TCCTTGACACCCCAACTACAAAGAGTGTATGAGTTCAATGATTTATGSCATAGATCTT 360

121 G1yLySAlaIaG1yCysThrPheThrLyMetArgSerAsnSerAlaLeuARgValLeu 140
DB 361 GGGAAATATGCGAGGTATACATTACAAAGATCGTTCAAAATGTCCTTCAAGAGTTTGG 420

141 PheSerG1ySerLeuARgLeuLySArgAsnAlaCysCysGInARgLyTrpThrPheThr 160
DB 421 TTGAGTGCTCATCTTGCTTGAATATGCAAGATGCTGAGGTGGATTTTTCACA 480

161 PheAsnG1yAlaG1yCysSerG1yProLeuProIleG1yAlaIleIleTyrlLeuAspGIn 180
DB 481 TTCAATGAGAGTGAATGTTGAGGACCTCTTCCCATTTGAAGCTATATTTATTTGAGCA 540

181 G1ySerProG1yMetCysAsnSerThrIleAsnIleHisArgThSerSerValG1yGInLeu 200
DB 541 GGAAGCCCTGAATGATTCACAAATTAATTCATCGCACTTCTGAGGAAAGACATT 600

201 CysG1yG1yIleG1yAlaG1yLeuValAspValAlaIleTrpValG1yThrCysSerArg 220
DB 601 TGTGAAGAAATGTGTGTGATTAAGTGAATGTTGCTATCTGGGTGGCACTTTGAGAT 660

221 TyrlProLySgLyAspAlaSerThrG1yTrpAsnSerValSerArgIleIleIleG1yGIn 240
DB 661 TACCAAAAGAGAGATGTTCTTACGTGATGGAATTCAGTTTCTGCAATCATTTATGAAGA 720
```

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QY 241 LeuProLyS 243
DB 721 CTACCAAAA 729

RESULT 10
US-09-834-759-512
; Sequence 512, Application US/09834759
; Publication No. US2002008598A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 512
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-512

Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-512 (1-837)

QY 1 MetATGProGInGlyProAlaIaSerProGInARgLeuARgLyLeuLeuLeuLeu 20
DB 106 ATGCGACCCCGAGGGCCCCCGCCCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCG 165

21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProLyGInLySAla 40
DB 166 CTGCTGCACTGCCCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGAAAGAGGCG 225

41 GInLeuARgInARgGInValAlaAspLeuTyraSngLyMetCysLeuGInGlyProAla 60
DB 226 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 285

61 G1yValProG1yARgARgLySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 286 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345

166 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345
DB 286 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345

81 ProG1yARgARgLyPheLySgLyGInLySgLyCysLeuARgLySerPheGInGIn 100
DB 41 GInLeuARgInARgGInValAlaAspLeuTyraSngLyMetCysLeuGInGlyProAla 60

226 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 285
DB 226 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 285

61 G1yValProG1yARgARgLySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 286 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345

286 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345
DB 286 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345

81 PheSerG1ySerLeuARgLeuLySArgAsnAlaCysCysGInARgLyTrpThrPheThr 160
DB 81 ProG1yARgARgLyPheLySgLyGInLySgLyCysLeuARgLySerPheGInGIn 100

346 CCGAGTCCGGATGATTTCAAGAGAAAGAGGAAATGCTGAGGAAAGCTTTGAGGAG 405
DB 346 CCGAGTCCGGATGATTTCAAGAGAAAGAGGAAATGCTGAGGAAAGCTTTGAGGAG 405

101 SerTrpThrProAsnTyrlYsGInCysSerTrpSerSerLeuAsnTyrgIyIleAspLeu 120
DB 101 SerTrpThrProAsnTyrlYsGInCysSerTrpSerSerLeuAsnTyrgIyIleAspLeu 120

406 TCTTGACACCCCAACTACAAAGAGTGTATGAGTTCAATGATTTATGSCATAGATCTT 465
DB 406 TCTTGACACCCCAACTACAAAGAGTGTATGAGTTCAATGATTTATGSCATAGATCTT 465

121 G1yLySAlaIaG1yCysThrPheThrLyMetArgSerAsnSerAlaLeuARgValLeu 140
DB 466 GGAAGAAATGCGAGGTATACAAAGATGCGTTCAAAATGATGCTTAAAGATTTTGG 525

466 GGAAGAAATGCGAGGTATACAAAGATGCGTTCAAAATGATGCTTAAAGATTTTGG 525
DB 466 GGAAGAAATGCGAGGTATACAAAGATGCGTTCAAAATGATGCTTAAAGATTTTGG 525

141 PheSerG1ySerLeuARgLeuLySArgAsnAlaCysCysGInARgLyTrpThrPheThr 160
DB 141 PheSerG1ySerLeuARgLeuLySArgAsnAlaCysCysGInARgLyTrpThrPheThr 160

526 TTCAAGTGCTCATCTTGCTTGAATATGCAAGATGCTGAGGTGGATTTTTCACA 585
DB 526 TTCAAGTGCTCATCTTGCTTGAATATGCAAGATGCTGAGGTGGATTTTTCACA 585

161 PheAsnG1yAlaG1yCysSerG1yProLeuProIleG1yAlaIleIleTyrlLeuAspGIn 180
QY 161 PheAsnG1yAlaG1yCysSerG1yProLeuProIleG1yAlaIleIleTyrlLeuAspGIn 180
```


Db 586 TTCATGGAGCTGAATGTTACAGACCTCTCCATGAGCTATATTATTATTTGACCAA 645
Qy 181 GYSerProGluMeTAsnSerThrIleAsnIleHisArgThSerSerValGluGluLeu 200
Db 646 GGAAGCCCTGGAATGATTAATCAACAATTAATTAATTCATCGACCTCTCTGGAAGACTT 705
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 706 TGTGAAGGAATGGTGCTGATTAAGATGTTGCTATCTGGTGGCACTGTTGAGAT 765
Qy 221 TyrProLysGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGlu 240
Db 766 TACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTGCATCATTTATTGAAGA 825
Qy 241 LeuProLys 243
Db 826 CTACCAAAA 834
RESULT 11
US-09-834-759-513
; Sequence 513, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-513
Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-063-734-122 (1-243) x US-09-834-759-513 (1-837)
Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 106 ATGGAGCCCGAGGGGCGCGCCCTCCCGCAGCGCTCCCGGCGCTCCTGCTGCTCTG 165
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyIleGlnIleVal 40
Db 166 CTGCTGCAAGTCCCGCCCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAGAGCG 225
Qy 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 226 CAGCTCCGGCAGAGGAGAGTGTGAGCTGTATATGAAATGCTTCAAGGGCCACACA 285
Qy 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
Db 286 GGAATGCTGCTGTCAGACGAGGAGCCCTGGGCGCAATGTATTCCCGGTTACACCTGGGATC 345
Qy 81 ProGlyIArgAspGlyPheIleGlyIleValGlyGluCysLeuArgGlnSerPheGlnIle 100
Db 346 CCAAGTGGGATGATTCATAAGAGCAAAAGGGGAGATGCTGAGGAGAAAGCTTTGAGAG 405

Qy 101 SerTyrThrProAsnTyrIleGlnCysSerTyrPserSerLeuAsnTyrGlyIleAspLeu 120
Db 406 TCTTGACACCCCACTACAGACAGTGTTCAGAGTTCATTGAATTTATGCAATAGACTT 465
Qy 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 466 GGGAAATTTGGGAGTGTACATTTCAAAGATGGCTTCAATAGTGTCTTAAGATTG 525
Qy 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 526 TTCACTGCTCACTCGGCTAAATGCAAGAAATCAGCTGTCAGCGTGTGATTTCACA 585
Qy 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrIleAspGln 180
Db 586 TTCATGGAGCTGAATGTTACAGACCTCTTCCATTAGCTATATTATTATTGACCAA 645
Qy 181 GlySerProGluMeTAsnSerThrIleAsnIleHisArgThSerSerValGluGlyLeu 200
Db 646 GGAAGCCCTGGAATGATTAATCAACAATTAATTCATCGACCTTCTCTGGAAGACTT 705
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 706 TGTGAAGGAATGGTGCTGATTAAGATGTTGCTATCTGGTGGCACTGTTGAGAT 765
Qy 221 TyrProLysGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGlu 240
Db 766 TACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTGCATCATTTATTGAAGA 825
Qy 241 LeuProLys 243
Db 826 CTACCAAAA 834
RESULT 12
US-10-007-805-512
; Sequence 512, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margalita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 512
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-512
Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-063-734-122 (1-243) x US-10-007-805-512 (1-837)
Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20

```

Db      106 ATGCGACCCAGAGGCCCCCGCCCTCCCGCAGCGGCTCGCGGCTCCGCTGCTCTG 165
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlysglylysglnlyVala 40
Db      166 CTGCTGCACCTGCCCCCGCGCTCGAGCGCTCTGAGATCCCGAAGGGGAAGCAAGGGCG 225
Qy      41 GlnLeuArgGlnArgGlnValValaAspLeuTyrAsnGluMetCysLeuGlnGlyProAla 60
Db      226 CAGCTCCGGGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 285
Qy      61 GlnValProGlnYArgAspGlySerProGlnYalaAsnValIleProGlyThrProGlyIle 80
Db      286 GAGAGTCCCTGCTGAGACCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 345
Qy      81 ProGlnYArgAspGlyPheIlysglylyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db      346 CCAGGTCCGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
Qy      101 SerTrpThrProAsnTyrIlysglyGlySerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db      406 TCCTGGACACCCCACTACAGACGCTGTTCAAGAGTTCAATGATTAATGACATGATCTT 465
Qy      121 GlnYlyIleAlaGlnCysThrPheThrIlysmetArgSerAsnSerAlaLeuArgValIleu 140
Db      466 GGGAAATTTGGCGAGTGTACATTTACAAAGATCGCTTCAAAATGCTCTCAAGATTTTG 525
Qy      141 PheSerGlySerLeuArgLeuIlyGlyCysArgAsnAlaCysGlnGlnArgTrpIlyPheThr 160
Db      526 TTCAGTGGCTCACTTCGGCTTAAATGCAAGAAATGCAATGCTGTCAGCGTGGTATTCACA 585
Qy      161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db      586 TTCAGTGGAGCTGAAATGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
Qy      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db      646 GGAAGCCCTGAATGAATTCACAAATTAATTCATCGACCTCTCTGCGAAGAGACTT 705
Qy      201 CysGlnGlyIleGlnYalaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      706 TGTGAAGGAATGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
Qy      221 TyrProIlyGlnYAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240
Db      766 TACCCAAAAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 825
Qy      241 LeuProIly 243
Db      826 CTACCAAAA 834

RESULT 13
US-10-007-805-513
; Sequence 513, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuguin
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Ronger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593

```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-513

Alignment Scores:
Pred. No.: 1,286-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-734-122 (1-243) x US-10-007-805-513 (1-837)
Qy      1 MetArgProGlnGlyProAlaIleSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db      106 ATGCGACCCAGAGGCCCCCGCCCTCCCGCAGCGGCTCGCGGCTCCGCTGCTCTG 165
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlysglylysglnlyVala 40
Db      166 CTGCTGCACCTGCCCCCGCGCTCGAGCGCTCTGAGATCCCGAAGGGGAAGCAAGGGCG 225
Qy      41 GlnLeuArgGlnArgGlnValValaAspLeuTyrAsnGluMetCysLeuGlnGlyProAla 60
Db      346 CCAGGTCCGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
Qy      101 SerTrpThrProAsnTyrIlysglyGlySerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db      406 TCCTGGACACCCCACTACAGACGCTGTTCAAGAGTTCAATGATTAATGACATGATCTT 465
Qy      121 GlnYlyIleAlaGlnCysThrPheThrIlysmetArgSerAsnSerAlaLeuArgValIleu 140
Db      466 GGGAAATTTGGCGAGTGTACATTTACAAAGATCGCTTCAAAATGCTCTCAAGATTTTG 525
Qy      141 PheSerGlySerLeuArgLeuIlyGlyCysArgAsnAlaCysGlnGlnArgTrpIlyPheThr 160
Db      526 TTCAGTGGCTCACTTCGGCTTAAATGCAAGAAATGCAATGCTGTCAGCGTGGTATTCACA 585
Qy      161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db      586 TTCAGTGGAGCTGAAATGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
Qy      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db      646 GGAAGCCCTGAATGAATTCACAAATTAATTCATCGACCTCTCTGCGAAGAGACTT 705
Qy      201 CysGlnGlyIleGlnYalaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      706 TGTGAAGGAATGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
Qy      221 TyrProIlyGlnYAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240
Db      766 TACCCAAAAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 825
Qy      241 LeuProIly 243
Db      826 CTACCAAAA 834

RESULT 14
US-10-076-622-512
; Sequence 512, Application US/10076622
; Publication No. US20030023036A1

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```

GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C11
CURRENT APPLICATION NUMBER: US/10/076,622
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 512
LENGTH: 837
TYPE: DNA
ORGANISM: Homo sapiens
US-10-076-622-512

Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-10-063-734-122 (1-243) x US-10-076-622-512 (1-837)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
DB 106 ATGCACCCCAAGGCGCGCGCTCCCGACGCGCTCCGCGCTCCGCTCCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGly 40
DB 166 CTGCTGACGCTGCGCGCGCGCTGAGCGCTGAGATCCCAAGGGAAGCAAGGCG 225
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGCGACAGGAGGAGTGTGACCTGTATTAATGATGATGCTTACAGAGCCAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GAGAGCTGCTGCTGAGAGCGGAGCCCTGGGCAATGTTATTCGGGTACACTGGGATC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 346 CCAAGTCCGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 101 SerTrpThrProAsnTyrllysGlnCysSerTrpSerSerLeuAsnTyrllysLeuAsp 120
DB 406 TCCCTGACACCACTACAGACAGTGTTCATGAGTTCATTGAATTAATGACATAGATCTT 465
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATTTGGGAGTGTATCAATTTCACAAAGATGCTTCAATATGCTTAAAGATTTTG 525
QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
DB 526 TTCAGTGGCTCACTTCGCTTAAATGCAAGATGATGCTGACAGCTTGGATTTTCA 585
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 586 TTCAATGAGCTGATGATGTTCAAGACCTCTCCCATTTGAAGCATTAATTAATTTGACCAA 645
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 646 GGAAGCCCTCAAAATTCATCAACATTAATTCACCACTTCTTCTGGAAGAGACTT 705
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrPvalGlyThrCysSerAsp 220
DB 706 TGTAAAGAAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
QY 221 TyrProIysGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240

```

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DB 766 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 825
QY 241 LeuProIys 243
DB 826 CTACCAAAA 834

RESULT 15
US-10-076-622-513
Sequence 513, Application US/10076622
Publication No. US20030023036A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C11
CURRENT APPLICATION NUMBER: US/10/076,622
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 513
LENGTH: 837
TYPE: DNA
ORGANISM: Homo sapiens
US-10-076-622-513

Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 14

US-10-063-734-122 (1-243) x US-10-076-622-513 (1-837)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
DB 106 ATGCACCCCAAGGCGCGCGCTCCCGACGCGCTCCGCGCTCCGCTCCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGly 40
DB 166 CTGCTGACGCTGCGCGCGCGCTGAGCGCTGAGATCCCAAGGGAAGCAAGGCG 225
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGCGACAGGAGGAGTGTGACCTGTATTAATGATGATGCTTACAGAGCCAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GAGAGCTGCTGCTGAGAGCGGAGCCCTGGGCAATGTTATTCGGGTACACTGGGATC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 346 CCAAGTCCGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 101 SerTrpThrProAsnTyrllysGlnCysSerTrpSerSerLeuAsnTyrllysLeuAsp 120
DB 406 TCCCTGACACCACTACAGACAGTGTTCATGAGTTCATTGAATTAATGACATAGATCTT 465
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATTTGGGAGTGTATCAATTTCACAAAGATGCTTCAATATGCTTAAAGATTTTG 525
QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
DB 526 TTCAGTGGCTCACTTCGCTTAAATGCAAGATGATGCTGACAGCTTGGATTTTCA 585
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 586 TTCAATGAGCTGATGATGTTCAAGACCTCTCCCATTTGAAGCATTAATTAATTTGACCAA 645

```

QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGluLeu 200
DB 646 GGAAGCCCTCGAATGATTCACCAATTATTCATCGACCTCTCTGGAGAGACTT 705
QY 201 CysGluGlyIleGlyValAlaGlyLeuValAlaIleTyrValGlyThrCysSerAsp 220
DB 706 TGTGAAGGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 765
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPanserValSerArgIleIleIleGluGlu 240
DB 766 TACCCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 825
QY 241 LeuProGly 243
DB 826 CTACCAAAA 834
RESULT 16
US-10-060-036-4557
; Sequence 4557, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yudi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4557
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4557
Alignment Scores:
Pred. No.: 1,286-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-063-734-122 (1-243) x US-10-060-036-4557 (1-837)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 106 ATGCCAGCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyLeuGlnValAla 40
DB 166 CTGCTGCACTGCCCGCCGCGCTGACCGCTCTGACATCCCAAGGAGAAAGGAGGAGGAG 225
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GGAAGTCCCTGCTGACACCGGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGGAGTC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyValGlyCysLeuArgGlyLeuSerPheGluGlu 100
DB 346 CCAAGTCCGGAATGATTCACCAAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405
QY 101 SerTyrThrProAsnTyrIleGlyGlySerTyrPheSerSerLeuAsnTyrIleIleAspLeu 120
DB 406 TCCTGGACACCACTACCAAGCAGTGTTCATGATGATGATGATGATGATGATGATGATGAT 465

QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAAATTCGCGATGTACATTTACAAAAGATGCTTCAANATGCTCTAAGAGTTTGG 525
QY 141 PheSerGlySerLeuArgLeuLeuCysArgAlaAlaCysCysGlnArgTyrPheThr 160
DB 526 TTCAGTGCCTCACTTCGCGCTAAATGCAAAATGATCATCTGTCACGCTGGATTTTCA 585
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 586 TTCATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGluLeu 200
DB 646 GGAAGCCCTCGAATGATTCACCAATTATTCATCGACCTCTCTGTGGAAGAGACTT 705
QY 201 CysGluGlyIleGlyValAlaGlyLeuValAlaIleTyrValGlyThrCysSerAsp 220
DB 706 TGTGAAGGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 765
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPanserValSerArgIleIleIleGluGlu 240
DB 766 TACCCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 825
QY 241 LeuProGly 243
DB 826 CTACCAAAA 834
RESULT 17
US-10-124-805-512
; Sequence 512, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 512
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-512
Alignment Scores:
Pred. No.: 1,286-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-10-063-734-122 (1-243) x US-10-124-805-512 (1-837)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 106 ATGCCAGCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyLeuGlnValAla 40
DB 166 CTGCTGCACTGCCCGCCGCGCTGACCGCTCTGACATCCCAAGGAGAAAGGAGGAGGAG 225
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 226 CAGCTCCCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80

```

Db      286  GGAGTGCCTGTGAGACGGGAGCCTCGGGCCAAATGTTATTCGGGTACACCTGGGATC 345
OY      81  PROGLYARGASpGLyPhelysGLyGLyGLyGLyGLyGLyGLyGLyGLyGLyGLyGLyGLy 100
Db      346  CCGAGTGGGATGATTCATTCAAAGAGAAAGAGGAGAAAGTGTGAGGAAAGCTTGGAGAG 405
OY      101  SerTTPThProAsnTYrLYsGLINcySerTTPSerSerLeuAsnTYrGLyILEAspLeu 120
Db      406  TCCTGGACACCCCAACTACAAAGCAGTGTTCATGAGTTCAATTGATTTAGGCATAGATCTT 465
OY      121  GLyGLyILEAlaGLyCyrThrPheThrLYsMetArgSerAsnSerAlaLeuArgValLeu 140
Db      466  GGGAAAATTTGGCGAGGTATCATTTTAAACAAGATCGTTCAAAATGTGCTCTTAAAGATTTC 525
OY      141  PheSerGlySerLeuArgLeuLYsCysArgAsnAlaCysGlyGlnArgTTPYrPheThr 160
Db      526  TTCAGTGGCTCACTTGCGCTTAAATGCAAGAAATGCATGTCGTAGCGGTGGTATTTTCACA 585
OY      161  PheAsnGLyAlaGLyCysSerGlyProLeuProILEGlnAlaILEILETYrLeuAspGln 180
Db      586  TTCAAAGGAGCTGAATGTTTCAGACACCTCTCCCATTTGAAGCTATTAATTATTTGACCAA 645
OY      181  GLySerProGLyMetAsnSerThrILEAsnILEHisArgThrSerGlyValGLyGLyLeu 200
Db      646  GGAAGCCCTGAATGAATGAATTCACAAATTAATTCATGCACTTCTCTGTGGAAAGACATT 705
OY      201  CysGLyGLyTYrLEGLyAlaGLyLeuValAspValAlaILETYrValGLyThrCysSerAsp 220
Db      706  TGTGAAGGAATGTGCTCTGGAATTAGTGAATGTTGCTATCTGGGTGGCATTTGTCAGAT 765
OY      221  TYrProLYsGLyAspAlaSerThrGLyTYrPheAsnSerValSerArgILEILEILEGLyGLu 240
Db      766  TACCCAAAGAGAGATCTTCTACTGATGAGAAATTCAGTTCTTCGCATCATTTATGAAGAA 825
OY      241  LeuProLYs 243
Db      826  CTACCAAAA 834

RESULT 18
US-10-124-805-513
; Sequence 513, Application US/10124805
; Publication No. US2003016022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: AND DIAGNOSIS OF BREAST CANCER
; CURRENT APPLICATION NUMBER: US/10/124,805
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-513

Alignment Scores:
Pred. No.:      1,286-144      Length:      837
Score:          1301.00      Matches:      243
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    100.00%      Indels:      0
DB:             15          Gaps:         0

US-10-063-734-122 (1-243) x US-10-124-805-513 (1-837)
OY      1  MetArgProGlnGLyProAlaAlaSerProGlnArgGluArgGLyLeuLeuLeuLeuLeu 20
Db      106  ATGCACACCCACGAGGCCCGCCGCTTCCTCCGACAGCGACTTCGGGAGCTCTCTGTGCTCTCG 165

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QY	21	LeuLeuGluGlnLeuProAlaProSerSerAlaSerGluIleProIleGlyIleGlyValAla	4
Db	166	CTGCTGCAGCTGCCCGCGCGCTCGAGGCGCTCTGNAATCCCAAGGAGGAGCAAAAGCCG	22
QY	41	GluIleuArgGlnArgGluValValaApleuTYTAenGlyMetCysLeuGlnGlyProAla	60
Db	226	CAGCTCCGGCAGAGAGGAGGTGGTGACCTGTGTAAAGAAATGCTGTTCAGAGGCGACACA	28
QY	61	GlyValProGlyArgArgIleSerProGlyValaAenValIleProGlyYThrProGlyIle	80
Db	286	GGAGTGCCTGGTGGAGACGGGAGCCCTCGGGGCCCAAGTTATTCGGGCTACACTGGGATC	34
QY	81	ProGlyArgArgGlyPheIleGlyIleGlyIleGlyCysLeuArgGlnSerPheGluGlu	100
Db	346	CCAGTGGCGGATGATTCAAAGACAGAAAGGGGGAAATGCTGACGGAGAAAGCTTTGAGGAG	40
QY	101	SerTrpThrProAenTYrlYsgIleCysSerTrpSerSerLeuAenTYrGlyIleApleu	120
Db	406	TCTCGACACCCCACTACAGACAGTGTTCATGGAGTTCAITGAATTAATGCAATGATCTT	46
QY	121	GlyIleValIleAglucYthrPheThrIlySmetArgSerSerSerAlaLeuArgValIleu	140
Db	466	GGGAAATTTCCGGGAGTGTCATTTTCAAAAGATGCCGTTCAATATAGTCTCTAAGAGTTTG	52
QY	141	PheSerIleSerLeuArgLeuIleYsgIleCysArgAenAlaCysCysGlnArgTrpTYrPheThr	160
Db	526	TTTCATGGCTCACTTGGCTTAATATCAGAAATGCAATGCTGACGCGTGGATTTTACA	58
QY	161	PheAenGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTYrLeuAspGln	180
Db	586	TTCAATGAGACTGAATGTTCAGACCTCTTCCATTTGAAGCTATATTTATTTGGACCA	64
QY	181	GlySerProGluMetLeuSerThrIleAenIleHisArgTrpSerSerValGluGlyLeu	200
Db	646	GGAGGCCCTTAATATGAAATTCACAAATTAATATTCACACTCTCTCTGTGGAAAGACTT	70
QY	201	CysGluGlyIleGlyAlaGlyLeuValaApleuAlaIleIleTPValGlyTYrCysSerAsp	220
Db	706	TGCGAAGAAATGGTGTCTGGAATTAAGATGTTGCTATCTGGGTTGGCACTTGTTCAGAT	76
QY	221	TYrProIleGlyAspAlaSerThrGlyTYrPaenSerValSerArgIleIleIleGluGlu	240
Db	766	TACCCAAAGAAAGATCTTCTACATGATGCAATTCAGTTCTCGCATCATTAATGAAGAA	82
QY	241	LeuProIleYs 243	
Db	826	CTACCAAAA 834	
RESULT 19			
US-09-938-418-2			
; Sequence 2, Application US/09938418			
; Patent No. US20020161199A1			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi J.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Polakis, Paul			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; APPLICANT: Wu, Thomas D.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
; TITLE OF INVENTION: TREATMENT OF TUMOR			
; FILE REFERENCE: P5009R1			
; CURRENT APPLICATION NUMBER: US/09/938,418			
; PRIOR APPLICATION NUMBER: 2001-08-23			
; PRIOR FILING DATE: 1998-04-07			
; PRIOR APPLICATION NUMBER: 60/085,697			
; PRIOR FILING DATE: 1998-05-15			
; PRIOR APPLICATION NUMBER: 60/097,022			

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; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-938-418-2
Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-063-734-122 (1-243) x US-09-938-418-2 (1-1257)
QY 1 MetArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATCGACGCCAGGAGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlyGlyGly 40
DB 198 CTGCTCAGCTGCGCCGCGCGCTGAGACGCTTGAAGTCCCAAGGGAAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGGTGGAGCTGTATTAAGGATGTGTACAAAGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGGTCCCTGCTGCAACGGGAGCCCTGGGGCCAAATTTATTCGGGTACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAGGTCCGGATGATTCAAAGAGAAAGGGGAATGTCTGAGGAAAGCTTTGAGGAG 437
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QY 101 SerTPThrProAsnTyrIleGlnCysSerTPSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGACACCCCACTACAGCAGTCTTCATGAGATTCAATTAAATGATGATGATCTT 497
QY 121 GlyIleIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATATGCCGAGGTGATTCATTTACAAAGATGCCCTTCAAAATAGTCTCTAAGATTGG 557
QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
DB 558 TTCAGTGGCTCACTTCGCTAAATGCAAAATGCAATGCAATGCAATGCAATGCAATGCA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleIleGln 180
DB 618 TTCATATGAGCTGAAATGTTTCAAGACCTCTTCCCATTTGAAGCTTATTTATTTGACCA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleIleIleIleIleIleIleIleIle 200
DB 678 GGAAGCCCTGAATGATTCATCAATTAATTAATTCATGCACTTCTCTGAGAGGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220
DB 738 TGTGAAGGATTTGGTCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProIleGlyAspAlaSerThrGlyTPAsnSerValSerArgIleIleIleGln 240
DB 798 TACCCAAAGGAGATGCTTCTACTGATGATTCAGTTTCTGATCATTATTTAGAGA 857
QY 241 LeuProIleGly 243
DB 858 CTRACCAAA 866
RESULT 20
US-09-946-374-430
; Sequence 430, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
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PRIOR APPLICATION NUMBER: 60/1014712	PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/1014740	PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/1014755	PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/1014766	PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/1014779	PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/1014798	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/1017411	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/1017433	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/1019155	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/1019166	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/1020707	PRIOR FILING DATE: 1998-09-26	PRIOR APPLICATION NUMBER: 60/1020730	PRIOR FILING DATE: 1998-09-26	PRIOR APPLICATION NUMBER: 60/1022440	PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/1023070	PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/1023300	PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/1023311	PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/1024844	PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/1024870	PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/1025700	PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/1025711	PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/1026644	PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/1026870	PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/1029655	PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/1032558	PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/1033144	PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/1033155	PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/1033288	PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/1033955	PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/1033966	PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/1036788	PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/1036799	PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/1036799	PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/1037111	PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/1042570	PRIOR FILING DATE: 1998-10-14	PRIOR APPLICATION NUMBER: 60/1049870
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;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807
Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnGlyAla 40
DB 198 CTGCTGAGCTGCTCCCGCGCTGAGCGCTCTGAGATCCCGAGGAGGAGGAGGAGCG 257
QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyraSnglyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGATATGCTTACAGGCGCCAGCA 317
QY 61 GlyValProGlyArgArgGlySerProGlyValAlaSnglyMetCysLeuGlnGlyPro 80
DB 318 GAGTGTCTGTGTGAGAGCGGAGCCCTCGGCGCAATGTATTTCCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheIysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAGCTCGGATGATTCAG 437
QY 101 SerTrpThrProSnglyTyrosGlnCysSerTrpSerSerLeuSnglyIleAspLeu 120
DB 438 TCCTGGACACCAACATCAAGAGTGTTCATGAGTTCAATTAATGCAATAGATCTT 497
QY 121 GlyValIleAlaGlyCysThrPheThrIysMetArgSerArgSnglyIleAspLeu 140
DB 498 GGGAAATATGCGAGGTATTAATTAACAAAGATCGTTCAATATGCTCTTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuIysCysArgSnglyCysGlyGlnArgTrpIlePheThr 160
DB 558 TTGAGTGCTCCTGCTGCTTAATATGAGAAATGACATGCTGACGCTGTGATTTTCA 617
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleIleTyrosAspGln 180
DB 618 TTCAAATGAGAGCTGAATGTTAGAGACCTCTCCCATTAAGCTATTAATTTTGGACCA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeu 200
DB 678 GGAAGCCCTGAATGATTCACAAATTAATTCATCGCATCTCTCTGGAAGAGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAlaIleIleTyrosValGlyThrCysSerAsp 220
DB 738 TGTGAAGAGATTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProIysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlyGln 240

DB 798 TACCAAAAGAGAGATCTTACTGATGAGAAATTCAGTTCTCGCATTAATTGAGAA 857
QY 241 LeuProIys 243
DB 858 CTACCAAAA 866
RESULT 21
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; Sequence 121, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William J.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
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PRIOR FILING DATE: 1999-05-14
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PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142
Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-063-734-122 (1-243) x US-10-066-867-121 (1-1257)

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QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
DB 138 ATGGGAGCCCAAGGAGCCCGCCCTCCCGACGGGCTCCGCGCTCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGly 40
DB 198 CTGCTGACACCTGCGCCGCGCTGACGCGCTGAGATCCCAAGGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValValAlaLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 258 CAGCTCCGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
QY 61 GlyValProGlyArgArgProGlySerProGlyAlaAlaValLeuProGlyGly 80
DB 318 GGAAGTCCCTGCTGACACGGGAGCCCTGGGCGCAATGTTATTCGGGTACCTGGGATC 377
QY 81 ProGlyArgArgProGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAGGTCCGGATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
QY 101 SerTrpThrProAsnTrpLeuGlnCySerTrpSerSerLeuAsnTrpGlyLeu 120
DB 438 TCCTGGACACCCCACTACAGAGGTTCATGAGATTGATTAATGAGCATAGATCTT 497
QY 121 GlyLeuAlaGluCySerPheThrLeuMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTCGGAGGTACATTACAAAGATCGTTCAATAGTGTCTAGAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuCySerAsnAlaCySerGlnArgTrpTrpPheThr 160
DB 558 TTCAGTGGCTCACTCGGCTAAATCAGAAATGATGCTGAGGCTTGATTTCA 617
QY 161 PheAsnGlyAlaGluCySerGlyProLeuProGlnAlaLeuLeuLeuLeu 180
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DB 678 GGAAGCCCTGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
QY 201 CyGlnGlyLeuGlyAlaGlyLeuValAspValAlaLeuTrpValGlyTrpCySerAsp 220
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QY 221 TyrProGlyGlyAspAlaSerTrpGlyTrpAsnSerValSerArgLeuLeuLeu 240
DB 798 TACCCAAAAGAGATCTTCTACTGATGATGAAATTCAGTTCTGCAATTAATTAAGAA 857
QY 241 LeuProLeu 243
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RESULT 22
US-10-052-586-365
; Sequence 365, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15

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;; PRIOR APPLICATION NUMBER: 60/089908

Alignment Scores:

Pred. No.: 2,21e-144 Length: 1257
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Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-734-122 (1-243) x US-10-052-586-365 (1-1257)

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QY 41 GInuLeuArgGInuArgGInuArgLeuArgLeuArgLeuArgLeuArgLeu 60
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DB 318 GGAAGTCCCTGTCAAGCGGAGCGCTGCGGCAATGTATTCGGGTACCTGGGATC 377
QY 81 ProGInuArgAArgGInuArgGInuArgLeuArgLeuArgLeuArgLeuArgLeu 100
DB 378 CCAGTCCGAGTGTGATTCAGAGGAAAGGAGGAAATGTCTGAGGAAAGCTTTGAGG 437
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DB 438 TCCTGACACCACTCAAGCAGTGTCTGAGTTCATTAATGAAATGAGCATAGATCTT 497
QY 121 GInuArgLeuArgGInuArgGInuArgLeuArgLeuArgLeuArgLeuArgLeu 140
DB 498 GGGAAATTCGAGAGTGTATTAATGAAATGCTCTCAAGAGTTTGG 557

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DB 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTCCCATTTGAACTATATTTATTTGACCA 677
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DB 678 GGAAGCCCTGAAATGATTAATCAATTAATTCATGACACTTCTCTGGAAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAAATGCTGCTGATTAAGAGATGTTGCTATCTGGTGGCACTGTGTCAAGT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGln 240
DB 798 TACCCAAAAGAGATCTTCTACTGATGATGAAATTCAGTTTCTGCAATCATATTAAGA 857
QY 241 LeuProGly 243
DB 858 CTACCAAAA 866

RESULT 23
US-10-063-547-121
; Sequence 121, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; PRIORITY FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-547-121 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGGCCCGCGCTCCCGCAGCGGCTCGCGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlySerGlyLeuValAla 40
DB 198 CTGCTCAGCTGCGCCGCGCGCTGAGAGCTTCCCAAGGGAAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGAGAGGTGCTGACCTGTATTAATGAAATGTGCTTAACAAGGCCAGCA 317
```

```
QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGAGTCCGCTGAGAGCGGAGCCCTGGGCAATGTTATTCGGGTACACTTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuSerGlyGluCysLeuArgGluSerPheGluGln 100
DB 378 CCAAGTCGGGAGATTCAAAGAGAAAGGGGAGATGCTCAGGGAAGCTTGAAGAG 437
QY 101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGGACACCCCACTACAGCAGTGTTCATGAGCTTCATTAATTAATGCAATGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrThrIleAsnValSerSerAsnSerAlaLeuArgValLeu 140
DB 498 GGAAGAAATTCGGAGGTACATTTACAAAGATGCGTTCAATATGATGCTCTTAAGATTTC 557
QY 141 PheSerGlySerLeuArgLeuValAspValAlaCysCysGlnArgTrpTyrPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGATGCTGTCAGCGTTGATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTCCCATTTGAAGCTATTAATTTGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGAAATGATTAATCAATTAATTCATGACACTTCTCTGGAAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAAATGCTGCTGATTAAGAGATGTTGCTATCTGGTGGCACTGTGTCAAGT 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGln 240
DB 798 TACCCAAAAGAGATCTTCTACTGATGATGAAATTCAGTTTCTGCAATCATATTAAGA 857
QY 241 LeuProGly 243
DB 858 CTACCAAAA 866

RESULT 24
US-10-063-551-121
; Sequence 121, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; PRIORITY FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0
 US-10-063-734-122 (1-243) x US-10-063-551-121 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 |||||
 DB 138 ATGGACCCCGAGGCGCCCGCCCTCCCGCAGCGGCTCCGGCGGCTCTGCTGCTCCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGlyGly 40
 |||||
 DB 198 CTGCTGACAGCTGCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGGAGGAGGAGG 257

QY 41 GlnLeuArgGlnArgGlnValValaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
 |||||
 DB 258 CAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 317

QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 |||||
 DB 318 GGAGTGCTGTGTGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 377

QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 |||||
 DB 378 CAGGTCGGGAGTGATTCAG 437

QY 101 SerTrpThrProAsnTrpLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 |||||
 DB 438 TCCTGGACACCCAC 497

QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 |||||
 DB 498 GGGAAATTTGCGGAGTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557

QY 141 PheSerGlySerLeuArgLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
 |||||
 DB 558 TTCACTGGCTCACTTCGGCTTAAATGCAAGAAATGCAATGCTGCTGAGGCTTGATTTTCA 617

QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyreLeuAspGln 180
 |||||
 DB 618 TTCATGTGAGCTGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
 |||||
 DB 678 GGAAGCCCTGAAATTAATTCATTAATTCATTCATTCATTCATTCATTCATTCATTCAT 737

QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
 |||||
 DB 738 TGTGAAGAAATGCTGTGATTAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 797

QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlu 240
 |||||
 DB 798 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGATTCAGATTCAGATTCAGATTCAG 857

QY 241 LeuProlys 243
 |||||
 DB 858 CTACCAAAA 866

RESULT 25
 US-10-174-590-365
 ; Sequence 365, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Yian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 365
 ; LENGTH: 1257
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-174-590-365

Alignment Scores:
 Pred. No.: 2,21e-144 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-590-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
 |||||
 DB 138 ATGGACCCCGAGGCGCCCGCCCTCCCGAGGAGGCTCCGGCGGCTCTGCTGCTCCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGlyGly 40
 |||||
 DB 198 CTGCTGACAGCTGCCCGCCGCTGAGCGCTCTGAGATCCCAAGGAGGAGGAGGAGGAG 257

QY 41 GlnLeuArgGlnArgGlnValValaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
 |||||
 DB 258 CAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 317

QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
 |||||
 DB 318 GGAGTGCTGTGTGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 377

QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 |||||
 DB 378 CAGGTCGGGAGTGATTCAG 437

QY 101 SerTrpThrProAsnTrpLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 |||||
 DB 438 TCCTGGACACCCAC 497

QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
 |||||
 DB 498 GGGAAATTTGCGGAGTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557

QY 141 PheSerGlySerLeuArgLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
 |||||
 DB 558 TTCACTGGCTCACTTCGGCTTAAATGCAAGAAATGCAATGCTGCTGAGGCTTGATTTTCA 617

QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyreLeuAspGln 180
 |||||
 DB 618 TTTCAATGAGCTGATTCAG 677

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
 |||||
 DB 678 GGAAGCCCTGAAATTAATTCATTAATTCATTCATTCATTCATTCATTCATTCATTCAT 737

QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
 |||||
 DB 738 TGTGAAGAAATGCTGTGATTAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 797

QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlu 240
 |||||
 DB 798 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGATTCAGATTCAGATTCAGATTCAG 857

QY 241 LeuProlys 243
 |||||

DB 858 CTACCAAAA 866

RESULT 26

US-10-176-758-365

/ Sequence 365, Application US/10176758

/ Publication No. US20030008353A1

/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Chen, Jian

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Pan, James

/ APPLICANT: Smith, Victoria

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ TITLE OF INVENTION: ACIDS ENCODING THE SAME

/ FILE REFERENCE: P3430R1C104

/ CURRENT APPLICATION NUMBER: US/10/176,758

/ PRIOR FILING DATE: 2002-06-21

/ Prior Application removed - See File Wrapper or Palm

/ NUMBER OF SEQ ID NOS: 612

/ SEQ ID NO 365

/ LENGTH: 1257

/ TYPE: DNA

/ ORGANISM: Homo Sapien

US-10-176-758-365

Alignment Scores:

Pred. No.:	2,21e-144	Length:	1257
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-063-734-122 (1-243) x US-10-176-758-365 (1-1257)

QY 1 MetArpProGlnGlyProAlaAlaSerProGlnArGlyLeuLeuLeu 20

DB 138 ATCCGACCCCGAGGGGCGCGCTCCCGCAGCGGCTCCGCGCTCCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuVala 40

DB 198 CTGCTCAGCTGCCCGCGCGCTGAGCGCTGAGATCCCAAGGGGAAGCAAGGCG 257

QY 41 GlnLeuArGlnArGlyValaValaPleuTyrAnGlyMetCysLeuGlnGlyProAla 60

DB 258 CAGCTCCGGAGGGAGGGAGGTGTGACCTGTATTAAGAAATGTGTACAAAGGCCAGCA 317

QY 61 GlyValProGlyArGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80

DB 318 GAGGTCCCTGTGTGAGACGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377

QY 81 ProGlyArGlySerProGlyPheLeuGlyGlyGlyCysLeuArGlySerPheGluGlu 100

DB 378 CCAGGTCCGGATGATTCAAAGAGAAAGGGGAATGTCTGAGGAAAGCTTGAAGAG 437

QY 101 SerTrpThrProAsnTyrLeuGlnCysSerTrpSerSerLeuAsnTyrGlyIleAsn 120

DB 438 TCTTGACACCCCACTACCAAGAGGTCTACAGAGTTCATTAATATGCAATAGATCTT 497

QY 121 GlyLeuIleAlaGluCysThrPheThrIleMetArGlySerSerAsnSerAlaLeuArVala 140

DB 498 GGGAAATATGCGAGGTACATTTACAAAGATCGTTCAAAATGTCTCTAAGATTTTG 557

QY 141 PheSerGlySerLeuArGlyLeuValaValaPleuTyrAnGlyMetCysLeuGlnGlyProAla 160

DB 558 TTCAGTGTGCTCACTTGGCTAAATATGCAAGAAATGATGTGTGAGGCTGTGATTTTCA 617

QY 161 PheAnGlyAlaGluCysSerGlyProLeuProIleGluValaIleIleTyrLeuAsnGln 180

DB 618 TTCATGAGCTGAAATGTTTCAAGACCTCTCCCATTTGAAGCATATATTATTGAGCA 677

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArGlnSerSerValaGluGlyLeu 200

DB 678 GGAAGCCCTGAAATGATTCACAAATTAATTCATTCGCACTTCTGTGTGAGAGACTT 737

QY 201 CysGluGlyIleGlyAlaGlyLeuValaAsnValaIleIleTyrValaGlyThrCysSerAsp 220

DB 738 TGTGAAGAAATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797

QY 221 TyrProGlyArGlySerThrGlyTyrAsnSerValSerArGlyIleIleIleGluGlu 240

DB 798 TACCCAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 857

QY 241 LeuProGly 243

DB 858 CTACCAAAA 866

RESULT 27

US-10-175-737-365

/ Sequence 365, Application US/10175737

/ Publication No. US20030013153A1

/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Chen, Jian

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Pan, James

/ APPLICANT: Smith, Victoria

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ TITLE OF INVENTION: ACIDS ENCODING THE SAME

/ FILE REFERENCE: P3430R1C50

/ CURRENT APPLICATION NUMBER: US/10/175,737

/ PRIOR FILING DATE: 2002-06-19

/ Prior Application removed - See File Wrapper or Palm

/ NUMBER OF SEQ ID NOS: 612

/ SEQ ID NO 365

/ LENGTH: 1257

/ TYPE: DNA

/ ORGANISM: Homo Sapien

US-10-175-737-365

Alignment Scores:

Pred. No.:	2,21e-144	Length:	1257
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-063-734-122 (1-243) x US-10-175-737-365 (1-1257)

QY 1 MetArpProGlnGlyProAlaAlaSerProGlnArGlyLeuLeuLeu 20

DB 138 ATCCGACCCCGAGGGGCGCGCTCCCGCAGCGGCTCCGCGCTCCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuVala 40

DB 198 CTGCTCAGCTGCCCGCGCGCTGAGCGCTGAGATCCCAAGGGGAAGCAAGGCG 257

QY 41 GlnLeuArGlnArGlyValaValaPleuTyrAnGlyMetCysLeuGlnGlyProAla 60

DB 258 CAGCTCCGGAGGGAGGGAGGTGTGACCTGTATTAAGAAATGTGTACAAAGGCCAGCA 317

QY 61 GlyValProGlyArGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80

Db 318 GGAGTGCTGTGAGACGGAGCCCTGGGGCCCAATGTTATTCGGGTACACCTGGGATC 377
Qy 81 ProglYAAspGlyPheLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 100
Db 378 CCAAGTCCGAGATGATTCAG 437
Qy 101 SerTPThrProAsnTyrLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 120
Db 438 TCCTGACACCCCACTACAGACAGTGTTCATGAGATTCATGATTCATGATTCATGATTCATG 497
Qy 121 GlyLysIleAlaGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 140
Db 498 GGGAAATTTGGAGAGTACATTACAAAGATGCTTCAATAGTCTCTCAAGAGCTTTGG 557
Qy 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160
Db 558 TTCATGCTGCTCCTTCGCTTAAATGCAAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 617
Qy 161 PheAsnGlyAlaGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 180
Db 618 TTCATGAGAGTGAATGTTCAAGACCTTCCCATTTGAGCTATATTTTGGACCA 677
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyLysLeu 200
Db 678 GGAACCCCTGAATGAAATTCACAAATTAATTCATGCACTTCTCTGAGAGACTT 737
Qy 201 CysGlyLysIleGlyAlaGlyLysValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlyLys 240
Db 798 TACCAGAAAGAGATGCTTCTACTGATGAAATTCAGTTCTCGCATCATTAATGAGAA 857
Qy 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 28
US-10-063-616-121
; Sequence 121. Application US/10063616
; Publication No. US20030013855A1
GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gutney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) X US-10-063-616-121 (1-1257)
Qy 1 MetAtrProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCATCCCAAGGCGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleLeuProLysGlyLysGlyLysVal 40
Db 198 CTGCTGACGCTCCCGCCCGCTCAGAGCTCTTGAAGATCCCAAGGGAGAGAGAGAGAGCG 257
Qy 41 GlnLeuArgGlnArgGlyValAlaAspLeuTyrAsnGlyLysCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGAGAGAGTGTGTGACCTGTATATAGAAATGTGCTTACAGAGGCGACGA 317
Qy 61 GlyValProGlyAAspGlyLysProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GGAGTGCTGTGATC 377
Qy 81 ProglYAAspGlyPheLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 100
Db 378 CCAAGTCCGAGATGATTCAG 437
Qy 101 SerTPThrProAsnTyrLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 120
Db 438 TCCTGACACCCCACTACAGACAGTGTTCATGAGATTCATGATTCATGATTCATGATTCATG 497
Qy 121 GlyLysIleAlaGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 140
Db 498 GGGAAATTTGGAGAGTACATTACAAAGATGCTTCAATAGTCTCTCAAGAGCTTTGG 557
Qy 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160
Db 558 TTCATGCTGCTCCTTCGCTTAAATGCAAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 617
Qy 161 PheAsnGlyAlaGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 180
Db 618 TTCATGAGAGTGAATGTTCAAGACCTTCCCATTTGAGCTATATTTTGGACCA 677
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyLysLeu 200
Db 678 GGAACCCCTGAATGAAATTCACAAATTAATTCATGCACTTCTCTGAGAGACTT 737
Qy 201 CysGlyLysIleGlyAlaGlyLysValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlyLys 240
Db 798 TACCAGAAAGAGATGCTTCTACTGATGAAATTCAGTTCTCGCATCATTAATGAGAA 857
Qy 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 29
US-10-174-581-365
; Sequence 365. Application US/10174581
; Publication No. US20030017540A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, J'ian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gutney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41


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PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
```

Alignment Scores:

```

Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
```

US-10-063-734-122 (1-243) x US-10-174-581-365 (1-1257)

```

QY 1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGAGCCCGCCCTCCCGCAGCGGCTCCGCGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyLeuGInLeu 40
DB 198 CTGCTGAGCTGCGCGCCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 257
QY 41 GInLeuArgGInArgGInValValAlaSerLeuTYraGInGlyMetCysLeuGInGlyProAla 60
DB 258 CAGCTCCGCGAGAGGAGGAGTGTGAGCTGTATATGAAATGCTTCAAGGGCCACACA 317
QY 61 G1yValProG1yArgAspG1ySerProG1yAlaAsnVal11leProG1yThhProG1y1le 80
DB 318 GGAATGCTGCTGATCGAAGCGAGCCCTGGGCGCAATGTTATTCGCGTACACTGGGATC 377
QY 81 ProG1yArgAspG1yPheLeuG1yG1uLysG1yG1uG1yCysLeuArgG1uSerPheG1uG1u 100
DB 378 CCAGGTGCGGATGATTCAAAGAGAAAGGGGAGATGTGAGGAGAAAGCTTTGAGAG 437
QY 101 SerThhProAsnTYrLeuG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1nG1n 120
DB 438 TCCGGAACCCCACTACAGACAGTGTTCATGAGATTCATGAATATATGAGATGATCTT 497
QY 121 G1yLys1leAlaG1uG1yThhPheThhLysMetArgSerAsnSerAlaLeuArgValLeu 140
```

```

DB 498 GGGAAATTGGGAGTGTACATTATCAAAAGATGCGTTCAATATGCTCTAAGGTTTG 557
QY 141 PheSerG1ySerLeuArgLeuLysCysArgAsnAlaCysCysGInArgTYrPheThr 160
DB 558 TTCAGTGTCTCACTTCGCGCTAAATGCAAGAAATCAGTGTCTGAGCTGTGATTTTACA 617
QY 161 PheArgG1yAlaG1uG1yCysSerG1yProLeuPro11leG1uAl1le11eTYrLeuAspG1n 180
DB 618 TTCATGAGCTGATGATGTTCCAGACCTCTTCCATGAGCTATATATTTTGGACCAA 677
QY 181 G1ySerProG1uMetAsnSerThr11eAsn11eHisArgThhSerSerValG1uG1yLeu 200
DB 678 GGAAGCCCTGAATGAATTCAACAATTATTCATGCACTTCTTGGAAGACTT 737
QY 201 CysG1uG1y11eG1yAlaG1yLeuValAspValAla11eTYrPValG1yThhCysSerAsp 220
DB 738 TGTGAAGAAATGCTGCTGATGTGTGATGTGTCTATCTGCGGTGCGCACTGTTCAGAT 797
QY 221 TYrProLysG1yAspAlaSerThhG1yThhPheAsnSerValSerArg11e11eG1uG1u 240
DB 798 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGTTCTGCACTATTTAAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866
```

RESULT 30

```

US-10-176-483-365
Sequence 365, Application US/10176483
Publication No. US20030017541A1
GENERAL INFORMATION:
```

```

APPLICANT: Baker, Kevin P.
APPLICANT: Chan, Jian
APPLICANT: Deenoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C68
CURRENT APPLICATION NUMBER: US/10/176,483
PRIOR FILING DATE: 2002-06-20
Prior application removed - See file wrapper or Paim
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-483-365
```

Alignment Scores:

```

Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
```

US-10-063-734-122 (1-243) x US-10-176-483-365 (1-1257)

```

QY 1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGAGCCCGCCCTCCCGCAGCGGCTCCGCGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyLeuGInLeu 40
DB 198 CTGCTGAGCTGCGCGCCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 257
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QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGAGGTGGAGCTGTATTAAGAAATGCTTACAGGGCCAGCA 317
QY 61 G1yValProG1yArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 318 GGAGTCCCTGCTCGAAGACGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 377
QY 81 ProG1yArgAspG1yPheIySerG1yGluValCysLeuArgGluSerPheG1yGlu 100
DB 378 CCAGGTCGGAGTGGATTCAAGAGAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrIySerGlnCysSerTrpSerSerLeuAsnTyrG1yIleAspLeu 120
DB 438 TCCTGGACACCCCACTACAGACAGTGTCTCATGAGATTCAATTAATGACATAGATCTT 497
QY 121 G1yIyValIleAlaGluCysThrPheThrIyMetArgSerAsnSerAlaLeuArgValIleu 140
DB 498 GGGAAATTTGGCGAGGTACATTATTAAGATGCTTCAAAATGATGCTCTAAGAGTTTG 557
QY 141 PheSerG1ySerLeuArgLeuIySyrValArgAsnAlaCysCysGlnArgTrpIyPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGACAGAAATGATGCTGTCAGCGTTGGTATTTCACA 617
QY 161 PheAsnG1yAlaGluCysSerG1yProLeuProIleGluAlaIleIleTyrIleuAspGln 180
DB 618 TTCAAATGAGAGCTGAATGTTCAAGACCTCTTCCCATTAAGCTATTAATTTATTTGACCAA 677
QY 181 GlySerProG1yMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGAATGATTCACAAATTAATTCATCGACCTTCTGTGGAGAGACTT 737
QY 201 CysGluGlyIleG1yAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProIyG1yAspAlaSerThrGlyTTPanSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProIyS 243
DB 858 CTACCAAAA 866

RESULT 31
US-10-176-749-365
; Sequence 365, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-365

```

```

Alignment Scores:
Pred. No.: 2 21e-144
Score: 1301.00
Percent Similarity: 100.00%
Beet Local Similarity: 100.00%
Query Match: 100.00%
DB: 14

US-10-063-734-122 (1-243) x US-10-176-749-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaIleAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 20
DB 138 ATCCGACCCCAAGGGCCCGCCGCTCCCGGACGGGCTCCGGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProIyG1ySerG1yValIle 40
DB 198 CTGCTGCACTGCTCCCGCCGCTGAGCCGCTCTGAGATCCCAAGGGGAAAGAGGGCG 257
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGTGGAGCTGTATTAAGAAATGCTTACAGGGCCAGCA 317
QY 61 G1yValProG1yArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 318 GGAGTCCCTGCTCGAAGACGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 377
QY 81 ProG1yArgAspG1yPheIySerG1yGluValCysLeuArgGluSerPheG1yGlu 100
DB 378 CCAGGTCGGAGTGGATTCAAGAGAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrIySerGlnCysSerTrpSerSerLeuAsnTyrG1yIleAspLeu 120
DB 438 TCCTGGACACCCCACTACAGACAGTGTCTCATGAGATTCAATTAATGACATAGATCTT 497
QY 121 G1yIyValIleAlaGluCysThrPheThrIyMetArgSerAsnSerAlaLeuArgValIleu 140
DB 498 GGGAAATTTGGCGAGGTACATTATTAAGATGCTTCAAAATGATGCTCTAAGAGTTTG 557
QY 141 PheSerG1ySerLeuArgLeuIySyrValArgAsnAlaCysCysGlnArgTrpIyPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGACAGAAATGATGCTGTCAGCGTTGGTATTTCACA 617
QY 161 PheAsnG1yAlaGluCysSerG1yProLeuProIleGluAlaIleIleTyrIleuAspGln 180
DB 618 TTCAAATGAGAGCTGAATGTTCAAGACCTCTTCCCATTAAGCTATTAATTTATTTGACCAA 677
QY 181 GlySerProG1yMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGAATGATTCACAAATTAATTCATCGACCTTCTGTGGAGAGACTT 737
QY 201 CysGluGlyIleG1yAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProIyG1yAspAlaSerThrGlyTTPanSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProIyS 243
DB 858 CTACCAAAA 866

RESULT 32
US-10-176-914-365
; Sequence 365, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemlin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-914-365

```

DB 498 GGGAAATTGCGAGTGTACATTTCACAAAGATGCGTTCAAAATGATGCTTAAGATTGTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnAArgTrpYrPheThr 160
DB 558 TTCAGTGGCTCAGCTTCGGCTTAAGATGCAAAATGATGCTGCAAGGTTGATTTTCACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATATGAGCTGATGTTTCAAGACCTCTTCCCATTTGAAGCTATATTTATTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAACCCCTGGAATGATTAATCAATTAATATTCATGCACTTCTCTGGAAGACATT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGATTTGCTGCTGATTAAGATGATGCTGATCTGGATGGACCTTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTTCGATCATTTATTGAAGA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

RESULT 34
US-10-063-569-121
; Sequence 121, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION: US/10/063,569
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-569-121 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGCGCCCGCTCCCGCAGCGGCTCCGCGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLeuGlnValAla 40
DB 198 CTGCTGCACTGCTCCGCGGCTGACGCGCTCTGAAATCCCAAGGGAAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60

DB 258 CAGCTCCGACAGAGGAGAGTGTGAGCTGTATTAATGAAATGTGCTTACAAAGGCCACGA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAATGCTGCTGAGAGCGGAGCGCTCCGCTCAATGTTATTCGGGATCACCTGGAGATC 377
QY 81 ProGlyArgAspGlyPheIleGlyGluLysGlyCysLeuArgGluSerPheGluGlu 100
DB 378 CCAAGTCCGGAGATTTCAAGAGAAAGAGGAGATGCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGAGACCCCACTCAAGACAGATGTTCAATGATTCATTAATTAATGAGCATGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGGAAATTTGCGAGTGTACATTTCACAAAGATGCTTCACAAATGATGCTCTTAAGATTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpYrPheThr 160
DB 558 TTCAGTGGCTCAGCTTCGGCTTAAGATGCAAAATGATGCTGCAAGCTTTGATTTTCACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATATGAGCTGATGTTTCAAGACCTCTTCCCATTTGAAGCTATATTTATTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAACCCCTGGAATGATTAATCAATTAATATTCATGCACTTCTCTGGAAGACATT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGATTTGCTGCTGATTAAGATGATGCTGATCTGGATGGACCTTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGATGATTAATTCAGTTCTTCGATCATTTATTGAAGA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

RESULT 35
US-10-063-513-121
; Sequence 121, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION: US/10/063,513
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0

	Best Local Similarity:	100.00%	Mismatches:	0
	Query Match:	100.00%	Indels:	0
DB:	14		Gaps:	0

US-10-063-734-122 (1-243) x US-10-063-513-121 (1-1257)	
OY	1 MetArgProGInglYProAlAalAsErProGlInArghLeuArGlyLeuLeuLeuLeu 20
Db	138 ANGCGACCCCAAGGGCCCCGCCCTCCGCCAAGGGGCTCCGGGCCTCCTGCTCTTG 197
OY	21 LeuLeuGlnLeuProAlAPrOsErSerAlASerGluLeuProIyLySGInLYSAIA 40
Db	198 CTGTCTCACACTTCCCGCCGCGCTGAGGGCCCTGTGAATGCCCAAGGGAAAGCAAAGGCG 257
OY	41 GlnLeuArGlnArGlnValValAspLeuTYrAsnLIWetCySLeugInGIProAlA 60
Db	258 CAGCTCCGGCAGAGGAGGTGTGTGACCTGTATATGATGTGCTTACAAGGGCCAGCA 317
OY	61 GIYValProGIYAraApGIYSerProGIYAlAsnValIIeProGIYThrProGIYIle 80
Db	318 GGAGTTCCTGTGTGACAGCGGACCCTCGGGCCNAATTATTTCCGGGTACACCTGGGATC 377
OY	81 ProGIYAraAsnGlyPheLYSGInLYSGInGLUCyleuArGlyUSeRPhieGlnGU 100
Db	378 CAGGTCCGAGATGATTCANAGAAGAAAGGGAAATGTGAGGGAAACCTTGGAGAG 437
OY	101 SerTPThrProAsnTYrLYSGInCYSeRTripSerSerLeuAsnTYrGIYIleAspLeu 120
Db	438 TCCTGGACACCCCACTACAAGCAGTGTTCATGAGTTCAATTGAATTATGGCATTAAGNCTT 457
OY	121 GIYLYSIIeAlAGlucYsrThrPheThrLYMeLArgSerAnSerAlaleuArGVallLeu 140
Db	498 GGGAAATATGGAGAGTACATTACAAAAGATCGTTCAAAATGTGCTTMAAGATTG 557
OY	141 PHeSerGIYSerLeuArGrLeuLYScYArGAsnAlACYSCysGlnArGTPrYrPheThr 160
Db	558 TTCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGACGCTTGATTTTCACA 617
OY	161 PHeArngIYAlAGlucYSerGIYProLeuProIGluAlalleIleTYrLeuAspGln 180
Db	618 TTCATATGAGCTGAATGTTCAGAGACCTCTCCCATGAAGCTATAATTATTGGACCAA 677
OY	181 GlYSerProGIWMeLAnsErTrIIeAnIIeHISArGhsErSerValGIUGLYLeu 200
Db	678 GGAACCCCTGAATGAATTCACACATTAATATTCAATGCACTTCTGTGGAAAGACTT 737
OY	201 CYSGInGIYIeGIYAlAGlYLeuValAspValAlAlIleTYrValGIYThrCYSeSaSP 220
Db	738 TGTGAAGGAATGTGGCTCGATTAAGGATGGTGTATCTGGGTGGCACTTGTCAGAT 797
OY	221 TYrPOLYSGIYAspAlAsErThrGIYTTPanSerValSerArGIIeIIeGIUGln 240
Db	798 TACCAAAAGGAGATGCTTCACTGATGATGAATTCAGTTCTTCGACATCAATTATGAAGA 857
OY	241 LeuProLYs 243
Db	858 CTACCAAAA 866

RESULT 36

US-10-063-515-121

/ Sequence 121, Application US/10063515

/ Publication No. US2003018173A1

/ GENERAL INFORMATION:

/ APPLICANT: Eaton, Dan L.

/ APPLICANT: Filvaroff, Ellen

/ APPLICANT: Gerritsen, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Grimaldi, Christopher J.

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Macanabe, Colin K.

/ APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

	FILE OF INVENTION: ACIDS ENCODING THE SAME
	FILE REFERENCE: P3230R1C1
	CURRENT APPLICATION NUMBER: US/10/063,515
	CURRENT FILING DATE: 2002-05-01
	Prior Application removed - See File Wrapper or Palm
	NUMBER OF SEQ ID NOS: 170
	SEQ ID NO 121
	LENGTH: 1257
	TYPE: DNA
	ORGANISM: Homo Sapien
	US-10-063-515-121
	Alignment Scores:
	Pred. No.: 2,21e-144 Length: 1257
	Score: 1301.00 Matches: 243
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 100.00% Indels: 0
	Gaps: 0
	US-10-063-724-122 (1-243) x US-10-063-515-121 (1-1257)
QY	1 MetAArgProGInGlyPProAlaAlaSerProGInaGLeuAArgGlyLeuLeuLeuLeu 20
Db	138 ATGGGACCCAGGGAGCCCGCCGCTCCCGCAGCGGCTCCGGGCTCTGCTGCTCTG 197
QY	21 LeuLeuGInLeuPProAlaProSerSerAlaSerGInuLeProGlyVLYeGILtLYaAla 40
Db	198 CTGCTGGACGTCGCCCGCCGCTGAGACGCTCTGAGATCCCGAGGGAGCAAAAGCGC 257
QY	41 GInLeuAArgGInaArgGluValValaApleuTYraeNglyMetCYaLeuGInGlyProAla 60
Db	258 CAGCTCCGGCAGAGAGGAGGTGTGTGACCTGTATTGCAATGTGCTTCAAGAGCCACGCA 317
QY	61 GLYValProGlyAArgAArgGlySerProGlyAlaAenValIleProGlyTYThProGlyTYIle 80
Db	318 GGAATGCTCTGTGAGAGCGGAGCCCTGGGGCCAAATGTATTTCGGGTACCTGGAGATC 377
QY	81 ProGlyAArgAArgGlyPheuArgGlyGluGlyCySeLeuAArgGluSerPheGluGlu 100
Db	378 CCAAGTCGGAGATGATTCAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTGGAGAG 437
QY	101 SerTYrPheProAenTYrTYIeGInCYaSerTYrPSeSerLeuAenTYrGlyTYIleApleu 120
Db	438 TCCGTGACACCACTACAAAGCAGGTTCATGAGATTCATTGAATTTATGGCATATGATCTT 497
QY	121 GLYYseIleAAGluCYeThrPheThryLysMeLcAArgSerAenSerAlaLeuAArgValLeu 140
Db	498 GGGAAATTCGGAAGCTACATTTCAAAGATGCTTCAATATGCTCTTAAGATTTTG 557
QY	141 PheSerGlySerLeuAArgLeuLYCyAArgAenAlaCYCySeGInaArgTYrPheThr 160
Db	558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATCTGTGACGCTGGATTTTACA 617
QY	161 PheAenGlyValAGluCYaSerGlyProLeuProIleGInuAlaIleTYrLeuAArgGIn 180
Db	618 TTCATATGACCTAAATGTTCAAGACCTCTTCCCATTTGAAGCATTAATTTATTTGGACAA 677
QY	181 GlySerProGluAerAenSerThryIleAenIleHisArgThrSerSerValGluGlyLeu 200
Db	678 GGAAGCCCTGAATTAATGAAATTCACATTAATTAATTCATGCACTTCTCTGTGGAAAGACTT 757
QY	201 CyGGLuGlyTYIleGlyAlaGlyLeuValaApleuAlaIleTYrValAGlyThrCYaSerAap 220
Db	738 TGTGAAGGAATTTGCTGATTAAGATGTGTCATCTGGTGGCTGACCTGTTCATGAT 797
QY	221 TYrProLYeGlyAAspAlaSerThrGlyTYrAAsenValIserArgIleIleIleGluGIn 240
Db	798 TACCCAAAAGAGATCTCTTCTGAGTGAATTCAGTTTCTCCGATCATTTATTTGAAGAA 857
QY	241 LeuProLYs 243
Db	858 CTACCAAAA 866


```
RESULT 37
US-10-063-512-121
; Sequence 121, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIOR FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-512-121 (1-1257)
QY 1 MetArgProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGAGGCGCGCGCTCCGCGACGCGCTCCGCGCTCCGCTGCTC 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlnVala 40
DB 198 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValaValaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGCAGAGGAGGTGTGACCTGTATATGAAATGTCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyValArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGAGTCCGTGTGAGACCGGAGCCCTGGGGCCAATGTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyCysLeuArgGlnSerPheGlnGlu 100
DB 378 CCAAGCTCGGATGATTTCAAAGAGAAAGGGGAATGTCTGAGGAACCTTTGAGAG 437
QY 101 SerTyrThrProAsnTyrlsGlnCysSerTyrSerSerLeuAsnValIleAspLeu 120
DB 438 TCTGTGACACCCAACTACAAGCAGTGTTCATGAGTTCAATGAAATATGGCATAGATCTT 497
QY 121 GlyValIleAlaGlyCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGAATAATTCGAGAGTACATTTTAAAGATGCTTCAATAGTCTCTTAAAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuValArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGTGAGGCTTGATTTTCA 617
QY 161 PheAsnGlyValaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleTyrLeuAspGln 180
DB 618 TTCAAATGAGAGCTGAATGTTTCAAGACCTTCCCATTTGAAGCTATATTTATTTGACCA 677
```

```
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 678 GGAAGCCCTGGAATGATTAATCAACATTAATATTCATCGACTTCTGTGAGAGACTT 737
QY 201 CysGlnGlyIleGlyValaGlyLeuValaAspValaIleIleTyrValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATTTGGTGTGATTTAGTGAATGTGTGATCTGTGAGTGTGCACTTGTTCAGAT 797
QY 221 TyrProLeuGlyValaAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240
DB 798 TACCCAAAGAGAGATGCTTCTACTGAGATGAATTCAGTTCTGCAATCATTAATGAAGA 857
QY 241 LeuProIle 243
DB 858 CTACCAAAA 866

RESULT 38
US-10-173-706-365
; Sequence 365, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; PRIOR FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-706-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-173-706-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGAGGCGCGCGCTCCGCGACGCGCTCCGCGCTCCGCTGCTC 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlnVala 40
DB 198 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValaValaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGCAGAGGAGGTGTGACCTGTATATGAAATGTCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyValArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGAGTCCGTGTGAGACCGGAGCCCTGGGGCCAATGTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyCysLeuArgGlnSerPheGlnGlu 100
```

Db 378 CCAAGTCGGAGATGATTCAGAGAGAAAGGGGGAATGCTGAGGAGAAAGCTTTGAGAG 437
QY 101 SerTPthrProAsnTyrIleGlnCysSerTrpSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCCTGGACCCCACTACAGACAGTGTCAATGAGATTGAAATTAAGCATAGATCTT 497
QY 121 GlyIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGAGTGAATTCATTACAAAGATCGCTTCAAAATAGTCTCTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db 558 TTCAGTGGCTCACTTCGCTTAAATGCAAGAAATGCAATGCTGTCAGCGTTGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGAGCTGAATGTTTCAAGACCTCTTCCCATTAAGACTAATTAATTTGACCAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGATTCATCAACATTAATTCATGCACTTCTCTGGAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGCTGCTGATTAAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAGAGATGCTTCTTACTGATGATGATGATGATGATGATGATGATGATGATG 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 39
US-10-175-738-365
; Sequence 365, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175, 738
; CURRENT FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-738-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-175-738-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 138 ATTCACCCCAAGGCCCCCGCCCTCCCGAGGCGCTCCGCGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyIleGlnValAla 40
Db 198 CTGCTGAGCTGCCCCGCGCTGAGAGCCCTCTAGATCCCAAGGGGAAAGCAAGCGC 257
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCCGCAGAGGAGAGTGTGACCTGTATATGAAATGTGCTTAAAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
Db 318 GGAGTCCCTGCTCGAGACGGAGGAGCCCTGGGSCCAATGTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLysGlyGluLysGlyCysLeuArgGlyIleSerPheGluGlu 100
Db 378 CCAAGTCGGAGATGATTCAGAGAGAAAGGGGGAATGCTGAGGGAAGACTTTGAGAG 437
QY 101 SerTPthrProAsnTyrIleGlnCysSerTrpSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCCTGGACCCCACTACAGACAGTGTCAATGAGATTGAAATTAAGCATAGATCTT 497
QY 121 GlyIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGAGTGAATTCATTACAAAGATCGCTTCAAAATAGTCTCTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db 558 TTCAGTGGCTCACTTCGCTTAAATGCAAGAAATGCAATGCTGTCAGCGTTGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGAGCTGAATGTTTCAAGACCTCTTCCCATTAAGACTAATTAATTTGACCAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGATTCATCAACATTAATTCATGCACTTCTCTGGAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGCTGCTGATTAAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAGAGATGCTTCTTACTGATGATGATGATGATGATGATGATGATGATGATG 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 40
US-10-175-752-365
; Sequence 365, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jjian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175, 752

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; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-752-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-175-752-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 138 ATGCGACCCAGAGGCCCCCGCGCTCCCGACGCGCTCCGCGCTCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlnGly 40
Db 198 CTGCTGACAGTCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGATGTGCTTACAAAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTGCTGTGTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAAGTCCGGATGATTTCAAGAGAGAAAGGGGAATGTCTGAGGAAAGCTTGAAGAG 437
QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrIleAspLeu 120
Db 438 TCCTGACACCCCAATCAAGACAGTGTTCATGAGATTCAATGATGATGATCTT 497
QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerSerSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGGTGTACATTACAAAGATCGTTCAAAATGCTCTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
Db 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGCAAGCTTGTATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCAAATGAGACTGAATGTTCAAGACCTCTCCCATGAACTAATATTATTGACCAA 677
QY 181 GlySerProGlnMetLeuSerThrIleAsnIleHisArgThrSerSerValIleGluLeu 200
Db 678 GGAAGCCCTGAAATGATTTCAACAAATTAATTCATGCACTTCTTGAGAGAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATTTGCTGTGATTAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTG 797
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlu 240
Db 798 TACCCAAAAGAAATGCTTCTACTGATGATGAAATTCAGTTTCTGCAATATTAAAGAA 857
QY 241 LeuProGly 243
Db 858 CTACCAAAA 866

RESULT 41
US-10-176-482-365
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; Sequence 365, Application US/10176482
; Publication No. US2003002296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-482-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-482-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 138 ATGCGACCCAGAGGCCCCCGCGCTCCCGACGCGCTCCGCGCTCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlnGly 40
Db 198 CTGCTGACAGTCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGGAGGTGTGACCTGTATATGATGTGCTTACAAAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTGCTGTGTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAAGTCCGGATGATTTCAAGAGAGAAAGGGGAATGTCTGAGGAAAGCTTGAAGAG 437
QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrIleAspLeu 120
Db 438 TCCTGACACCCCAATCAAGACAGTGTTCATGAGATTCAATGATGATGATCTT 497
QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerSerSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGGTGTACATTACAAAGATCGTTCAAAATGCTCTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
Db 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGCAAGCTTGTATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCAAATGAGACTGAATGTTCAAGACCTCTCCCATGAACTAATATTATTGACCAA 677
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QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
| | | | |
Db 678 GGAAGCCCTGGAATGATTAATCAATTAATATTCATCGACCTTCTGTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTTPValGlyThrCysSerAsp 220
| | | | |
Db 738 TGTGAAGGAATGGTGTGATTAAGAGATGGTTCATCTGGGTGGCACTTGTTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTTPAsnSerValSerArgIleIleIleGluGlu 240
| | | | |
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATTAATTGAAGA 857
QY 241 LeuProLys 243
| | | | |
Db 858 CTACCAAAA 866

RESULT 42
US-10-176-757-365
; Sequence 365, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Pan, James
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C86
; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-757-365

Alignment Scores:
Pred. No.: 2,216-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-757-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnaGLeuArgGlyLeuLeuLeuLeu 20
| | | | |
Db 138 ATGCGACCCCGAGGGGCGCCGCGCTCCCGCAGCGCTCCGCGGCGCTCCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyIleGlnVala 40
| | | | |
Db 198 CTGCTGACGCTGCCCGCCCTCGAGCGCTCTGAGATCCCCAGGAGGAGCAAAAGCG 257
QY 41 GlnLeuArgGlnaGlyValaValaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
| | | | |
Db 258 CAGCTCCGGCAGAGGAGAGTGTGAGCTGTATATATGAGATGCTTCAAGGGGCAACA 317
QY 61 GlyValaProGlyArgAspGlySerProGlyValaAsnValaIleProGlyThrProGlyTle 80
| | | | |
Db 318 GGAAGTGGCTGTGTGACAGAGGAGCCCTGGGCGCAATGTTATTCGCGTACACTGGGATC 377
QY 81 ProGlyArgAspGlyPheIleGlyGluGlyGluCysLeuArgGluSerPheGlnIlu 100
| | | | |
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Db 378 CCAGTCCGGATGATTCAAAGAGAGAGGGGGAATGCTTGAGGAAGACTTTGAGAG 437
QY 101 SerTPThrProAsnTyrIleGlyIleCysSerTPSerSerLeuAsnTyrGlyTleAspLeu 120
| | | | |
Db 438 TCTTGACACCCCACTACAGACAGATGTTCAATGAGATTCATTAATTAATGATGATCTT 497
QY 121 GlyIleIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValaLeu 140
| | | | |
Db 498 GGGAAATATTCGCGATGTCATCTTACAAAGATGCGTTCAATAGCTCTTAAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuIleCysArgAsnAlaCysCysGlnaGlyTyrPheThr 160
| | | | |
Db 558 TTCAGTGGCTCCTTCGCGCTAAATGCGAATATCATGCTGTACGCGCTGGTATTTCACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
| | | | |
Db 618 TTCATGAGAGCTGATGATGTCAGACCTTCCCATTAAGCTAATTAATTTTGGACAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
| | | | |
Db 678 GGAAGCCCTGGAATGATTAATCAATTAATATTCATCGCACTTCTTGTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTTPValGlyThrCysSerAsp 220
| | | | |
Db 738 TGTGAAGGAATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTTPAsnSerValSerArgIleIleIleGluGlu 240
| | | | |
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATTAATTGAAGA 857
QY 241 LeuProLys 243
| | | | |
Db 858 CTACCAAAA 866

RESULT 43
US-10-176-913-365
; Sequence 365, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C86
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-913-365

Alignment Scores:
Pred. No.: 2,216-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-913-365 (1-1257)
```

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QY 1 MetatpProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
Db 138 ATGCCACCCCAAGGCCCCCGCTCCCGACGCGCTCCGCGCTCTGCTGCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGly 40
Db 198 CTGCTGACAGCTCCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValValAlaPleuTyraGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCCGCAGAGGAGGTGTGAGCCTGTATTAAGATGTCTTACAAAGGCGCAGCA 317
QY 61 GlyValProGlyArgGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80
Db 318 GAGAGTCCCTGCTGAGACCGGACCTCGGGCCAAATGTTATTCGCGGTACCTGGAGATC 377
QY 81 ProGlyArgAspGlyPheLeuSerGlyGlyGlyGlyCysLeuArgGlyLeuSerPheGln 100
Db 378 CCAGGTCCGGATGATTAAGAGAAAGGGAATGTCGAGGAAAGCTTTGAGAG 437
QY 101 SerTPThrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlsIleAspleu 120
Db 438 TCCTGGACACCCCAACTACAGAGTGTTCATGAGATTGATTAATGCAATGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGGAGTGTACATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTPThrPheThr 160
Db 558 TTCAGTGGCTCACTTGCGCTAAATGCAAAATGCAATGCTGAGGCTTGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlsLeuAspGln 180
Db 618 TTCAATGAGCTGGAATGTTTCAAGACCTTCTCCATGAAGCTAATATTTATTTGAGCAA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737
QY 201 CysGlnGlyIleGlyValAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGTTGCTATCTGGGTGGCACTTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTPAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCAATCATTAATGAAGA 857
QY 241 LeuProLys 243
Db 858 CTAACAAA 866
RESULT 44
US-10-180-552-365
; Sequence 365, Application US/10180552
; Publication No. US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Ausetin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C153
; CURRENT APPLICATION NUMBER: US/10/180,552
; CURRENT FILING DATE: 2002-06-25
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO. 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-180-552-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-180-552-365 (1-1257)
QY 1 MetatpProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 20
Db 138 ATGCCACCCCAAGGCCCCCGCTCCCGACGCGCTCCGCGCTCTGCTGCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGly 40
Db 198 CTGCTGACAGCTCCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValValAlaPleuTyraGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCCGCAGAGGAGGTGTGAGCCTGTATTAAGATGTCTTACAAAGGCGCAGCA 317
QY 61 GlyValProGlyArgGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80
Db 318 GAGAGTCCCTGCTGAGACCGGACCTCGGGCCAAATGTTATTCGCGGTACCTGGAGATC 377
QY 81 ProGlyArgAspGlyPheLeuSerGlyGlyGlyGlyCysLeuArgGlyLeuSerPheGln 100
Db 378 CCAGGTCCGGATGATTAAGAGAAAGGGAATGTCGAGGAAAGCTTTGAGAG 437
QY 101 SerTPThrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlsIleAspleu 120
Db 438 TCCTGGACACCCCAACTACAGAGTGTTCATGAGATTGATTAATGCAATGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGGAGTGTACATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTPThrPheThr 160
Db 558 TTCAGTGGCTCACTTGCGCTAAATGCAAAATGCAATGCTGAGGCTTGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlsLeuAspGln 180
Db 618 TTCAATGAGCTGGAATGTTTCAAGACCTTCTCCATGAAGCTAATATTTATTTGAGCAA 677
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737
QY 201 CysGlnGlyIleGlyValAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGTTGCTATCTGGGTGGCACTTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTPAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCAATCATTAATGAAGA 857
QY 241 LeuProLys 243
Db 858 CTAACAAA 866
RESULT 45
US-10-180-557-365
; Sequence 365, Application US/10180557
```

```
Publication No. US20030022301A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
PRIORITY FILING DATE: 2002-06-25
PRIORITY APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-734-122 (1-243) x US-10-180-557-365 (1-1257)

Alignment Scores:
Pred. No.: 2,21e-144      Length: 1257
Score: 1301.00           Matches: 243
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 14                     Gaps: 0

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuLeuLeuLeu 20
Db 138 ATGGACCCCGAGGCGCCGCCCTCCCGCAGCGGCTCCGCGGCTCCTGCTGCTCCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyLeuGlnIle 40
Db 198 CTGCTGCGAGCTGCCCGCCGCTCGAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyraAngIyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGGAGGTGGTGAACCTGTATATGGAATGCTTCAAGGGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTGCTGTGTCAGACGAGGAGCCCTGGGGCCAAATGTTATTCGCGGTACACCTGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGluTyraAngIyGluCysLeuArgGlySerPheGlnGlu 100
Db 378 CCAAGTCCGAGATGATTCAAAGAGAAAAGGGGGAATGCTCGAGGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrlYsGlnCysSerTrpSerSerLeuAsnTyrlIleAspLeu 120
Db 438 TCCGTGACACCCCACTACAGACAGTGTTCATGATGATTAATGAGCATAGATCTT 497
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTCGGAGGTGATCTTTCACAAAGATGCTTCAAAATAGTCTTAAAGATTG 557
QY 141 PheSerGlySerLeuArgLeuLeuTyraArgAsnAlaCysCysGlnArgTrpIysPheThr 160
Db 558 TTCAGTGGCTCACTTCGGCTAAATGCAAGATGATCTGTACGCGTGTGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlLeuAspGln 180
Db 618 TTCATATGAGCTGATGATTCAAGACCTTCTCCATTTGAAGCTATATTAATTATGAGCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGluLeu 200
```

```
Db 678 GGAAGCCCTGGAATATTCACATTAATTAATTCACACTTCTTCTGGAAGGACTT 737
QY 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGTGTGTGATTAAGTATGATGTGTGTATCTGGTGGCACTGTTCAGAT 797
QY 221 TyrProGlyArgAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCAAAAGAGAGATCTTCACTGATGATGAGAAATTCAGTTCTCCATCATTAATTGAAGAA 857
QY 241 LeuProIys 243
Db 858 CTACCAAAA 866

RESULT 46
US-10-063-502-121
Sequence 121, Application US/10063502
Publication No. US20030023042A1
GENERAL INFORMATION:
APPLICANT: Baton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
PRIORITY FILING DATE: 2002-05-01
PRIORITY APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 121
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-502-121

Alignment Scores:
Pred. No.: 2,21e-144      Length: 1257
Score: 1301.00           Matches: 243
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 14                     Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-502-121 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuLeuLeuLeu 20
Db 138 ATGGACCCCGAGGCGCCGCCCTCCCGCAGCGGCTCCGCGGCTCCTGCTGCTCCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyLeuGlnIle 40
Db 198 CTGCTGAGAGCTGCCCGCCGCTCGAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyraAngIyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGGAGGTGGTGAACCTGTATTAATGATGATGCTTCAAGGGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTGCTGTGTCAGACGAGGAGCCCTGGGGCCAAATGTTATTCGCGGTACACCTGGATC 377
QY 81 PheGlyArgAspGlyPheLeuGlyGluTyraAngIyGluCysLeuArgGlySerPheGlnGlu 100
Db 378 CCAAGTCCGAGATGATTCAAAGAGAAAAGGGGGAATGCTCGAGGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrlYsGlnCysSerTrpSerSerLeuAsnTyrlIleAspLeu 120
```

```
Db 438 TCCTGGACACCCAACTACAGAGAGTGTTCATGAGTTCAATTATATGACATAGATCTT 497
Qy 121 G1yVsl1eAlaGluCyThrPheThrlyMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGATGATCATTTACAAAGATGCCCTTCAAAATAGTCTCTAAGAGTTTGG 557
Qy 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160
Db 558 TTCAGTGGCTCACTTGGCTTAAATACAGAAATGATGCTGTCAAGCTTGGATTTCACA 617
Qy 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyLeuAspGln 180
Db 618 TTCAAATGGAGCTGAATGTTCAAGACCTCTTCCATTGAAGCTATATTTATTTGACCAA 677
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGATTCACAAATTAATTCATCGACATTCCTCTGGAAGACATTT 737
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAAATGGTGTCTGATATGATGATGTGCTATCTGGGTGCACTGTGTCAAGT 797
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAAGAGAGATGCTTCTACTGATGAGATTCAGTTTCTCGCATCATTTATGAAGA 857
Qy 241 LeuProLys 243
Db 858 CTACCAAAA 866
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RESULT 47

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US-10-173-700-365
; Sequence 365, Application US/10173700
; Publication No. US20030027262A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C14
; CURRENT APPLICATION NUMBER: US/10/173,700
; PRIOR FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-700-365
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Alignment Scores:

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Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
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US-10-063-734-122 (1-243) x US-10-173-700-365 (1-1257)

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Qy 1 MetArgProGlnGlyProAlaAspProGlnArgGlyLeuLeuLeuLeu 20
Db 138 ATCGACCCCGAGGCCCGCGCTCCCGCCAGCGGCTCGGGGCTCCGCTGCTCTCG 197
```

```
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLeuGlnLysAla 40
Db 138 CTGCTGCACTGCTCCCGCCCGCTCGAGCCCTCTGAGATCCCAAGGGAAGGAAAAAGCGG 257
Qy 41 GlnLeuArgGlnArgGlyValValAspLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCCGCAGAGGAGGAGGTGGTGAAGCTGTATATGAAATGTGCTTCAAGAGGCCAGCA 317
Qy 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GGAGTGGCTGTGAGAGCGGAGCCCTGGGGCAATGTATTTCCGGATACACTGGAGATC 377
Qy 81 ProGlyArgAspGlyPheLysGlyValLysGlyGluCysLeuArgGlySerPheGluGln 100
Db 378 CAGGTCCGAGTGAATTCACAAAGAAAGAGGAGAAATGTCTGAGGAAAGACTTTTGAAGAG 437
Qy 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120
Db 438 TCCTGGACACCCAACTACAGACAGTGTTCATGAGATTCATTGAATTAATGACATAGATCTT 497
Qy 121 G1yVsl1eAlaGluCyThrPheThrlyMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGATGATCATTTACAAAGATGCCCTTCAAAATAGTCTCTAAGAGTTTGG 557
Qy 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160
Db 558 TTCAGTGGCTCACTTGGCTTAAATACAGAAATGATGCTGTCAAGCTTGGATTTCACA 617
Qy 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyLeuAspGln 180
Db 618 TTCAAATGGAGCTGAATGTTCAAGACCTCTTCCATTGAAGCTATATTTATTTGACCAA 677
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGATTCACAAATTAATTCATCCACTTCTCTGTGGAAGACATTT 737
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAAATGGTGTCTGATATGATGATGTGCTATCTGGGTGCACTGTGTCAAGT 797
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAAGAGAGTCTTCTACTGATGAGATTCAGTTTCTCGCATCATTTATGAAGA 857
Qy 241 LeuProLys 243
Db 858 CTACCAAAA 866
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RESULT 48

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US-10-174-572-365
; Sequence 365, Application US/10174572
; Publication No. US20030027263A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C40
; CURRENT APPLICATION NUMBER: US/10/174,572
; PRIOR FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
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; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-572-365

Alignment Scores:
Pred. No.: 2,21e-144      Length: 1257
Score: 1301.00           Matches: 243
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 14                     Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-572-365 (1-1257)

QY 1 MetArpProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 138 ATGCGACCCCAAGGCCCCCGCCCTCCCGCAGCGGCTCGGGCTTCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnYsAla 40
Db 198 CTGCTGCACTCCCGCGCCGCTGAGCGCTCTGAGATCCCAAGGGGAAGCAAGGG 257
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGGCAGAGGAGGTGTGTGACCTGTATTAATGAAATGCTTACAGAGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80
Db 318 GGAAGTCCCTGCTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 377
QY 81 ProGlyArgAspGlyPheIysGlyGlyIysGlyCysLeuArgGlnSerPheGlnGln 100
Db 378 CCAAGTCCGGAGATGATTCAAAGAGAGAAAGGGGGAATGTCTAGGGAAAGCTTGAAGAG 437
QY 101 SerTPhrProAsnTyrIysGlnCysSerTyrPseSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCTCGACACCCCACTACAGACAGTGTTCATGAGATTCATTAATTAATGCAATGATCTT 497
QY 121 GlyIysIleAlaGlnCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTTGGCGAGTGTATCAATTCAAAAGATGCGTTCAAAATGCTCTTAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
Db 558 TTCAGTGGCTCACTTCGGCTAAATAAGCAAAATGATGCTGTCAAGGTGGATTTCA 617
QY 161 PheAsnGlnValGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
Db 618 TTCAATGAGAGCTGATGTTCAGGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCA 677
QY 181 GlySerProGlnMetArgSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db 678 GGAAGCCTGAAATGATTCACAAATTAATTAATTCAGCACTTCTGTGGAAGAGACTT 737
QY 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
Db 738 TGTAAAGGAATGTGGTGTGATTAATGATGTTCATCTGGGTGGGCACTTGTTCAAGAT 797
QY 221 TyrProIysGlyAspAlaSerThrGlyTyrPheAsnSerValSerArgIleIleIleGlnGln 240
Db 798 TACCAAAAGAGAGATGCTTCTACTGATGATGATTCAGATTTCTCGCATCTATTAAGAA 857
QY 241 LeuProIys 243
Db 858 CTACCAAAA 866

RESULT 49
US-10-174-579-365
; Sequence 365, Application US/10174579
; Publication No. US20030027264A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

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; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C31
; CURRENT APPLICATION NUMBER: US/10/174,579
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-579-365

Alignment Scores:
Pred. No.: 2,21e-144      Length: 1257
Score: 1301.00           Matches: 243
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 14                     Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-579-365 (1-1257)

QY 1 MetArpProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db 138 ATGCGACCCCAAGGCCCCCGCCCTCCCGCAGCGGCTCGGGCTTCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnYsAla 40
Db 198 CTGCTGCACTCCCGCGCCGCTGAGCGCTCTGAGATCCCAAGGGGAAGCAAGGG 257
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C36
; CURRENT APPLICATION NUMBER: US/10/174,582
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
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GenCore version 5.1.6
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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6      ; APPLICANT: Ashkenazi, Avi J.
7      ; APPLICANT: Goddard, Audrey
8      ; APPLICANT: Godowski, Paul
9      ; APPLICANT: Gutney, Austin L.
10     ; APPLICANT: Polakis, Paul
11     ; APPLICANT: Williams, P. Mickey
12     ; APPLICANT: Wood, William I.
13     ; APPLICANT: Mu, Thomas D.
14     ; APPLICANT: Zhang, Zhenh.
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16     ; FILE REFERENCE: P5009R1
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23     ; PRIOR APPLICATION NUMBER: 60/097,022
24     ; PRIOR FILING DATE: 1998-08-18
25     ; PRIOR APPLICATION NUMBER: 60/101,922
26     ; PRIOR FILING DATE: 1998-09-24
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US-09-938-418-2

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Db 901 TTATTATGCTTGAATGTTCACTTAATGACATTTTAATTAAGTTATGTAATACATCT 960
Qy 961 GAATGAAAAGCAAGCTAAATAATGTTTACAGACCAAAAGTGATTTTACACTGTTTAA 1020
Db 961 GAATGAAAAGCAAGCTAAATAATGTTTACAGACCAAAAGTGATTTTACACTGTTTAA 1020
Qy 1021 ACTGACATTATTCATTTTGTCTTCAATCAAAAGTGTTCAATTTTATTTAGTTGCT 1080
Db 1021 ACTGACATTATTCATTTTGTCTTCAATCAAAAGTGTTCAATTTTATTTAGTTGCT 1080
Qy 1081 AGAATACCTTCTTCATAGTCACTTCTCAACCTTAATTTGGAATTTGTTGCTCT 1140
Db 1081 AGAATACCTTCTTCATAGTCACTTCTCAACCTTAATTTGGAATTTGTTGCTCT 1140
Qy 1141 TTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
Db 1141 TTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
Qy 1201 AATTTGTAATGTTAGAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1257
Db 1201 AATTTGTAATGTTAGAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1257

RESULT 2

US-09-946-374-430
Sequence 430, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCES: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821

PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
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PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23

1	PRIOR APPLICATION NUMBER: 60/101447
2	PRIOR FILING DATE: 1998-09-23
3	PRIOR APPLICATION NUMBER: 60/101475
4	PRIOR FILING DATE: 1998-09-23
5	PRIOR APPLICATION NUMBER: 60/101476
6	PRIOR FILING DATE: 1998-09-23
7	PRIOR APPLICATION NUMBER: 60/101477
8	PRIOR FILING DATE: 1998-09-23
9	PRIOR APPLICATION NUMBER: 60/101479
10	PRIOR FILING DATE: 1998-09-23
11	PRIOR APPLICATION NUMBER: 60/101738
12	PRIOR FILING DATE: 1998-09-24
13	PRIOR APPLICATION NUMBER: 60/101744
14	PRIOR FILING DATE: 1998-09-24
15	PRIOR APPLICATION NUMBER: 60/102207
16	PRIOR FILING DATE: 1998-09-24
17	PRIOR APPLICATION NUMBER: 60/102240
18	PRIOR FILING DATE: 1998-09-29
19	PRIOR APPLICATION NUMBER: 60/102307
20	PRIOR FILING DATE: 1998-09-29
21	PRIOR APPLICATION NUMBER: 60/102330
22	PRIOR FILING DATE: 1998-09-29
23	PRIOR APPLICATION NUMBER: 60/102331
24	PRIOR FILING DATE: 1998-09-29
25	PRIOR APPLICATION NUMBER: 60/102484
26	PRIOR FILING DATE: 1998-09-30
27	PRIOR APPLICATION NUMBER: 60/102487
28	PRIOR FILING DATE: 1998-09-30
29	PRIOR APPLICATION NUMBER: 60/102570
30	PRIOR FILING DATE: 1998-09-30
31	PRIOR APPLICATION NUMBER: 60/102571
32	PRIOR FILING DATE: 1998-09-30
33	PRIOR APPLICATION NUMBER: 60/102684
34	PRIOR FILING DATE: 1998-10-01
35	PRIOR APPLICATION NUMBER: 60/102687
36	PRIOR FILING DATE: 1998-10-01
37	PRIOR APPLICATION NUMBER: 60/102965
38	PRIOR FILING DATE: 1998-10-02
39	PRIOR APPLICATION NUMBER: 60/103258
40	PRIOR FILING DATE: 1998-10-06
41	PRIOR APPLICATION NUMBER: 60/103314
42	PRIOR FILING DATE: 1998-10-07
43	PRIOR APPLICATION NUMBER: 60/103315
44	PRIOR FILING DATE: 1998-10-07
45	PRIOR APPLICATION NUMBER: 60/103328
46	PRIOR FILING DATE: 1998-10-07
47	PRIOR APPLICATION NUMBER: 60/103395
48	PRIOR FILING DATE: 1998-10-07
49	PRIOR APPLICATION NUMBER: 60/103396
50	PRIOR FILING DATE: 1998-10-07
51	PRIOR APPLICATION NUMBER: 60/103401
52	PRIOR FILING DATE: 1998-10-07
53	PRIOR APPLICATION NUMBER: 60/103449
54	PRIOR FILING DATE: 1998-10-06
55	PRIOR APPLICATION NUMBER: 60/103633
56	PRIOR FILING DATE: 1998-10-08
57	PRIOR APPLICATION NUMBER: 60/103678
58	PRIOR FILING DATE: 1998-10-08
59	PRIOR APPLICATION NUMBER: 60/103679
60	PRIOR FILING DATE: 1998-10-08
61	PRIOR APPLICATION NUMBER: 60/103711
62	PRIOR FILING DATE: 1998-10-08
63	PRIOR APPLICATION NUMBER: 60/104257
64	PRIOR FILING DATE: 1998-10-14
65	PRIOR APPLICATION NUMBER: 60/104987
66	PRIOR FILING DATE: 1998-10-20
67	PRIOR APPLICATION NUMBER: 60/105000

[illegible]

Db 781 TTGGCAGCTTGTTCAGATTACCCAAAAGAGATGCTTCTACGTGATGGAATTCAGTTCTC 840
Qy 841 GGATGATTTATGAGAACTACCAAAATTAATGCTTAATTTTCACTTGCTACTCTTTT 900
Db 841 GGATGATTTATGAGAACTACCAAAATTAATGCTTAATTTTCACTTGCTACTCTTTT 900
Qy 901 TTATTAATGCTTGAATGCTTCACTTAATTAATGATTTAATTAATGATTAATCATCT 960
Db 901 TTATTAATGCTTGAATGCTTCACTTAATTAATGATTTAATTAATGATTAATCATCT 960
Qy 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTGACAGCTGTTTAA 1020
Db 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTGACAGCTGTTTAA 1020
Qy 1021 ATCTGACATTAATTCATTTGCTTCATCAAAAGTGCTTCATTAATTTTATGTTGCT 1080
Db 1021 ATCTGACATTAATTCATTTGCTTCATCAAAAGTGCTTCATTAATTTTATGTTGCT 1080
Qy 1081 AGAATACCTTCTTCATAGTACATCTCTCAACCTTAATTTGGAATTTGTTGCTCT 1140
Db 1081 AGAATACCTTCTTCATAGTACATCTCTCAACCTTAATTTGGAATTTGTTGCTCT 1140
Qy 1141 TTTGTTTTTCTCTTAGTATAGATTTTAAAAAATATPAAAGCTACCAATCTTTGAC 1200
Db 1141 TTTGTTTTTCTCTTAGTATAGATTTTAAAAAATATPAAAGCTACCAATCTTTGAC 1200
Qy 1201 AATTGTAAATGTAGATTTTATTAATCTGTTAAATTAATTAATTTTCCAA 1257
Db 1201 AATTGTAAATGTAGATTTTATTAATCTGTTAAATTAATTAATTTTCCAA 1257

RESULT 3
US-10-006-867-121
Sequence 121, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Baton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/006, 867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/064215
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088734
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PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101475
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PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24

DB 781 TTGGCATTGTTGAGATTACCCAAAGAGAGTCCTTCTAGTGAGTAATTCAGTTTC 840
QY 841 GGATCATTTATGAGAACTACCAATAATGCTTAATTTTCATTGCTGCTCTTTT 900
DB 841 GGATCATTTATGAGAACTACCAATAATGCTTAATTTTCATTGCTGCTCTTTT 900
QY 901 TTATTTGCTTGGATGTTGCTTCACTTAATGACATTTTAATGTTTATGTTATCATCT 960
DB 901 TTATTTGCTTGGATGTTGCTTCACTTAATGACATTTTAATGTTTATGTTATCATCT 960
QY 961 GAATGAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTTACAGCTGTTTAA 1020
DB 961 GAATGAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTTACAGCTGTTTAA 1020
QY 1021 ACTGACATTTATTCATTTTCTGCTTCAATCAAAAGTGTGATTTTATGTTTATGTT 1080
DB 1021 ACTGACATTTATTCATTTTCTGCTTCAATCAAAAGTGTGATTTTATGTTTATGTT 1080
QY 1081 AGAATACCTTCTTCATGATGACATTCCTCAACCTTAATTTGGAATATGTTGCTG 1140
DB 1081 AGAATACCTTCTTCATGATGACATTCCTCAACCTTAATTTGGAATATGTTGCTG 1140
QY 1141 TTTGTTTTTCTCTAGTATGATGATTTTAAAAAATATAAAGCTACCAATCTTTGAC 1200
DB 1141 TTTGTTTTTCTCTAGTATGATGATTTTAAAAAATATAAAGCTACCAATCTTTGAC 1200
QY 1201 AATTTGTAATGTTAAGAAATTTTAAAAAATATAAAGCTACCAATCTTTGAC 1257
DB 1201 AATTTGTAATGTTAAGAAATTTTAAAAAATATAAAGCTACCAATCTTTGAC 1257

RESULT 4
US-10-052-586-365
Sequence 365, Application US/10052586
Publication No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
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PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/077649
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06

[illegible]

Db 781 TTGGCACTTGTTCAGATTACCCAAAGAGAGTCTTCTACTGATGAGTAATTCAGTTTC 840
QY 841 GGATCATTTATGAGAACTACCAAAATPAATGCTTAATTTTCACTTGTGACTCTTTT 900
Db 841 GCACTATTATGAGAACTACCAAAATPAATGCTTAATTTTCACTTGTGACTCTTTT 900
QY 901 TTATTATGCTTGGAAATGCTTCACTTAAATGACATTTTAAATAGTTATGATACATCT 960
Db 901 TTATTATGCTTGGAAATGCTTCACTTAAATGACATTTTAAATAGTTATGATACATCT 960
QY 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAAAGTGTGATTTTCACTGTTTTTA 1020
Db 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAAAGTGTGATTTTCACTGTTTTTA 1020
QY 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTGTTT 1080
Db 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTGTTT 1080
QY 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGTCT 1140
Db 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGTCT 1140
QY 1141 TTGTTTCTTCTCTAGTATGATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200
Db 1141 TTGTTTCTTCTCTAGTATGATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257
Db 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257

RESULT 5

US-10-063-547-121
; Sequence 121, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Malanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-121

Query Match 100.0%; Score 1257; DB 13; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGGCGCGCGGTGAAAGCGGATGATGACAGCTGCGGCGGCTCGAGAGCGG 60
Db 1 GGAGAGAGGCGCGCGGTGAAAGCGGATGATGACAGCTGCGGCGGCTCGAGAGCGG 60
QY 61 CGGAGCAGAGCGGTGCAAGCTTCTCTGCTGCTCGGCTCGAGCTCGGCGCTG 120
Db 61 CGGAGCAGAGCGGTGCAAGCTTCTCTGCTGCTCGGCTCGAGCTCGGCGCTG 120
QY 121 CCGGAGCGCGGAGCGGATCGAAGCGGAGCGCGCGCTCGGCGAGCGGCTCGGCG 180
Db 121 CCGGAGCGCGGAGCGGATCGAAGCGGAGCGCGCGCTCGGCGAGCGGCTCGGCG 180

QY 181 GCCTCTGCTGCTCTGCTGCTGCTGAGCTGCCGCGCGCTGAGCGGCTGAGATCCCA 240
Db 181 GCCTCTGCTGCTCTGCTGCTGCTGAGCTGCCGCGCGCTGAGCGGCTGAGATCCCA 240
QY 241 AGGGAGAGCAAAAGCGAGCTCCGCGAGAGGAGTGTGACCTGTATTAATGAAATG 300
Db 241 AGGGAGAGCAAAAGCGAGCTCCGCGAGAGGAGTGTGACCTGTATTAATGAAATG 300
QY 301 GCTTACAAAGGCGCAGAGAGTGCCTGTCGAGAGCGGAGCCCTGGGCGCAATGTAATC 360
Db 301 GCTTACAAAGGCGCAGAGAGTGCCTGTCGAGAGCGGAGCCCTGGGCGCAATGTAATC 360
QY 361 CGGCTACACCTGAGATCCAGAGTGGAGATGATTTCAAGAGAAAAGGGGAAATGCTGA 420
Db 361 CGGCTACACCTGAGATCCAGAGTGGAGATGATTTCAAGAGAAAAGGGGAAATGCTGA 420
QY 421 GGAGAAAGCTTGAAGAGTCTGAGACCCCACTACAGAGAGTGTCAAGAGTTCATGA 480
Db 421 GGAGAAAGCTTGAAGAGTCTGAGACCCCACTACAGAGAGTGTCAAGAGTTCATGA 480
QY 481 ATTATGAGATAGATCTTGGGAAATGCGGAGTGTACATTTACAAAGATGCCCTCAATA 540
Db 481 ATTATGAGATAGATCTTGGGAAATGCGGAGTGTACATTTACAAAGATGCCCTCAATA 540
QY 541 GTGCTTAAGAGTGTTCAGAGGCTCACTCGGCTAAATGACAAATGACATGCTGTC 600
Db 541 GTGCTTAAGAGTGTTCAGAGGCTCACTCGGCTAAATGACAAATGACATGCTGTC 600
QY 601 AGCGTGTATTTTCAATTCATTAAGAGTGAATGTTTCAAGAGCTCTTCCATGAAGTA 660
Db 601 AGCGTGTATTTTCAATTCATTAAGAGTGAATGTTTCAAGAGCTCTTCCATGAAGTA 660
QY 661 TAATTTATTTGACCAAGAGAGCGCTGAATGATTTCAACATTTATTCATGCACTT 720
Db 661 TAATTTATTTGACCAAGAGAGCGCTGAATGATTTCAACATTTATTCATGCACTT 720
QY 721 CTTCTGAGAGAGACTTGTGAAGAAATGAGTGTGATGATGATGATGATGATGATG 780
Db 721 CTTCTGAGAGAGACTTGTGAAGAAATGAGTGTGATGATGATGATGATGATGATG 780
QY 781 TTGGCACTTGTTCAGATTACCCAAAGAGAGTCTTCACTGAGTGAATTCAGTTTCTC 840
Db 781 TTGGCACTTGTTCAGATTACCCAAAGAGAGTCTTCACTGAGTGAATTCAGTTTCTC 840
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCACTTGTCTCTTTT 900
Db 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCACTTGTCTCTTTT 900
QY 901 TTATTATGCTTGGAAATGCTTCACTTAATGACATTTTAAATAGTTATGATACATCT 960
Db 901 TTATTATGCTTGGAAATGCTTCACTTAATGACATTTTAAATAGTTATGATACATCT 960
QY 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAAAGTGTGATTTTCACTGTTTTTA 1020
Db 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAAAGTGTGATTTTCACTGTTTTTA 1020
QY 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTGTTT 1080
Db 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTGTTT 1080
QY 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGTCT 1140
Db 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGTCT 1140
QY 1141 TTGTTTCTTCTTATGATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200
Db 1141 TTGTTTCTTCTTATGATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257
Db 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257

```
RESULT 6
US-10-063-551-121
; Sequence 121, Application US/10063551
; Publication No. US20020183494A1
GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-121

Query Match      100.0%; Score 1257; DB 13; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAAAGCGCATTTGAGCTTCGGCGGCGCTCGAGAGCGCG 60
DB 1 GGAAGAGAGCGCGCGGGTGAAAAGCGCATTTGAGCTTCGGCGGCGCTCGAGAGCGCG 60
QY 61 CGAGAGCGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCGCGGAGCGCATGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCCGCGAGCGCGGAGCGCATGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGT 300
DB 241 AGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGT 300
QY 301 GCTTACAAAGGCGCGAGAGGTCTGTGAGAGCGGAGCCCTGCGGCGCAATGTATTC 360
DB 301 GCTTACAAAGGCGCGAGAGGTCTGTGAGAGCGGAGCCCTGCGGCGCAATGTATTC 360
QY 361 CGGGAACCTGGAATCCAGGTGCGGATGATTCAAAGAGAAAAGGCGGAGTGTCTGA 420
DB 361 CGGGAACCTGGAATCCAGGTGCGGATGATTCAAAGAGAAAAGGCGGAGTGTCTGA 420
QY 421 GGGAAAGCTTGGAGAGTCTGAGACCCCACTAACACAGTTCATGAGTTTATTTGA 480
DB 421 GGGAAAGCTTGGAGAGTCTGAGACCCCACTAACACAGTTCATGAGTTTATTTGA 480
QY 481 ATATGAGCATAGATCTTGGAGAAAATTTGGAGGTGACATTTACAAAGATGCTTCAATA 540
DB 481 ATATGAGCATAGATCTTGGAGAAAATTTGGAGGTGACATTTACAAAGATGCTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCATCTCGGCTAAATGCGAATGATGCTGTCT 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCATCTCGGCTAAATGCGAATGATGCTGTCT 600
QY 601 AGGCTTGATTTTCACTCAATGAGAGTGAATGTTTCAGAGCTCTTCCCATGAGCTA 660
```

```
DB 601 AGGCTTGATTTTCACTCAATGAGAGTGAATGTTTCAGAGCTCTTCCCATGAGCTA 660
QY 661 TAATTTATTTGGAGCAAGAAAGCCCTGAATGAATTTCAACATTAATTTATGTCACCT 720
DB 661 TAATTTATTTGGAGCAAGAAAGCCCTGAATGAATTTCAACATTAATTTATGTCACCT 720
QY 721 CTTCTGTGGAAGAGCTTGTGAGAGAAATGCTGTGAGTGTAGTGAATGCTGATCTGCGG 780
DB 721 CTTCTGTGGAAGAGCTTGTGAGAGAAATGCTGTGAGTGTAGTGAATGCTGATCTGCGG 780
QY 781 TTGGCACTTGTGAGATTTACCAAGAGAGATGCTTCTACTGATGAGTGAATTCAGTTTCTC 840
DB 781 TTGGCACTTGTGAGATTTACCAAGAGAGATGCTTCTACTGATGAGTGAATTCAGTTTCTC 840
QY 841 GCATATATTTGAAGACTACCAAAATTAATGCTTTAATTTTCTACTGATCTCTTTT 900
DB 841 GCATATATTTGAAGACTACCAAAATTAATGCTTTAATTTTCTACTGATCTCTTTT 900
QY 901 TTATATGCTTGTGAATGCTTCACTTAATGACATTTTAATAGTTTATGATATACCT 960
DB 901 TTATATGCTTGTGAATGCTTCACTTAATGACATTTTAATAGTTTATGATATACCT 960
QY 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGGTGATTTCACTGTTTAA 1020
DB 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGGTGATTTCACTGTTTAA 1020
QY 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGGTTTCAATTTTGTGTTGTT 1080
DB 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGGTTTCAATTTTGTGTTGTT 1080
QY 1081 AGAATACCTTCTTCAATGACATTTCTCAACCTTATATTTGGAATATGTTGTGCTCT 1140
DB 1081 AGAATACCTTCTTCAATGACATTTCTCAACCTTATATTTGGAATATGTTGTGCTCT 1140
QY 1141 TTTGTTTCTCTTGAATGACATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTCTCTTGAATGACATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTATTTTCAACA 1257
DB 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTATTTTCAACA 1257

RESULT 7
US-10-174-590-365
; Sequence 365, Application US/10174590
; Publication No. US2003008352A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-365
```


Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGAGAGAGGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGCGCG 60
DB 1 GGAGAGAGGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGCGCG 60
QY 61 CGAGAGCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CGGAGAGCGGAGAGCGATCCGACCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
DB 121 CGGAGAGCGGAGAGCGATCCGACCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGAGAGAGAAAAGGCGAGCTCCGCGAGAGAGAGTGTGACCTGTATATGAAATGT 300
DB 241 AGGAGAGAGAAAAGGCGAGCTCCGCGAGAGAGAGTGTGACCTGTATATGAAATGT 300
QY 301 GCTTACAAAGGCGCAGAGAGAGTCCGTGTGAGAGCGGAGCCCTGAGGCGCAATGTATTC 360
DB 301 GCTTACAAAGGCGCAGAGAGAGTCCGTGTGAGAGCGGAGCCCTGAGGCGCAATGTATTC 360
QY 361 CGGAGTACACCTGAGGATCCAGGTCGGAGTGTGATTCAGAGAGAGAAAAGGAGGATGTCTGA 420
DB 361 CGGAGTACACCTGAGGATCCAGGTCGGAGTGTGATTCAGAGAGAGAAAAGGAGGATGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGAGAGTGTATGAGAGTTCATGTA 480
DB 421 GGGAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGAGAGTGTATGAGAGTTCATGTA 480
QY 481 ATTATGAGCATAGATCTTGGGAAAATTGGCGAGTGTACATTTACAAAGATGCCGTCAATA 540
DB 481 ATTATGAGCATAGATCTTGGGAAAATTGGCGAGTGTACATTTACAAAGATGCCGTCAATA 540
QY 541 GTGCTCTAAGAGTGTGTCTCAAGTGTCTCACTTCGGCTAAATGACAGAAATGACATGCTGTTC 600
DB 541 GTGCTCTAAGAGTGTGTGTCTCAAGTGTCTCACTTCGGCTAAATGACAGAAATGACATGCTGTTC 600
QY 601 AGCGTGTGATTTCAATTCATGATGAGCTGATGTTTCAAGACCTCTTCCCATTTGAAGCTTA 660
DB 601 AGCGTGTGATTTCAATTCATGATGAGCTGATGTTTCAAGACCTCTTCCCATTTGAAGCTTA 660
QY 661 TAATTTATTTGAGCAAGAGAGCCCTGAATGAAATGAAATTCATTAATTTATTCAGACTT 720
DB 661 TAATTTATTTGAGCAAGAGAGCCCTGAATGAAATGAAATTCATTAATTTATTCAGACTT 720
QY 721 CTTCCTGTGAGAGACTTTGTGAGAAATGATGCTGATGATGATGATGATGATGATGATG 780
DB 721 CTTCCTGTGAGAGACTTTGTGAGAAATGATGCTGATGATGATGATGATGATGATGATG 780
QY 781 TTGGCACTTTGATGATTAACCAAAAGAGAGTCTTCTACTGTGATGAAATTCAGTTCTTC 840
DB 781 TTGGCACTTTGATGATTAACCAAAAGAGAGTCTTCTACTGTGATGAAATTCAGTTCTTC 840
QY 841 GGATCATTTATTAAGAACTACCAAAATTAATGCTTTAAATTTTCAATTTGCTACCTCTTTT 900
DB 841 GGATCATTTATTAAGAACTACCAAAATTAATGCTTTAAATTTTCAATTTGCTACCTCTTTT 900
QY 901 TTATTAATGCTTGAATGATGCTTAATTAATGATGATGATGATGATGATGATGATGATG 960
DB 901 TTATTAATGCTTGAATGATGCTTAATTAATGATGATGATGATGATGATGATGATGATG 960
QY 961 GAATGAAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTTAA 1020
DB 961 GAATGAAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTTAA 1020
QY 1021 ATCTAGCATATTCATTTGCTTCAATCAAAAGTGTTCATATATTTTATTTAGTTGTT 1080
  
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DB 1021 ATCTAGCATATTCATTTGCTTCAATCAAAAGTGTTCATATATTTTATTTAGTTGTT 1080
QY 1081 AGAATACCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 AGAATACCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTTATTCGTTAATATTAATTAATTTTCAACA 1257
DB 1201 AATTTGTAATGTTAAGATTTTATTTATTCGTTAATATTAATTAATTTTCAACA 1257

```

RESULT 8
 US-10-176-758-365
 ; Sequence 365, Application US/10176758
 ; Publication No. US20030008353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C104
 ; CURRENT APPLICATION NUMBER: US/10/176/758
 ; PRIOR FILING DATE: 2002-06-21
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 365
 ; LENGTH: 1257
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-176-758-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGAGAGAGGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGCGCG 60
DB 1 GGAGAGAGGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGCGCG 60
QY 61 CGAGAGCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CGGAGAGCGGAGAGCGATCCGACCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
DB 121 CGGAGAGCGGAGAGCGATCCGACCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGAGAGAGAAAAGGCGAGCTCCGCGAGAGAGAGTGTGACCTGTATATGAAATGT 300
DB 241 AGGAGAGAGAAAAGGCGAGCTCCGCGAGAGAGAGTGTGACCTGTATATGAAATGT 300
QY 301 GCTTACAAAGGCGCAGAGAGAGTCCGTGTGAGAGCGGAGCCCTGAGGCGCAATGTATTC 360
DB 301 GCTTACAAAGGCGCAGAGAGAGTCCGTGTGAGAGCGGAGCCCTGAGGCGCAATGTATTC 360
  
```


QY 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840
DB 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840
QY 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTGCTACCTCTTTT 900
DB 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTGCTACCTCTTTT 900
QY 901 TTAATTAAGCTTGGATGCTGATCACTTAATGATATTTAAATAGTTAATGATATCT 960
DB 901 TTAATTAAGCTTGGATGCTGATCACTTAATGATATTTAAATAGTTAATGATATCT 960
QY 961 GAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTTTTAA 1020
DB 961 GAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTTTTAA 1020
QY 1021 ATCTAGCAATTATCAATTTGCTTCAATCAAAAGTGTTCATATATTTTAAAGTTGTT 1080
DB 1021 ATCTAGCAATTATCAATTTGCTTCAATCAAAAGTGTTCATATATTTTAAAGTTGTT 1080
QY 1081 AGAATCTTCTTCATAGTCACATCTCTCAACCTAATTTGGAATATGTTGCTGCT 1140
DB 1081 AGAATCTTCTTCATAGTCACATCTCTCAACCTAATTTGGAATATGTTGCTGCT 1140
QY 1141 TTGTTTCTTCTTCTAGTATAGCAATTTTAAATTAATTAAGCTACCAATCTTTGAC 1200
DB 1141 TTGTTTCTTCTTCTAGTATAGCAATTTTAAATTAATTAAGCTACCAATCTTTGAC 1200
QY 1201 AATTGTAAATGTTAAGAAATTTTAAATGCTTAAATTAATTAATTTTCAACA 1257
DB 1201 AATTGTAAATGTTAAGAAATTTTAAATGCTTAAATTAATTAATTTTCAACA 1257

RESULT 10

US-10-063-616-121
; Sequence 121, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerstlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Matarabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-121
Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3 4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCGCTCGGCGCCTCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCGCTCGGCGCCTCGAGCGCG 60
QY 61 CGAGAGCAAGCGTGACGAGCTTCTCTCGGTCTCTCCGCGCTCCGAGCTCCGGCTG 120
DB 61 CGAGAGCAAGCGTGACGAGCTTCTCTCGGTCTCTCCGCGCTCCGAGCTCCGGCTG 120
QY 1201 CCCGAGCGCGGAGCATGCGACCCGAGGCGCGCGCTCCGCGAGCGGCTCCGCG 180

DB 121 CCCGAGCGCGGAGCATGCGACCCGAGGCGCGCGCTCCGCGAGCGGCTCCGCG 180
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AAGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAGCTGTAAATGGAATGT 300
DB 241 AAGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAGCTGTAAATGGAATGT 300
QY 301 GCTTACAGGCGCAGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCTTACAGGCGCAGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CGGCTACCTGCGGATCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 CGGCTACCTGCGGATCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 GGGAAAGCTTGAAGAGTCTGGAACACCACTACCAAGAGTGTGCTGCTGCTGCTGCT 480
DB 421 GGGAAAGCTTGAAGAGTCTGGAACACCACTACCAAGAGTGTGCTGCTGCTGCTGCT 480
QY 481 ATTATGCAATGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCTTCAATA 540
DB 481 ATTATGCAATGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCTTCAATA 540
QY 541 GTGCTTAAGAGTTTGTTCAGTGTCTCACTTCCGCTAAATGCAAAATGCAATGCTG 600
DB 541 GTGCTTAAGAGTTTGTTCAGTGTCTCACTTCCGCTAAATGCAAAATGCAATGCTG 600
QY 601 AGGCTGTAAATTCATCAATGAGCTGAATGTTCAAGAGCTCTTCCCATGGAAGCTA 660
DB 601 AGGCTGTAAATTCATCAATGAGCTGAATGTTCAAGAGCTCTTCCCATGGAAGCTA 660
QY 661 TAATTAATTTGCAACCAAGAGGCGCTGAATGATTAATTAATTAATTTTCAACTG 720
DB 661 TAATTAATTTGCAACCAAGAGGCGCTGAATGATTAATTAATTAATTTTCAACTG 720
QY 721 CTTCGTGAGAGACTTGTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CTTCGTGAGAGACTTGTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840
DB 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTC 840
QY 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTGCTACCTCTTTT 900
DB 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTGCTACCTCTTTT 900
QY 901 TTAATTAAGCTTGGATGCTGATCACTTAATGATATTTAAATAGTTAATGATATCT 960
DB 901 TTAATTAAGCTTGGATGCTGATCACTTAATGATATTTAAATAGTTAATGATATCT 960
QY 961 GAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTTTTAA 1020
DB 961 GAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTTTTAA 1020
QY 1021 ATCTAGCAATTATCAATTTGCTTCAATCAAAAGTGTTCATATATTTTAAAGTTGTT 1080
DB 1021 ATCTAGCAATTATCAATTTGCTTCAATCAAAAGTGTTCATATATTTTAAAGTTGTT 1080
QY 1081 AGAATCTTCTTCATAGTCACATCTCTCAACCTAATTTGGAATATGTTGCTGCT 1140
DB 1081 AGAATCTTCTTCATAGTCACATCTCTCAACCTAATTTGGAATATGTTGCTGCT 1140
QY 1141 TTGTTTCTTCTTCTAGTATAGCAATTTTAAATTAATTAAGCTACCAATCTTTGAC 1200
DB 1141 TTGTTTCTTCTTCTAGTATAGCAATTTTAAATTAATTAAGCTACCAATCTTTGAC 1200
QY 1201 AATTGTAAATGTTAAGAAATTTTAAATGCTTAAATTAATTAATTTTCAACA 1257

Db 1201 AATTGTAATGTAAGAAATTTTATATCTGTTAAATAAATATTCCACA 1257

RESULT 11

US-10-174-581-365

Sequence 365, Application US/10174581

Publication No. US20030017540A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C41

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US/10/174,581

PRIOR FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: 10/052586

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063564

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063734

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/063870

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066120

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/066466

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/066772

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/069335

PRIOR FILING DATE: 1997-12-11

PRIOR APPLICATION NUMBER: 60/069425

PRIOR FILING DATE: 1997-12-12

PRIOR APPLICATION NUMBER: 60/069870

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/068017

PRIOR FILING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/078886

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079786

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/080107

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080194

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080327

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333

PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/081049

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081070

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/081195

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: 60/081838

PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/082568

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/082569

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/082704

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082797

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/083495

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083496

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083499

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083559

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/084366

PRIOR FILING DATE: 1998-05-05

PRIOR APPLICATION NUMBER: 60/084414

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: 60/084639

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084640

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084643

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/085573

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085580

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085582

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085700

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/086023

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/086392

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/086486

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087098

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087208

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
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 PRIOR APPLICATION NUMBER: 60/088033
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 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
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 PRIOR APPLICATION NUMBER: 60/088212
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 PRIOR APPLICATION NUMBER: 60/088217
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 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088555
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088722
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088740
 PRIOR FILING DATE: 1998-06-10
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 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088863
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089090
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3 4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAGAGAGCGCGGGGTGAAGCGCATTTGATGACGCTCGGCGGCTCGGAGCGCG 60
 1 GGAGAGAGCGCGGGGTGAAGCGCATTTGATGACGCTCGGCGGCTCGGAGCGCG 60
 61 CGAGGCAACGCTGACCAAGTTCCTCTCGGCTCGGCTCGGCTCGGCTCGGCTCG 120
 61 CGAGGCAACGCTGACCAAGTTCCTCTCGGCTCGGCTCGGCTCGGCTCGGCTCG 120
 121 CCGGAGCGCGGAGCATGCGACCCAGGCGCCCGCGCTCCCGCAGCGGCTCGCG 180

121 CCGGAGCGCGGAGCATGCGACCCAGGCGCCCGCGCTCCCGCAGCGGCTCGCG 180
 181 GCTCTCTGCT 240
 181 GCTCTCTGCT 240
 241 AGGGAGAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGTGAACCTGTAAATGAAATG 300
 241 AGGGAGAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGTGAACCTGTAAATGAAATG 300
 301 GCTTCAAGGCGCAGAGAGTCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 301 GCTTCAAGGCGCAGAGAGTCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 361 CGGTAACCTGAGATCCAGGTCCGAGATGATTAAGAGAGAGAGAGAGAGAGAGAG 420
 361 CGGTAACCTGAGATCCAGGTCCGAGATGATTAAGAGAGAGAGAGAGAGAGAGAG 420
 421 GGGAAAGCTTTGAGAGTCTGGAACCCAGCTAACAGAGAGTTCATGAGATTCATGA 480
 421 GGGAAAGCTTTGAGAGTCTGGAACCCAGCTAACAGAGAGTTCATGAGATTCATGA 480
 481 ATTATGCAATGATCTTGGGAAATTCGAGGTGATCATTTTCAAAAGATGCTTCAATA 540
 481 ATTATGCAATGATCTTGGGAAATTCGAGGTGATCATTTTCAAAAGATGCTTCAATA 540
 541 GTGCTTAAGATTTTGTTCAGTGTCTCATCTTGGTAAATGCAAGATGCTGTCTC 600
 541 GTGCTTAAGATTTTGTTCAGTGTCTCATCTTGGTAAATGCAAGATGCTGTCTC 600
 601 AGCGTTGATTTTCAATTCANAGAGAGTGAATGTTTCAAGAGCTCTTCCATTTGAAGCTA 660
 601 AGCGTTGATTTTCAATTCANAGAGTGAATGTTTCAAGAGCTCTTCCATTTGAAGCTA 660
 661 TAATTTATTTGAGCAAGAGAGCCCTGAATGATTCACAAATTAATTTATTCATTCGACCTT 720
 661 TAATTTATTTGAGCAAGAGAGCCCTGAATGATTCACAAATTAATTTATTCATTCGACCTT 720
 721 CTTCGTGAGAGACTTTTGTGAAGATTTGTGTGAGATTTAGTGAATGTTCTATTCGGG 780
 721 CTTCGTGAGAGACTTTTGTGAAGATTTGTGTGAGATTTAGTGAATGTTCTATTCGGG 780
 781 TTGGCACTTGTCAAGTTACCAAAAGAGAGCTTCTTCAAGAGATTCAGTTCTC 840
 781 TTGGCACTTGTCAAGTTACCAAAAGAGAGCTTCTTCAAGAGATTCAGTTCTC 840
 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTTTT 900
 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTTTT 900
 901 TTATTATGCTTGAAGTGTCACTTAATGACATTTTAATTAATGATTTATGATACATCT 960
 901 TTATTATGCTTGAAGTGTCACTTAATGACATTTTAATTAATGATTTATGATACATCT 960
 961 GAATGAAAGCAAGGATTAATGTTTACAGCAAGAGTATTCACAGCTTTTAA 1020
 961 GAATGAAAGCAAGGATTAATGTTTACAGCAAGAGTATTCACAGCTTTTAA 1020
 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGGTGTTCAATTTTATTTAGTTGTT 1080
 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGGTGTTCAATTTTATTTAGTTGTT 1080
 1081 AGAATATCTTCTTCAATGATCAATTCCTCAACCTTAATTTGGAATATTTGTGTGCT 1140
 1081 AGAATATCTTCTTCAATGATCAATTCCTCAACCTTAATTTGGAATATTTGTGTGCT 1140
 1141 TTGTGTTTTCTTCAATGATCAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200
 1141 TTGTGTTTTCTTCAATGATCAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200
 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTTAATTAATTAATTTATTTCAACA 1257

Db 1201 AATTGTAAAGTAAAGATTTTATATCTGTAAATAAATAATTATTTCCACA 1257

RESULT 12
US-10-176-483-365
; Sequence 365, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; PRIORITY FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-483-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGAGCGCGCGGGAAGGCGCATTTGATGACCTTGCGGCGGCTCCGAGCGCG 60
Db 1 GGAGAGAGCGCGCGGGAAGGCGCATTTGATGACCTTGCGGCGGCTCCGAGCGCG 60

Qy 61 CGAGACGACGCTGACCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 61 CGAGACGACGCTGACCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120

Qy 121 CCGGCGACCGGAGACCATGCGACCCCGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 121 CCGGCGACCGGAGACCATGCGACCCCGCGCGCTCTCTCTCTCTCTCTCTCTCTCT 180

Qy 181 GCTCTCTGCT 240
Db 181 GCTCTCTGCT 240

Qy 241 AGGGAAGCAAAAGGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 241 AGGGAAGCAAAAGGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

Qy 301 GCTTAAGAGGCGCGACGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 301 GCTTAAGAGGCGCGACGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

Qy 361 CGGGAACCTTGAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 CGGGAACCTTGAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

Qy 421 GGGAAAGCTTGAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 421 GGGAAAGCTTGAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480

Qy 481 AATTAGCATGATCTTGGGAAATTTGGGAGTGTACATTTTCAAAAGATGGCTCAATA 540
Db 481 AATTAGCATGATCTTGGGAAATTTGGGAGTGTACATTTTCAAAAGATGGCTCAATA 540

Qy 541 GTGCTTAAGAGTCTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTCTC 600

Db 541 GTGCTTAAGAGTCTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTCTC 600

Qy 601 ACGTTGGTATTTCACATTCATGAGCTGATGTTTCAGACCTCTTCCATGAACTA 660
Db 601 ACGTTGGTATTTCACATTCATGAGCTGATGTTTCAGACCTCTTCCATGAACTA 660

Qy 661 TAATTATTTGGACCAAGAAAGCCCTGAATGAATTCACATTAATATTCATGCACTT 720
Db 661 TAATTATTTGGACCAAGAAAGCCCTGAATGAATTCACATTAATATTCATGCACTT 720

Qy 721 CTTCTGTGAAGAGCTTGTGAAGAAATGCTGATTAATGATGATGATGATGATGATG 780
Db 721 CTTCTGTGAAGAGCTTGTGAAGAAATGCTGATTAATGATGATGATGATGATGATG 780

Qy 781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGATGAAATTCAGTTCTC 840
Db 781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGATGAAATTCAGTTCTC 840

Qy 841 GCATCATTAATGAAAGATACCAAAATTAATGCTTAAATTTTCAATTTGCTTACTCTT 900
Db 841 GCATCATTAATGAAAGATACCAAAATTAATGCTTAAATTTTCAATTTGCTTACTCTT 900

Qy 901 TTATTATGCTTGAAGTGTCACTTAATGACATTTTAAATTAATGATTAATGATTAAT 960
Db 901 TTATTATGCTTGAAGTGTCACTTAATGACATTTTAAATTAATGATTAATGATTAAT 960

Qy 961 GAATGAAAGCAAAAGCTTAATATGTTTACAGCAAAAGTGAATTCACACTGTTTAA 1020
Db 961 GAATGAAAGCAAAAGCTTAATATGTTTACAGCAAAAGTGAATTCACACTGTTTAA 1020

Qy 1021 ATCTAGCATTAATTCATTTTGTCTCAATCAAAAGGTTTCAATATTTTGTGTTT 1080
Db 1021 ATCTAGCATTAATTCATTTTGTCTCAATCAAAAGGTTTCAATATTTTGTGTTT 1080

Qy 1081 AGAATACCTTCTCATATGATGACATTTCTCAACTATTAATTTGAAATATGTTGTGTC 1140
Db 1081 AGAATACCTTCTCATATGATGACATTTCTCAACTATTAATTTGAAATATGTTGTGTC 1140

Qy 1141 TTTGTTTTTCTCTTATTAATGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1200
Db 1141 TTTGTTTTTCTCTTATTAATGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1200

Qy 1201 AATTGTAAAGTAAAGATTTTATATCTGTAAATAAATAATTATTTCCACA 1257
Db 1201 AATTGTAAAGTAAAGATTTTATATCTGTAAATAAATAATTATTTCCACA 1257

RESULT 13
US-10-176-749-365
; Sequence 365, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; PRIORITY FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257

TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-749-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGAGAGCGCGCGGGGTAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGCGGGGTAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
QY 61 CGAGAGCAGACGCTGACACGTTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CGAGAGCAGACGCTGACACGTTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCGGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 CCGGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGAGGAGCAAAAGCGCGAGCTCCGCGAGAGGAGGTGGAGCCTGTAATGAATGT 300
DB 241 AGGAGGAGCAAAAGCGCGAGCTCCGCGAGAGGAGGTGGAGCCTGTAATGAATGT 300
QY 301 GCTTACAAAGCGCGAGAGGAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTTATTC 360
DB 301 GCTTACAAAGCGCGAGAGGAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTTATTC 360
QY 361 CGGAGTACCTGCGGATCCGAGGTGCGGATGAGATCAAGAGCAAAAGGCGGAAATGCTCTGA 420
DB 361 CGGAGTACCTGCGGATCCGAGGTGCGGATGAGATCAAGAGCAAAAGGCGGAAATGCTCTGA 420
QY 421 GGGAAAGCTTTGAGAGAGTCTGCGACCACTACAGAGGAGTTCATGAGATTCATGA 480
DB 421 GGGAAAGCTTTGAGAGAGTCTGCGACCACTACAGAGGAGTTCATGAGATTCATGA 480
QY 481 ATTATGCGATAGATCTTGGGAAATTCGAGAGTGAATTTACAAAGATGCGTTCAATA 540
DB 481 ATTATGCGATAGATCTTGGGAAATTCGAGAGTGAATTTACAAAGATGCGTTCAATA 540
QY 541 GTGCTTAAGAGTGTGTTGCTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GTGCTTAAGAGTGTGTTGCTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AGGCTGATATTTCAATTCATGAGAGTGAATGTTGAGAGCTCTTCCCATTTGAAGCTA 660
DB 601 AGGCTGATATTTCAATTCATGAGAGTGAATGTTGAGAGCTCTTCCCATTTGAAGCTA 660
QY 661 TAAATTAATTTGAGCAAGAGAGCCCTGAATGATTTCAACAATTAATTTATTCATGCACTT 720
DB 661 TAAATTAATTTGAGCAAGAGAGCCCTGAATGATTTCAACAATTAATTTATTCATGCACTT 720
QY 721 CTTCCTGAGAGAGCTTTGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGAT 780
DB 721 CTTCCTGAGAGAGCTTTGAGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGAT 780
QY 781 TTGGGACCTGTTAGATTTACCAAAAGAGAGTCTTCTAGTGAATGATGATGATGATGATGAT 840
DB 781 TTGGGACCTGTTAGATTTACCAAAAGAGAGTCTTCTAGTGAATGATGATGATGATGATGAT 840
QY 841 GCATCATTTATGAGAGAGTCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
DB 841 GCATCATTTATGAGAGAGTCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
QY 901 TTAATTAATGCTTGAATGCTTCACTTAATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 TTAATTAATGCTTGAATGCTTCACTTAATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 GAATGAAGCAAAAGCGAGCTCCGCGAGAGGAGTGTGAGCTGTAATGAATGT 1020

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DB 961 GAATGAAGCAAAAGCGAGCTTAATGTTTACAGCCAAAGTGTATTTACAGCTGTTTAA 1020
QY 1021 ATCTGACATTAATTTGCTTCAATCAAAAGGCTTCAATATTTTGTAGTGT 1080
DB 1021 ATCTGACATTAATTTGCTTCAATCAAAAGGCTTCAATATTTTGTAGTGT 1080
QY 1081 AGAATATCTTCTGATGACATTTCTCAACCTATAATTTGAATATGTTGTGTCT 1140
DB 1081 AGAATATCTTCTGATGACATTTCTCAACCTATAATTTGAATATGTTGTGTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATGACATTTTAAATAATAAAGTACCAATCTTTGATC 1200
DB 1141 TTTGTTTTTCTCTAGTATGACATTTTAAATAATAAAGTACCAATCTTTGATC 1200
QY 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAAATAATAATTTATTTCAACA 1257
DB 1201 AATTTGTAATGTTAAGATTTTATCTGTTAAATAATAATTTATTTCAACA 1257

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RESULT 14

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US-10-176-914-365
; Sequence 365, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176, 914
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-914-365

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Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGAGAGCGCGCGGGGTAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGCGGGGTAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
QY 61 CGAGAGCAGACGCTGACACGTTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CGAGAGCAGACGCTGACACGTTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCGGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 CCGGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGAGGAGCAAAAGCGCGAGCTCCGCGAGAGGAGTGTGAGCTGTAATGAATGT 300
DB 241 AGGAGGAGCAAAAGCGCGAGCTCCGCGAGAGGAGTGTGAGCTGTAATGAATGT 300

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TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-515-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCGCGCGCGCTCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCGCGCGCGCTCGAGCGCG 60
QY 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCGAGTCT 120
DB 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCGAGTCT 120
QY 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCTCGAGCGCG 180
DB 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCTCGAGCGCG 180
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAAT 300
DB 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAAT 300
QY 301 GCTTACAGAGGCGCAGAGAGTCTGCTGAGACCGGAGCCCTGGGCGCAATGTT 360
DB 301 GCTTACAGAGGCGCAGAGAGTCTGCTGAGACCGGAGCCCTGGGCGCAATGTT 360
QY 361 CGGCTACCTCGGAGATCCCGAGTCCGAGTGTGATTTCAAGAGAAAGGAGGAT 420
DB 361 CGGCTACCTCGGAGATCCCGAGTCCGAGTGTGATTTCAAGAGAAAGGAGGAT 420
QY 421 GGGAAAGCTTGAAGAGTCTGAGACACCACTACAGAGTGTGATGAGTTCAT 480
DB 421 GGGAAAGCTTGAAGAGTCTGAGACACCACTACAGAGTGTGATGAGTTCAT 480
QY 481 ATTATGAGCATAGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATG 540
DB 481 ATTATGAGCATAGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATG 540
QY 541 GTGCTCTAAGAGTGTGTGATGAGTCTCACTTGGGCTAAATGCAAAATGCT 600
DB 541 GTGCTCTAAGAGTGTGTGATGAGTCTCACTTGGGCTAAATGCAAAATGCT 600
QY 601 AGCGTGTATTTACATTCATGAGCTGATGATGTTGAGGACCTCTCCCAT 660
DB 601 AGCGTGTATTTACATTCATGAGCTGATGATGTTGAGGACCTCTCCCAT 660
QY 661 TAAATTTATTTGACCAAGAGGCTGAAATGATTCACAAATTAATTTAT 720
DB 661 TAAATTTATTTGACCAAGAGGCTGAAATGATTCACAAATTAATTTAT 720
QY 721 CTCTGTGAGAGACTTTGAGAGAAATGTGTGATGATGATGATGATGATG 780
DB 721 CTCTGTGAGAGACTTTGAGAGAAATGTGTGATGATGATGATGATGATG 780
QY 781 TTGGACATTTGATGATTTACCAAAAGAGATGCTTACTGATGATGATGAT 840
DB 781 TTGGACATTTGATGATTTACCAAAAGAGATGCTTACTGATGATGATGAT 840
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTGATGATGAT 900
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTGATGATGAT 900
QY 901 TTATTTATGCTTGAATGATGCTTCAATTAATGATGATGATGATGATGAT 960
DB 901 TTATTTATGCTTGAATGATGCTTCAATTAATGATGATGATGATGATGAT 960
QY 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTCACTGTT 1020

DB 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTCACTGTT 1020
QY 1021 ATCTAGCATTTATGATTTGCTTCAATCAAAAGTGTTCATATTTTATGTT 1080
DB 1021 ATCTAGCATTTATGATTTGCTTCAATCAAAAGTGTTCATATTTTATGTT 1080
QY 1081 AGAATACCTTCTTCAATGACATTTCTCAACTATATTTGAAATATTTGTTG 1140
DB 1081 AGAATACCTTCTTCAATGACATTTCTCAACTATATTTGAAATATTTGTTG 1140
QY 1141 TTTGTTTCTTCTTATGATGATTTTAAATATTAATTAATTAATTTGAT 1200
DB 1141 TTTGTTTCTTCTTATGATGATTTTAAATATTAATTAATTAATTTGAT 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTTATGCTGTTAAATTAATTTGAT 1257
DB 1201 AATTTGTAATGTTAAGATTTTATTTATGCTGTTAAATTAATTTGAT 1257

RESULT 19
US-10-063-512-121
; Sequence 121, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCGCGCGCGCTCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCGCGCGCGCTCGAGCGCG 60
QY 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCGAGTCT 120
DB 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCGAGTCT 120
QY 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCTCGAGCGCG 180
DB 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCTCGAGCGCG 180
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAAT 300
DB 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAAT 300
QY 301 GCTTACAGAGGCGCAGAGAGTCTGCTGAGACCGGAGCCCTGGGCGCAATGTT 360

Db 301 GCTTACAAAGGCCACAGAGAGTGCCTGCTGAGACGGAGCCCTGGGGCCCAATGTTATTC 360
Qy 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTCAAAGGAGAAAAGGGGAAATGCTCA 420
Db 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTCAAAGGAGAAAAGGGGAAATGCTCA 420
Qy 421 GGGAAAGCTTTGAGAGTCTTGACACCACTACAGAGAGTTCATGAGAGTTCAATGA 480
Db 421 GGGAAAGCTTTGAGAGTCTTGACACCACTACAGAGAGTTCATGAGAGTTCAATGA 480
Qy 481 ATTATGCAATAGATCTTGGGAAAATTCGGGAGTGTACATTTACAAAGATGCTTCAATA 540
Db 481 ATTATGCAATAGATCTTGGGAAAATTCGGGAGTGTACATTTACAAAGATGCTTCAATA 540
Qy 541 GTGCTCTAAGAGTCTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 GTGCTCTAAGAGTCTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTTCAAGAGCTCTTCCATTGAAGCTA 660
Db 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTTCAAGAGCTCTTCCATTGAAGCTA 660
Qy 661 TAATTTATTTGGACCAAGAGAGCCCTGAATGATTAATTCATTAATTCATTCGCACTT 720
Db 661 TAATTTATTTGGACCAAGAGAGCCCTGAATGATTAATTCATTAATTCATTCGCACTT 720
Qy 721 CTTCGTGGAGAGAGCTTGTGAGAGAAATGCTGCTGATTAAGTGAATGCTGCTGCTGCT 780
Db 721 CTTCGTGGAGAGAGCTTGTGAGAGAAATGCTGCTGATTAAGTGAATGCTGCTGCTGCT 780
Qy 781 TTGGACATTTGTCAATTAACCAAAAGAGAGTCTTCACTGAGTGAATGCAATTCCTC 840
Db 781 TTGGACATTTGTCAATTAACCAAAAGAGAGTCTTCACTGAGTGAATGCAATTCCTC 840
Qy 841 GCATCATATTGAGAGAGAGCTTCACTTAAATGCTTAAATTCATTTGCTTACTCTCTTT 900
Db 841 GCATCATATTGAGAGAGAGCTTCACTTAAATGCTTAAATTCATTTGCTTACTCTCTTT 900
Qy 901 TTATTTATGCTTGAATGCTTCACTTAAATGAGATTTTAAATGATTAATGATTAATC 960
Db 901 TTATTTATGCTTGAATGCTTCACTTAAATGAGATTTTAAATGATTAATGATTAATC 960
Qy 961 GAAATGAAAGCAAGAGCTTAAATGTTTACAGACCAAGTGTGATTCACATGTTTTTAA 1020
Db 961 GAAATGAAAGCAAGAGCTTAAATGTTTACAGACCAAGTGTGATTCACATGTTTTTAA 1020
Qy 1021 ATCTAGCATATTATCTTTTGTCTTCAATCAAAAGTGTTCATTTTGTGATTTTGTG 1080
Db 1021 ATCTAGCATATTATCTTTTGTCTTCAATCAAAAGTGTTCATTTTGTGATTTTGTG 1080
Qy 1081 AGAATACCTTCTTCATGATCAATCTCTCAACCTAATATTTGGAATATGTTGTGCT 1140
Db 1081 AGAATACCTTCTTCATGATCAATCTCTCAACCTAATATTTGGAATATGTTGTGCT 1140
Qy 1141 TTGTTTTTCTCTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1200
Db 1141 TTGTTTTTCTCTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1200
Qy 1201 AATTTGTAATGTTAAGATTTTATCTGTTAATTAATTAATTAATTAATTAATTAATTA 1257
Db 1201 AATTTGTAATGTTAAGATTTTATCTGTTAATTAATTAATTAATTAATTAATTAATTA 1257

RESULT 20

US-10-173-706-365

; Sequence 365, Application US/10173706

; Publication No. US20030022293A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jlan

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-706-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAGAGGCGCGCGGTGAAGGCGCATTTGATGACCTGCGCGGCTCGAGCGCG 60
Db 1 GAGAGAGGCGCGCGGTGAAGGCGCATTTGATGACCTGCGCGGCTCGAGCGCG 60
Qy 61 CGGAGCCAGAGCTGACCACTTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 61 CGGAGCCAGAGCTGACCACTTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Qy 121 CCCGCGAGCCGAGAGCCATGCGACCCGAGGAGCCCGCGCTCCGCGAGCGGCTCGG 180
Db 121 CCCGCGAGCCGAGAGCCATGCGACCCGAGGAGCCCGCGCTCCGCGAGCGGCTCGG 180
Qy 181 GCTCTCTGCT 240
Db 181 GCTCTCTGCT 240
Qy 241 AGGGGAGCAAAAGGCGGAGCTCCGCGAGAGAGGCTGTGAGCTGTATTAATGGAATGT 300
Db 241 AGGGGAGCAAAAGGCGGAGCTCCGCGAGAGAGGCTGTGAGCTGTATTAATGGAATGT 300
Qy 301 GCTTACAAAGGCGCAGAGAGTGTGAGAGCGGAGCCCTGCGGCGCAATGTTATTC 360
Db 301 GCTTACAAAGGCGCAGAGAGTGTGAGAGCGGAGCCCTGCGGCGCAATGTTATTC 360
Qy 361 CGGGTACACCTGGGATCCAGAGTGGGATGATTCAAAGGAGAAAGGGGAAATGCTGA 420
Db 361 CGGGTACACCTGGGATCCAGAGTGGGATGATTCAAAGGAGAAAGGGGAAATGCTGA 420
Qy 421 GGGAAAGCTTTGAGAGTCTTGACACCACTACAGAGAGTTCATGAGAGTTCAATGA 480
Db 421 GGGAAAGCTTTGAGAGTCTTGACACCACTACAGAGAGTTCATGAGAGTTCAATGA 480
Qy 481 ATTATGCAATAGATCTTGGGAAAATTCGGGAGTGTACATTTACAAAGATGCTTCAATA 540
Db 481 ATTATGCAATAGATCTTGGGAAAATTCGGGAGTGTACATTTACAAAGATGCTTCAATA 540
Qy 541 GTGCTCTAAGAGTCTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 GTGCTCTAAGAGTCTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTTCAAGAGCTCTTCCATTGAAGCTA 660
Db 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTTCAAGAGCTCTTCCATTGAAGCTA 660
Qy 661 TAATTTATTTGGACCAAGAGAGCCCTGAATGATTAATTCATTAATTCATTCGCACTT 720
Db 661 TAATTTATTTGGACCAAGAGAGCCCTGAATGATTAATTCATTAATTCATTCGCACTT 720
Qy 721 CTTCGTGGAGAGAGCTTGTGAGAGAAATGCTGATTAAGTGAATGTTGCTATCTGCG 780

Db 1141 TTGTTTTCTCTAGTATAGCATTTTAAAAAATATAAAGTACCAATCTTTGTAC 1200
QY 1201 AATTGTAATGTAAATTTTATATCTGTAATAAATAATTAATTCACACA 1257
Db 1201 AATTGTAAATGTAAATTTTATATCTGTAATAAATAATTAATTCACACA 1257

RESULT 22
US-10-175-752-365
; Sequence 365, Application US/10175752
; Publication No. US20030022295A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-752-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGAGAGCGCGCGGTGAAGGCGCATTTATGACGCTGGGCGGCGCTCGGAGCGCGG 60
Db 1 GAGAGAGAGCGCGCGGTGAAGGCGCATTTATGACGCTGGGCGGCGCTCGGAGCGCGG 60
QY 61 CGAGCCAGACGCTGACCAAGTTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 61 CGAGCCAGACGCTGACCAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGCGACCGCGGAGCCATGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 CCGCGACCGCGGAGCCATGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCCT 240
Db 181 GCCT 240
QY 241 AGGGAAGCAAAAGGCGGAGCTCTCGGCAAGGAGAGTGTGACCTGTATATAGGAATGT 300
Db 241 AGGGAAGCAAAAGGCGGAGCTCTCGGCAAGGAGAGTGTGACCTGTATATAGGAATGT 300
QY 301 GCTTAACAAGGGCCGACAGAGTGCCTGTCCAGAGCGGAGCCCTGGGGCCAAATGTTATTC 360
Db 301 GCTTAACAAGGGCCGACAGAGTGCCTGTCCAGAGCGGAGCCCTGGGGCCAAATGTTATTC 360
QY 361 CGGGTACACTGTGATCCAGAGTCCGAGTGTGATTAAGAAGAAAAGGGGGAATGTCTGA 420
Db 361 CGGGTACACTGTGATCCAGAGTCCGAGTGTGATTAAGAAGAAAAGGGGGAATGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGTCTCTGACACCCAACTACAGAGTGTCTATGAGTTCAATGA 480
Db 421 GGGAAAGCTTTGAGAGTCTCTGACACCCAACTACAGAGTGTCTATGAGTTCAATGA 480
QY 481 ATTATGATGATGATCTTGGGAAAATTTGGGAGTGTACATTTTAAACAAGATGGCTCAATA 540

Db 481 ATTATGATGATGATCTTGGGAAAATTTGGGAGTGTACATTTTAAACAAGATGGCTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTGTCAGTGCCTCACTTGGCTAAATATGCAAAATGATGCTGTC 600
Db 541 GTGCTCTAAGAGTTTGTGTCAGTGCCTCACTTGGCTAAATATGCAAAATGATGCTGTC 600
QY 601 AGCGTTGATTTTCAATTCATGAGTGTGAATGAGTGTGAAGTGTGAAGTGTGAAGTGTGA 660
Db 601 AGCGTTGATTTTCAATTCATGAGTGTGAATGAGTGTGAAGTGTGAAGTGTGAAGTGTGA 660
QY 661 TAAATTTATTTGACCAAGAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 661 TAAATTTATTTGACCAAGAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
QY 721 CTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAATGATGATGATGATGATGATGAT 780
Db 721 CTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAATGATGATGATGATGATGATGAT 780
QY 781 TTGGCACTGTTCAGATTTACCAAGAGAGATGCTGTCTAGTGAATGATGATGATGATGATGAT 840
Db 781 TTGGCACTGTTCAGATTTACCAAGAGAGATGCTGTCTAGTGAATGATGATGATGATGATGAT 840
QY 841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
Db 841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
QY 901 TTATTAAGCTTTGGAATGCTTCACTTAATTAATGACATTTTAATTAATTAATTAATTAAT 960
Db 901 TTATTAAGCTTTGGAATGCTTCACTTAATTAATGACATTTTAATTAATTAATTAATTAAT 960
QY 961 GAATGAAAAGCAAGCTAAATATGTTATGACAGCAAGAGTGTGATTTACACAGTGTGTTAA 1020
Db 961 GAATGAAAAGCAAGCTAAATATGTTATGACAGCAAGAGTGTGATTTACACAGTGTGTTAA 1020
QY 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGTGATTTTAAATTTTAAATTTTAAATTTTAA 1080
Db 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGTGATTTTAAATTTTAAATTTTAAATTTTAA 1080
QY 1081 AGAATACCTTTCTTATGACATCTCTCAACCTTAATTTGGAATTTGTTGCTGCT 1140
Db 1081 AGAATACCTTTCTTATGACATCTCTCAACCTTAATTTGGAATTTGTTGCTGCT 1140
QY 1141 TTGTTTTTCTCTTATATAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
Db 1141 TTGTTTTTCTCTTATATAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
QY 1201 AATTGTAAATGTAAATTTTATATCTGTAATAAATAATTAATTAATTCACACA 1257
Db 1201 AATTGTAAATGTAAATTTTATATCTGTAATAAATAATTAATTAATTCACACA 1257

RESULT 23
US-10-176-482-365
; Sequence 365, Application US/10176482
; Publication No. US20030022295A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 365
 ; LENGTH: 1257
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-482-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3,4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 60
 DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 60
 QY 61 CGAGAGCGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 120
 DB 61 CGAGAGCGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 120
 QY 121 CCGGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 180
 DB 121 CCGGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 180
 QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 AGGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 300
 DB 241 AGGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 300
 QY 301 GCTTAAAGGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 360
 DB 301 GCTTAAAGGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 360
 QY 361 CGGAGAGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 420
 DB 361 CGGAGAGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 420
 QY 421 GGGAGAGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 480
 DB 421 GGGAGAGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 480
 QY 481 ATTATGCGCATTAATCTTGGGAAATTTGCGAGGTGTCATTACAAAGATGCGTTCAAA 540
 DB 481 ATTATGCGCATTAATCTTGGGAAATTTGCGAGGTGTCATTACAAAGATGCGTTCAAA 540
 QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGGCTAAATGCGAAATGCAATGCTGTC 600
 DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGGCTAAATGCGAAATGCAATGCTGTC 600
 QY 601 AGGAGAGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 660
 DB 601 AGGAGAGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 660
 QY 661 TAATTTATTTGAGCAAGAGGCGCTGAAATGCAATTAATTAATTTGATGCACTT 720
 DB 661 TAATTTATTTGAGCAAGAGGCGCTGAAATGCAATTAATTAATTTGATGCACTT 720
 QY 721 CTTCTGAGAGAGCTTTGAGAGGAAATGAGTGGTGAATGATGATGATGATGATGATG 780
 DB 721 CTTCTGAGAGAGCTTTGAGAGGAAATGAGTGGTGAATGATGATGATGATGATGATG 780
 QY 781 TTGGGCACTTTGAGAGGAAATGAGTGGTGAATGATGATGATGATGATGATGATGATG 840
 DB 781 TTGGGCACTTTGAGAGGAAATGAGTGGTGAATGATGATGATGATGATGATGATGATG 840
 QY 841 GCATCATTTATGAGAGGAAATGAGTGGTGAATGATGATGATGATGATGATGATGATG 900
 DB 841 GCATCATTTATGAGAGGAAATGAGTGGTGAATGATGATGATGATGATGATGATGATG 900
 QY 901 TTATTTATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960

DB 901 TTATTTATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 QY 961 GAATGAGAGCAAGGCGCTGAAATGAGTGGTGAATGATGATGATGATGATGATGATG 1020
 DB 961 GAATGAGAGCAAGGCGCTGAAATGAGTGGTGAATGATGATGATGATGATGATGATG 1020
 QY 1021 ATCTGAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1021 ATCTGAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 AGAATATCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 DB 1081 AGAATATCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 QY 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 DB 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
 QY 1201 AATTTGTAATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
 DB 1201 AATTTGTAATGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1257

RESULT 24
 US-10-176-757-365
 ; Sequence 365, Application US/10176757
 ; Publication No. US20030022297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C86
 ; CURRENT APPLICATION NUMBER: US/10/176,757
 ; PRIOR APPLICATION DATE: 2002-06-20
 ; PRIOR APPLICATION removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 365
 ; LENGTH: 1257
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-757-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3,4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 60
 DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 60
 QY 61 CGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 120
 DB 61 CGAGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 120
 QY 121 CCGGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 180
 DB 121 CCGGAGCGCGCGGGTGAAGGCGCATTTGATGACCGTGGCGCGGCTCGAGGCGCG 180
 QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240


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Qy 241 AGGGGAGCAAAAGCGCAGCTCCGAGAGGAGGTGTGAGCTGTATATGAAATGT 300
Db 241 AGGGGAGCAAAAGCGCAGCTCCGAGAGGAGGTGTGAGCTGTATATGAAATGT 300
Qy 301 GCTTCAAGAGGCGCAGAGAGTCTGTGTGAGAGCGGAGCCTGGGGCCCAATGTATTC 360
Db 301 GCTTCAAGAGGCGCAGAGAGTCTGTGTGAGAGCGGAGCCTGGGGCCCAATGTATTC 360
Qy 361 CGGGTACACCTGGGATCCGAGGTGGGATGATTTCAAGAGAGAGAGAGAGAGTGTCTGA 420
Db 361 CGGGTACACCTGGGATCCGAGGTGGGATGATTTCAAGAGAGAGAGAGAGAGTGTCTGA 420
Qy 421 GGGAAAGCTTTGAGAGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GGGAAAGCTTTGAGAGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 ATTATGCAATGATCTGTGGGAAATTTGGGAGAGTCAATTTACAAAGATGCGTTCAATA 540
Db 481 ATTATGCAATGATCTGTGGGAAATTTGGGAGAGTCAATTTACAAAGATGCGTTCAATA 540
Qy 541 GTGCTCTAAGAGTTTGTCTAGTGTGCTCACTTGGCTAAATGCAAGAAATGAGTGTCTC 600
Db 541 GTGCTCTAAGAGTTTGTCTAGTGTGCTCACTTGGCTAAATGCAAGAAATGAGTGTCTC 600
Qy 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTCAAGAGAGAGAGAGAGAGAGAG 660
Db 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTCAAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TAATTTATTTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 TAATTTATTTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 CTTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 CTTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 TTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 TTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 GCATCATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GCATCATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 TTATATATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 TTATATATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy 961 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 ATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 ATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 AGAATACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 AGAATACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 1141 TTGTTTTTTTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 TTGTTTTTTTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy 1201 AATTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
Db 1201 AATTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257

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RESULT 25
 US-10-176-913-365
 ; Sequence 365, Application US/10176913
 ; Publication No. US20030022298A1

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P340R1C66
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-913-365

```

```

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 1 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Qy 61 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Qy 121 CCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 CCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 GCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 181 GCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Qy 241 AGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 AGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 GCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 GCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 CGGGTACACCTGGGATCCGAGGTGGGATGATTTCAAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 CGGGTACACCTGGGATCCGAGGTGGGATGATTTCAAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 GGGAAAGCTTTGAGAGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GGGAAAGCTTTGAGAGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 ATTATGCAATGATCTGTGGGAAATTTGGGAGAGTCAATTTACAAAGATGCGTTCAATA 540
Db 481 ATTATGCAATGATCTGTGGGAAATTTGGGAGAGTCAATTTACAAAGATGCGTTCAATA 540
Qy 541 GTGCTCTAAGAGTTTGTCTAGTGTGCTCACTTGGCTAAATGCAAGAAATGAGTGTCTC 600
Db 541 GTGCTCTAAGAGTTTGTCTAGTGTGCTCACTTGGCTAAATGCAAGAAATGAGTGTCTC 600
Qy 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTCAAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTTCAAGAGAGAGAGAGAGAGAGAGAG 660

```

QY 661 TAATTATTTGGACCAAGAGCCCTGAATGATTTCAAAATTAATTCATCGACT 720
DB 661 TAATTATTTGGACCAAGAGCCCTGAATGATTTCAAAATTAATTCATCGACT 720
QY 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGAATGCTTAC 780
DB 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGAATGCTTAC 780
QY 781 TTGGCACTTGTCAAGTTACCCAAAGAGAGTCTCTAATGATTAAGTGAATGCTTAC 840
DB 781 TTGGCACTTGTCAAGTTACCCAAAGAGAGTCTCTAATGATTAAGTGAATGCTTAC 840
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAAATTTGCTTACCTCTTTT 900
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAAATTTGCTTACCTCTTTT 900
QY 901 TTATTATGCTTGGAAATGCTTCAATTAATGATTTAAATTAATGATTAATGATTAATG 960
DB 901 TTATTATGCTTGGAAATGCTTCAATTAATGATTTAAATTAATGATTAATGATTAATG 960
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTACACTGTTTAA 1020
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTACACTGTTTAA 1020
QY 1021 ATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGGTTCAATATTTTGTGTTGTT 1080
DB 1021 ATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGGTTCAATATTTTGTGTTGTT 1080
QY 1081 AGAATACCTTCTTCATAGTCACTCTCTCAACCTTAATTTGGAATTTGTTGTTGTT 1140
DB 1081 AGAATACCTTCTTCATAGTCACTCTCTCAACCTTAATTTGGAATTTGTTGTTGTT 1140
QY 1141 TTTGTTTCTTCTTATGATAGATTTTAAAAAATATTAAGCTACCAATTTGTTAC 1200
DB 1141 TTTGTTTCTTCTTATGATAGATTTTAAAAAATATTAAGCTACCAATTTGTTAC 1200
QY 1201 AATTGTAAATGTTAAGATTTTAAATCTGTAATTAATTAATTAATTTTCCACA 1257
DB 1201 AATTGTAAATGTTAAGATTTTAAATCTGTAATTAATTAATTAATTTTCCACA 1257

RESULT 26

US-10-180-552-365
; Sequence 365, Application US/10180552
; Publication No. US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C153
; CURRENT APPLICATION NUMBER: US/10/180,552
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See file Wrapper or Palm
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-180-552-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAGAGAGCGCGCGGTGAAGGCGCATTTGATGAGCTTGGGCGGCTCCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGTGAAGGCGCATTTGATGAGCTTGGGCGGCTCCGAGCGCG 60
QY 61 CGAGCCAGACCGCTGACCACTTCTCTCTCTGATCTCTCGGCTCCAGCTCCGCGCTG 120
DB 61 CGAGCCAGACCGCTGACCACTTCTCTCTCTGATCTCTCGGCTCCAGCTCCGCGCTG 120
QY 121 CCCGCAAGCCGGAAGCCATGCACTCCCAAGGCGCCGCGCTCCCGCAAGCGGCTCCG 180
DB 121 CCCGCAAGCCGGAAGCCATGCACTCCCAAGGCGCCGCGCTCCCGCAAGCGGCTCCG 180
QY 181 GCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGGGAGCAAAAGCGCAGCTCCGCAAGGAGGTGTGAGCTGTATTAATGGAATGT 300
DB 241 AGGGGAGCAAAAGCGCAGCTCCGCAAGGAGGTGTGAGCTGTATTAATGGAATGT 300
QY 301 GCTTACAGAGGCGCAGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCTTACAGAGGCGCAGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CGGTAACCTGGGATCCCGGATGATTCAGAAAGGAGAAAGGGGGAATGCTGA 420
DB 361 CGGTAACCTGGGATCCCGGATGATTCAGAAAGGAGAAAGGGGGAATGCTGA 420
QY 421 GGGAAAGCTTTGAGAGTCTTGAACCACTACAGAGCTGTTCAATGAGTTCATTTGA 480
DB 421 GGGAAAGCTTTGAGAGTCTTGAACCACTACAGAGCTGTTCAATGAGTTCATTTGA 480
QY 481 AATTATGCAATGATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGTGCCTTCAAA 540
DB 481 AATTATGCAATGATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGTGCCTTCAAA 540
QY 541 GTGCTCTAAGATTTTGTTCATGCTGCTCACTCGGCTAAAGCAAGAAATGATGCTGTC 600
DB 541 GTGCTCTAAGATTTTGTTCATGCTGCTCACTCGGCTAAAGCAAGAAATGATGCTGTC 600
QY 601 AGCGTTGATTTTCACTTCAATGAGCTGAATGTTTCAAGGACTCTTCCCATTTGAAGCTA 660
DB 601 AGCGTTGATTTTCACTTCAATGAGCTGAATGTTTCAAGGACTCTTCCCATTTGAAGCTA 660
QY 661 TAATTATTTGGACCAAGAGCCCTGAATGATTTCAAAATTAATTAATTCATCGACTT 720
DB 661 TAATTATTTGGACCAAGAGCCCTGAATGATTTCAAAATTAATTAATTCATCGACTT 720
QY 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGAATGCTTACCTG 780
DB 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGAATGCTTACCTG 780
QY 781 TTGGCACTTGTCAAGTTACCCAAAGAGAGTCTCTAATGATTAAGTGAATGCTTAC 840
DB 781 TTGGCACTTGTCAAGTTACCCAAAGAGAGTCTCTAATGATTAAGTGAATGCTTAC 840
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAAATTTGCTTACCTCTTTT 900
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAAATTTGCTTACCTCTTTT 900
QY 901 TTATTATGCTTGGAAATGCTTCAATTAATGATTTAAATTAATGATTAATGATTAATG 960
DB 901 TTATTATGCTTGGAAATGCTTCAATTAATGATTTAAATTAATGATTAATGATTAATG 960
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTACACTGTTTAA 1020
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTACACTGTTTAA 1020
QY 1021 ATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGGTTCAATATTTTGTGTTGTT 1080
DB 1021 ATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGGTTCAATATTTTGTGTTGTT 1080

QY 1081 AGAATACCTTCTTCATGTCACATCTCTCAACCTATAATTTGGAAATATGTTGGTCT 1140
DB 1081 AGAATACCTTCTTCATGTCACATCTCTCAACCTATAATTTGGAAATATGTTGGTCT 1140
QY 1141 TTTGTTTTCTCTAGTATGATCTTTTAAAAAATATAAAAAGCTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTCTCTAGTATGATCTTTTAAAAAATATAAAAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGATTTTTTTTTATCTGTTAATTAATAAATTTATTTCCACA 1257
DB 1201 AATTTGTAATGTTAAGATTTTTTTTTATCTGTTAATTAATAAATTTATTTCCACA 1257

RESULT 27

US-10-180-557-365
; Sequence 365, Application US/10180557
; Publication No. US20030022301A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C147
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-180-557-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGAGAGGCGCGCGGTGAAGGCGCATTTGATGAGCCCTGCGGCGGCTCGGAGCGGCG 60
DB 1 GAGAGAGGCGCGCGGTGAAGGCGCATTTGATGAGCCCTGCGGCGGCTCGGAGCGGCG 60
QY 61 CGAGGCCAGAGCGTGAACCACTTCTCTCTGCTCTCTCGGCTCGAGCTCCGCGCTG 120
DB 61 CGAGGCCAGAGCGTGAACCACTTCTCTCTGCTCTCTCGGCTCGAGCTCCGCGCTG 120
QY 121 CCGGCGAGCGGGAAGCATGGAAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCGGCGAGCGGGAAGCATGGAAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGAGTGTGTATATATGGAATGT 300
DB 241 AGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGAGTGTGTATATATGGAATGT 300
QY 301 GCTTACAAGGCGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 GCTTACAAGGCGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 CGGAGTACCTGGAGTCCAGAGTCCAGATGGAATCAAGAGAAAGGGGGAATGTCTGA 420
DB 361 CGGAGTACCTGGAGTCCAGAGTCCAGATGGAATCAAGAGAAAGGGGGAATGTCTGA 420

QY 421 GGGAAAGCTTTGAGAGTCTTGACACCCCACTAACAGAGTGTTCATGAGTTCATTGA 480
DB 421 GGGAAAGCTTTGAGAGTCTTGACACCCCACTAACAGAGTGTTCATGAGTTCATTGA 480
QY 481 ATTATGCAATAGATCTTGGGAAAAATGGGAGGTGATCAATTTACCAAGATCGTTCAATA 540
DB 481 ATTATGCAATAGATCTTGGGAAAAATGGGAGGTGATCAATTTACCAAGATCGTTCAATA 540
QY 541 GTGCTCTAAGAGTGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GTGCTCTAAGAGTGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AGCGTTGATATTTCATTCATGAGTGAATGTCAGAGACCTCTCCCATGGAAGCTA 660
DB 601 AGCGTTGATATTTCATTCATGAGTGAATGTCAGAGACCTCTCCCATGGAAGCTA 660
QY 661 TAAATTAATTTGACCAAGAAAGCCCTGAAATGAATTCACAAATTAATTCATGCACTT 720
DB 661 TAAATTAATTTGACCAAGAAAGCCCTGAAATGAATTCACAAATTAATTCATGCACTT 720
QY 721 CTTCGTGGAAGAGCTTTGTGAGAGAAATGGTGTGATTAAGTGAATGTTGCTATCTGGG 780
DB 721 CTTCGTGGAAGAGCTTTGTGAGAGAAATGGTGTGATTAAGTGAATGTTGCTATCTGGG 780
QY 781 TTGGCACTTTTCAGATTAACCAAAAGAGATGCTTCACTGATGGAATTCAGATTTCTC 840
DB 781 TTGGCACTTTTCAGATTAACCAAAAGAGATGCTTCACTGATGGAATTCAGATTTCTC 840
QY 841 GCATCATTAATGAAGAACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
DB 841 GCATCATTAATGAAGAACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
QY 901 TTAATAGCCTTGAAGTGTCACTTAATGAATTTAATAGTAAATTTTATGTAATGTAATCT 960
DB 901 TTAATAGCCTTGAAGTGTCACTTAATGAATTTAATAGTAAATTTTATGTAATGTAATCT 960
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020
QY 1021 ATCTAGCATTAATTAATTTGCTCAATCAAAAGTGTGTAATTTTATGTTGTT 1080
DB 1021 ATCTAGCATTAATTAATTTGCTCAATCAAAAGTGTGTAATTTTATGTTGTT 1080
QY 1081 AGAATACCTTCTTCATGTCACATCTCTCAACCTATAATTTGGAAATATGTTGGTCT 1140
DB 1081 AGAATACCTTCTTCATGTCACATCTCTCAACCTATAATTTGGAAATATGTTGGTCT 1140
QY 1141 TTTGTTTTCTCTAGTATGATCTTTTAAAAAATATAAAAAGCTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTCTCTAGTATGATCTTTTAAAAAATATAAAAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGATTTTTTTTTATCTGTTAATTAATAAATTTATTTCCACA 1257
DB 1201 AATTTGTAATGTTAAGATTTTTTTTTATCTGTTAATTAATAAATTTATTTCCACA 1257

RESULT 28

US-10-063-502-121
; Sequence 121, Application US/10063502
; Publication No. US20030023042A1
GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gettisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

? TITLE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P3230RAC1
? CURRENT APPLICATION NUMBER: US/10/063,502
? CURRENT FILING DATE: 2002-05-01
? Prior Application removed - See File Wrapper or Patent
? NUMBER OF SEQ ID NOS: 170
? SEQ ID NO 121
? LENGTH: 1257
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-063-502-121

```

Query Match	100.0%;	Score 1257;	DB 14;	length 1257;
Best Local Similarity	100.0%;	Pred. No. 3.4e-271;		
Matches 1257; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	GGAGAGAGGCGCGCGGTGAAAAGCGCATTTGAGCTCGCGGCGCTCGAGCGCGG	60
Db	1	GGAGAGAGGCGCGCGGTGAAAAGCGCATTTGAGCTCGCGGCGCTCGAGCGCGG	60
Qy	61	CGAGCGCAGCGCTGACCAAGTTCTCTCTCGGTCTCTCGGCTCGAGTCCGCGCTG	120
Db	61	CGAGCGCAGCGCTGACCAAGTTCTCTCTCGGTCTCTCGGCTCGAGTCCGCGCTG	120
Qy	121	CCGGGACGCCGGGAGGCATGCGACCCCAAGGGCCCGCGCGCTCCCGGAGCGCTCGCGG	180
Db	121	CCGGGACGCCGGGAGGCATGCGACCCCAAGGGCCCGCGCGCTCCCGGAGCGCTCGCGG	180
Qy	181	GCCTCCGTGCTCTCTGCTGCTGCAAGCTGCCCCGCGCTCGAGCGCTCTGAGATCCCA	240
Db	181	GCCTCCGTGCTCTCTGCTGCTGCAAGCTGCCCCGCGCTCGAGCGCTCTGAGATCCCA	240
Qy	241	AGGGAGAGCAAAAAGGCGCAGCTTCGGCAGAGGAGAGTGTGACCTGTATATAGAAATGT	3000
Db	241	AGGGAGAGCAAAAAGGCGCAGCTTCGGCAGAGGAGAGTGTGACCTGTATATAGAAATGT	3000
Qy	301	GCTTACAGAGGCGCAGAGAGTGCCTGCTGAGAGCGGAGCCCTGAGGSCCAATGTATTC	3600
Db	301	GCTTACAGAGGCGCAGAGAGTGCCTGCTGAGAGCGGAGCCCTGAGGSCCAATGTATTC	3600
Qy	361	CGGGTACACCTGGGATCCAGGTCCGGATGATTCAAAGAGAAAAGGGGAGATGTCTGA	4200
Db	361	CGGGTACACCTGGGATCCAGGTCCGGATGATTCAAAGAGAAAAGGGGAGATGTCTGA	4200
Qy	421	GGGAAAGCTTTGAGAGTCTCGACACCCAACTTAACAACAGTGTTCATGAGTTCATTGA	4800
Db	421	GGGAAAGCTTTGAGAGTCTCGACACCCAACTTAACAACAGTGTTCATGAGTTCATTGA	4800
Qy	481	ATTATGGCATAGATCTTGGGAAAAATTCGCGAGTGTACATTTACAAAGATGCTTCAATA	5400
Db	481	ATTATGGCATAGATCTTGGGAAAAATTCGCGAGTGTACATTTACAAAGATGCTTCAATA	5400
Qy	541	GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGCTTAAATGCAGAAATGCAATGCTGTC	6000
Db	541	GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGCTTAAATGCAAGAAATGCAATGCTGTC	6000
Qy	601	AGGGTGGTATTTCAATTCANATGAGAGCTGATGTCAGAGCTCTCCCATTAAGCTA	6600
Db	601	AGGGTGGTATTTCAATTCANATGAGAGCTGATGTCAGAGCTCTCCCATTAAGCTA	6600
Qy	661	TAAATTTATTTGACCAAGAGGCCCTGAATGAAATTCACAATTATATTCATGCGCACTT	7200
Db	661	TAAATTTATTTGACCAAGAGGCCCTGAATGAAATTCACAATTATATTCATGCGCACTT	7200
Qy	721	CTTCTGTGAAAGCATTTGTGAAAGAAATGGTGTGATTAATGATGTTGCTATCTGGG	7800
Db	721	CTTCTGTGAAAGCATTTGTGAAAGAAATGGTGTGATTAATGATGTTGCTATCTGGG	7800
Qy	781	TTGGCACTTGTTCAGATTAACCAAAAAGAGATGCTTCACTGATGATGAAATTCAGTTTCTC	8400
Db	781	TTGGCACTTGTTCAGATTAACCAAAAAGAGATGCTTCACTGATGATGAAATTCAGTTTCTC	8400
Qy	841	GCATCATTTATGAAGACTACCAAAATAATGCTTTAATTTATTCATTGGTACTCTTTT	9000

Db	841	GCATCATTTATGGAAGACTACCAAAATAAATGCTTAAATTTCACTTGTCACCTCTTTT	900
Qy	901	TTATTTATGCCCTTGGAAATGCTTCACTTAATGACATTTTAAATAGTTATGTATACACT	960
Db	901	TTATTTATGCCCTTGGAAATGCTTCACTTAATGACATTTTAAATAGTTATGTATACACT	960
Qy	961	GAATGAAGAAGCAAGCTAAATATGTTTACAGACCAAGGTGATTTCACACTGTTTTTAA	10200
Db	961	GAATGAAGAAGCAAGCTAAATATGTTTACAGACCAAGGTGATTTCACACTGTTTTTAA	10200
Qy	1021	ATCTAGCAATTATTCATTTTGGCTTCAATCAAAAGTGTTCAATATTTTTTTTAACTGGTT	10800
Db	1021	ATCTAGCAATTATTCATTTTGGCTTCAATCAAAAGTGTTCAATATTTTTTTTAACTGGTT	10800
Qy	1081	AGAACTACTTTCCTCATAGTCACATCTCTCAACCTATAATTTGGAAATATGTGTGCTCT	11400
Db	1081	AGAACTACTTTCCTCATAGTCACATCTCTCAACCTATAATTTGGAAATATGTGTGCTCT	11400
Qy	1141	TTTGTCTTTTTCTCTTAGTATAGCATTTTAAAAAAATATAAAGCTACCAATCTTGTAC	12000
Db	1141	TTTGTCTTTTTCTCTTAGTATAGCATTTTAAAAAAATATAAAGCTACCAATCTTGTAC	12000
Qy	1201	AATTTGTAATGTTAAGAAATTTTTTTTATATATGCTTAATATAAAAATATATTTCCACA	1257
Db	1201	AATTTGTAATGTTAAGAAATTTTTTTTATATATGCTTAATATAAAAATATATTTCCACA	1257

RESULT 29
US-10-173-700-365

```

, GENERAL INFORMATION:
, APPLICANT: Baker, Kevin P.
, APPLICANT: Chen, Jian
, APPLICANT: Desnoyers, Luc
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul J.
, APPLICANT: Gurney, Austin L.
, APPLICANT: Pan, James
, APPLICANT: Smith, Victoria
, APPLICANT: Matanabe, Colin K.
, APPLICANT: Wood, William I.
, APPLICANT: Zhang, Zemin
, TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
, TITLE OF INVENTION: ACIDS ENCODING THE SAME
, FILE REFERENCE: P3430R1C14
, CURRENT APPLICATION NUMBER: US/10/173,700
, CURRENT FILING DATE: 2002-06-17
, Prior Application removed - See File Wrapper or Palm
, NUMBER OF SEQ ID NOS: 612
, SEQ ID NO 365
, LENGTH: 1257
, TYPE: DNA
, ORGANISM: Homo Sapien
, US-10-173-700-365

```

Query Match	100.0%	Score 1257;	DB 14;	Length 1257;
Best Local Similarity	100.0%	Pred. No.3	4e-271;	
Matches 1257;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GGAGAGAGCGCGCGGGTGAAGGCGCATTTATGACGCTCGGCGGCTTCGGAGCGCGG	60
Db	1	GGAGAGAGGCGCGCGGGTGAAGGCGCATTTATGACGCTCGGCGGCTTCGGAGCGCGG	60
Qy	61	CGAGGCCAGACGCTGACCAACGTTCTCTTCCTCGGCTTCCTCCGCTCAGCTCCGCGCTG	120
Db	61	CGAGGCCAGACGCTGACCAACGTTCTCTCTCTCGGCTTCCTCCGCTCAGCTCCGCGCTG	120
Qy	121	CCGGGAGGCGGGAGGCAATGCGGCAACCCAGAGGCCCGCGCGCTCCCGCGAGAGGCTCCGGG	180
Db	121	CCGGGAGGCGGGAGGCAATGCGGCAACCCAGAGGCCCGCGCGCTCCCGCGAGAGGCTCCGGG	180

Qy	60	AGCGTTGGATTTCAACATTCAGAGAGCTGAATGTTCAGACGCTCTCCCATTTGAAGCTA	660
Db	601	AGCGTTGGATTTCAACATTCAGAGAGCTGAATGTTCAGACGCTCTCCCATTTGAAGCTA	660
Qy	661	TAATTTATTTGGACCAAGAGAGCCCTGAAATTCACAAATTAATATTCATGCACTT	720
Db	661	TAATTTATTTGGACCAAGAGAGCCCTGAAATTCACAAATTAATATTCATGCACTT	720
Qy	721	CTTCTGTGGAAAGCACTTGTGGAAGAAATTGGTGTCTGAATTAGTGGAGTGTCTATCTGGG	780
Db	721	CTTCTGTGGAAAGCACTTGTGGAAGAAATTGGTGTCTGAATTAGTGGAGTGTCTATCTGGG	780
Qy	781	TTGGCACTGTGTCAAGATTACCCAAAGAGANGCTTCACTGAGATGGAATTCAGATTCTC	840
Db	781	TTGGCACTGTGTCAAGATTACCCAAAGAGANGCTTCACTGAGATGGAATTCAGATTCTC	840
Qy	841	GCATCATTTATGGAAGACTACCAAAATTAATGTCTTTAATTTTCATTTTGCTACTCTTTT	900
Db	841	GCATCATTTATGGAAGACTACCAAAATTAATGTCTTTAATTTTCATTTTGCTACTCTTTT	900
Qy	901	TTATTTAGCCCTTGGAAAGGTTCACTTAAATGACATTTTAATTAAGTTATGATACACT	960
Db	901	TTATTTAGCCCTTGGAAAGGTTCACTTAAATGACATTTTAATTAAGTTATGATACACT	960
Qy	961	GAATGAAAGCAAAAGCTAAATATGTGTTACAGACCAAGTGTGATTTTCACTGTGTTTTAA	1020
Db	961	GAATGAAAGCAAAAGCTAAATATGTGTTACAGACCAAGTGTGATTTTCACTGTGTTTTAA	1020
Qy	1021	ATCTAGCATTAATTCATTTTGCTTCACATCAAAAGTGTGTTCAATATTTTGTAGTGGTT	1080
Db	1021	ATCTAGCATTAATTCATTTTGCTTCACATCAAAAGTGTGTTCAATATTTTGTAGTGGTT	1080
Qy	1081	AGAAATACCTTCTTCATAGTCAATTCCTCAACACTTAATTAATTTGGAAATGTGTGGTCT	1140
Db	1081	AGAAATACCTTCTTCATAGTCAATTCCTCAACACTTAATTAATTTGGAAATGTGTGGTCT	1140
Qy	1141	TTTGTGTTTTCTCTAGTATAGCAATTTTAAAAAAATATAAAGCTACCAATCTTGTGAC	1200
Db	1141	TTTGTGTTTTCTCTAGTATAGCAATTTTAAAAAAATATAAAGCTACCAATCTTGTGAC	1200
Qy	1201	AAATTTGTAAGTTAAGAAATTTTTTTTAATATCTGTAAATTAATAATTAATTTCCACAA	1257
Db	1201	AAATTTGTAAGTTAAGAAATTTTTTTTAATATCTGTAAATTAATAATAATTTTCACAA	1257

Query Match		Similarity	100.0%	Score 1257	DB 171	Length 1257
Best Local Match		Similarity	100.0%	Pred. No. 3.4e-271		
Matches 1257		Conservative	0	Mismatches	0	Indels
			0	Gaps	0	
Qy	1	GGAGAGAGGCGCGGGGTGAAAAGCGCATTTGATGACAGCTTGGCGGCGCTTCGAGGCGCG	60			
Db	1	GGAGAGAGGCGCGGGGTGAAAAGCGCATTTGATGACAGCTTGGCGGCGCTTCGAGGCGCG	60			
Qy	61	CGAGGCCAGAGCGCTGACAGAGTTCTCTCTCGGTCTCTCCGCGTCAGCTCCGCGCTG	120			
Db	61	CGAGGCCAGAGCGCTGACAGAGTTCTCTCTCGGTCTCTCCGCGTCAGCTCCGCGCTG	120			
Qy	121	CCGGGACGCGGGAGCCATGCGAACCCGAGGGCCCGCGCGCTCCCGCAGCGGCTCCGCG	180			
Db	121	CCGGGACGCGGGAGCCATGCGAACCCGAGGGCCCGCGCGCTCCCGCAGCGGCTCCGCG	180			
Qy	181	GCTCTCTGCTGCTCTCTGCTGCTGACGTGCCCGCGCGCTGAGCGGCTTCGAGATCCCCA	240			
Db	181	GCTCTCTGCTGCTCTCTGCTGCTGACGTGCCCGCGCGCTGAGCGGCTTCGAGATCCCCA	240			
Qy	241	AGGGGAAGCAAAAGGCGCAGCTCCGGAGAGGGAGGAGTGAGACCTGTATTAAGAAATGT	300			
Db	241	AGGGGAAGCAAAAGGCGCAGCTCCGGAGAGGGAGGAGTGAGACCTGTATTAAGAAATGT	300			
Qy	301	GCTTACAAAGGCGCCAGCAGAGTGCTGTGTGAGACGGAGAGCCCTGGGSCCAATGTATTC	360			
Db	301	GCTTACAAAGGCGCCAGCAGAGTGCTGTGTGAGACGGAGAGCCCTGGGSCCAATGTATTC	360			
Qy	361	CGGGTACACCTGGGATCCCCAGTGGGATGTGATTTCAAGAGAAAGGGGAAATGTCTGA	420			
Db	361	CGGGTACACCTGGGATCCCCAGTGGGATGTGATTTCAAGAGAAAGGGGAAATGTCTGA	420			
Qy	421	GGGAAAGCTTTGAGAGATCTCTGACACCCAACTACAAGAGTGTTCATGAGATTCATTTGA	480			
Db	421	GGGAAAGCTTTGAGAGATCTCTGACACCCAACTACAAGAGTGTTCATGAGATTCATTTGA	480			
Qy	481	ATTATGCGATAGATCTTGGGAAAATTGGCGAGTGTACATTTCAAGAATGCGTTCAATA	540			
Db	481	ATTATGCGATAGATCTTGGGAAAATTGGCGAGTGTACATTTCAAGAATGCGTTCAATA	540			
Qy	541	GTGCTTAAGAGTTTGTTCAGTGGGCTCACTGGGCTAAATGAGAAATGCATGCTGTC	600			
Db	541	GTGCTTAAGAGTTTGTTCAGTGGGCTCACTGGGCTAAATGAGAAATGCATGCTGTC	600			
Qy	601	AGCGTGGTATTTTCAATTCATATGAGCTGATGTTGAGACCTCTTCCCATGAACTGA	660			
Db	601	AGCGTGGTATTTTCAATTCATATGAGCTGATGTTGAGACCTCTTCCCATGAACTGA	660			
Qy	661	TAAATTTATTTGACACCAAGAAAGCCCTGAATGAAATTCACAAATTAATTCATGGCACTT	720			
Db	661	TAAATTTATTTGACACCAAGAAAGCCCTGAATGAAATTCACAAATTAATTCATGGCACTT	720			
Qy	721	CTTCTGAGAAAGACTTGTGAGAAATGGTGTGATTAAGTGAATGTTGCTATCTGCGG	780			
Db	721	CTTCTGAGAAAGACTTGTGAGAAATGGTGTGATTAAGTGAATGTTGCTATCTGCGG	780			
Qy	781	TTGGCACTTGTTCAGATTTACCCAAAGAGATGCTTCACTGATGGAATTCAGTTTCTC	840			
Db	781	TTGGCACTTGTTCAGATTTACCCAAAGAGATGCTTCACTGATGGAATTCAGTTTCTC	840			
Qy	841	GCATCATTAATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT	900			
Db	841	GCATCATTAATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT	900			
Qy	901	TTATTTATGCCCTTGGAAATGCTTCACTTAATGCAATTTTAAATTAAGTTATGTATACACT	960			
Db	901	TTATTTATGCCCTTGGAAATGCTTCACTTAATGCAATTTTAAATTAAGTTATGTATACACT	960			
Qy	961	GAATGAAAAGCAAGCTTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAA	1020			
Db	961	GAATGAAAAGCAAGCTTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAA	1020			


```
QY 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGTGGTTCAATATTTTGTAGTGGTT 1080
DB 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGTGGTTCAATATTTTGTAGTGGTT 1080
QY 1081 AGAATCTTTCTTCATAGTCAATTTCTCAACCTTAATTGGAAATTTGTGGTCT 1140
DB 1081 AGAATCTTTCTTCATAGTCAATTTCTCAACCTTAATTGGAAATTTGTGGTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAATATTAAGCTACCAATCTTGTAC 1200
DB 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAATATTAAGCTACCAATCTTGTAC 1200
QY 1201 AATTGTAAATGTAAAGATTTTATATCTGTTAAATAAAATTAATTTCCACA 1257
DB 1201 AATTGTAAATGTAAAGATTTTATATCTGTTAAATAAAATTAATTTCCACA 1257

RESULT 32
US-10-174-582-365
; Sequence 365, Application US/10174582
; Publication No. US20030027265A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C36
; CURRENT APPLICATION NUMBER: US/10/174,582
; PRIORITY FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-174-582-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCGCGGGTGAAAGCGCATTTGATGACCTTGCGGCGGCTCGGAGCGGCG 60
DB 1 GGAAGAGGCGCGCGGGTGAAAGCGCATTTGATGACCTTGCGGCGGCTCGGAGCGGCG 60
QY 61 CGAGAGCAGACGCTGACACGTTCTCTCTCGGCTCTCTCGGCTCTGACGCTCGGCGGCTG 120
DB 61 CGAGAGCAGACGCTGACACGTTCTCTCTCGGCTCTCTCGGCTCTGACGCTCGGCGGCTG 120
QY 121 CCGGAGCGCGGAGACCATTCGACCCCGGCGGCTCTCGGAGCGGCTCGGCGGCTCGGCG 180
DB 121 CCGGAGCGCGGAGACCATTCGACCCCGGCGGCTCTCGGAGCGGCTCGGCGGCTCGGCG 180
QY 181 GCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AGGGGAGAGCAAAAGCGCGAGCTCGGAGAGAGAGTGTGGAACCTGTATATGGAATGT 300
DB 241 AGGGGAGAGCAAAAGCGCGAGCTCGGAGAGAGAGTGTGGAACCTGTATATGGAATGT 300
QY 301 GCTTACAGGCGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 GCTTACAGGCGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
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QY 361 CGGGTACACTGGGATTCACAGCTGGGATGGATTCAAAGAGAAAGGGGGAATGTCTGA 420
DB 361 CGGGTACACTGGGATTCACAGCTGGGATGGATTCAAAGAGAAAGGGGGAATGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGAGCTCTGACACCACTCAAGACAGTGTTCATGAGGATTCATGA 480
DB 421 GGGAAAGCTTTGAGAGAGCTCTGACACCACTCAAGACAGTGTTCATGAGGATTCATGA 480
QY 481 ATTATGCAATGATCTTGGGAAAATTTGGGAGTGTATATTAACAAAGATCGTTCAATA 540
DB 481 ATTATGCAATGATCTTGGGAAAATTTGGGAGTGTATATTAACAAAGATCGTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGTCTCACTTGGGCTTAAATGTGCAAAATGACAGTGTCT 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGTCTCACTTGGGCTTAAATGTGCAAAATGACAGTGTCT 600
QY 601 AGCGTGTGATTTACATTCATGAGCTGAATGTTCAGACCTCTTCCCATTTGAAGCTA 660
DB 601 AGCGTGTGATTTACATTCATGAGCTGAATGTTCAGACCTCTTCCCATTTGAAGCTA 660
QY 661 TAATTTATTTGACCAAGAAAGCCCTGAATGAATTCACAAATTAATATTCATGCACTT 720
DB 661 TAATTTATTTGACCAAGAAAGCCCTGAATGAATTCACAAATTAATATTCATGCACTT 720
QY 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGTGTCTGATTTGATGAGATGTGTCTGCTG 780
DB 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGTGTCTGATTTGATGAGATGTGTCTGCTG 780
QY 781 TTGGCACTTGTTCAGATTTCCCAAGAGAGATGCTTCTACTGATGAGATTCAGTGTCTC 840
DB 781 TTGGCACTTGTTCAGATTTCCCAAGAGAGATGCTTCTACTGATGAGATTCAGTGTCTC 840
QY 841 GCATCATTTATGAAGATCCAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
DB 841 GCATCATTTATGAAGATCCAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
QY 901 TTATTAAGCCTTGAAGTGTCTCACTTAATGACATTTTAATGAATTTATGATATCATCT 960
DB 901 TTATTAAGCCTTGAAGTGTCTCACTTAATGACATTTTAATGAATTTATGATATCATCT 960
QY 961 GAATGAAGAAAGCAATTAATGATTTTACAGACCAAGTGTGATTCACATGTTTTTA 1020
DB 961 GAATGAAGAAAGCAATTAATGATTTTACAGACCAAGTGTGATTCACATGTTTTTA 1020
QY 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGTGGTTCAATATTTTGTAGTGGTT 1080
DB 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGTGGTTCAATATTTTGTAGTGGTT 1080
QY 1081 AGAATCTTTCTTCATAGTCAATTTCTCAACCTTAATTGGAAATTTGTGGTCT 1140
DB 1081 AGAATCTTTCTTCATAGTCAATTTCTCAACCTTAATTGGAAATTTGTGGTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAATATTAAGCTACCAATCTTGTAC 1200
DB 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAATATTAAGCTACCAATCTTGTAC 1200
QY 1201 AATTGTAAATGTAAAGATTTTATATCTGTTAAATAAAATTAATTTCCACA 1257
DB 1201 AATTGTAAATGTAAAGATTTTATATCTGTTAAATAAAATTAATTTCCACA 1257

RESULT 33
US-10-174-588-365
; Sequence 365, Application US/10174588
; Publication No. US20030027266A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
```


Dp	61	CGAGGCGAAGCGGTGACCAAGTTCCTCTCTCGGTCTCTCCGCTCCAGCTCCAGCTCCGGCTG	120
Qy	121	CCGGGCAAGCCGGGAGCCATTCGACCCCAAGGGCCCCGCTCGCTCCCGGACGGCTCCGGC	180
Dp	121	CCGGGCAAGCCGGGAGCCATTCGACCCCAAGGGCCCCGCTCGCTCCCGGACGGCTCCGGC	180
Qy	181	GCCTCTGCTGCTCTGCTGCTGCAAGCTGCGCGCGCTGAGAGGCTCTGAGATCCCA	240
Dp	181	GCCTCTGCTGCTCTGCTGCTGCAAGCTGCGCGCGCTGAGAGGCTCTGAGATCCCA	240
Qy	241	AGGGGAAGCAAAAGGGCGAGCTCCGGCAGAGGAGTGATGACCTGTATATGAAATGT	300
Dp	241	AGGGGAAGCAAAAGGGCGAGCTCCGGCAGAGGAGTGATGACCTGTATATGAAATGT	300
Qy	301	GCCTTACAAGGGCAGGAGGTGCTGCTGAGACCGGAGACCCCTGGGGCCAAATGTATTC	360
Dp	301	GCCTTACAAGGGCAGGAGGTGCTGCTGAGACCGGAGACCCCTGGGGCCAAATGTATTC	360
Qy	361	CGGGTACACCTGGGATCCAGGCTCGGAGTGAATTCAAAGAGAAAAGGGGAAATGCTGA	420
Dp	361	CGGGTACACCTGGGATCCAGGCTCGGAGTGAATTCAAAGAGAAAAGGGGAAATGCTGA	420
Qy	421	GGGAAAGCTTTGAGAGTCTCTGGAACCCCAACTACAGAGTGTTCATGAGCTTCAATGA	480
Dp	421	GGGAAAGCTTTGAGAGTCTCTGGAACCCCAACTACAGAGTGTTCATGAGCTTCAATGA	480
Qy	481	ATTATGGCATAGATCTTGGGAAAATTCGGAGATGATTCATTACAAAGATGCGTTCAAATA	540
Dp	481	ATTATGGCATAGATCTTGGGAAAATTCGGAGATGATTCATTACAAAGATGCGTTCAAATA	540
Qy	541	GTGCTCTAAGAGTTTGTGTTCACTGAGCTCACTTGCGTAAATGCAAGAAATGCATGCTGTC	600
Dp	541	GTGCTCTAAGAGTTTGTGTTCACTGAGCTCACTTGCGTAAATGCAAGAAATGCATGCTGTC	600
Qy	601	AGCGTGTGATTTTCACTTCAATGAGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTA	660
Dp	601	AGCGTGTGATTTTCACTTCAATGAGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTA	660
Qy	661	TAAATTTATTTGGACCAAGGAAGCCCTGAATGAATTCACAAATTAATATTCATCGCACTT	720
Dp	661	TAAATTTATTTGGACCAAGGAAGCCCTGAATGAATTCACAAATTAATATTCATCGCACTT	720
Qy	721	CTTCTGTGGAAGGACTTTGTGAAGAAATGGTGCTGGAATTAAGGATGTTGCTATCTGGG	780
Dp	721	CTTCTGTGGAAGGACTTTGTGAAGAAATGGTGCTGGAATTAAGGATGTTGCTATCTGGG	780
Qy	781	TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTTC	840
Dp	781	TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTTC	840
Qy	841	GCATCATTTATTAAGAACTACCAAAATAATGCTTTAATTTTCATTTGCTACTCTTTT	900
Dp	841	GCATCATTTATTAAGAACTACCAAAATAATGCTTTAATTTTCATTTGCTACTCTTTT	900
Qy	901	TTATTTATGCTTGAATGCTTCACTTAAATGACATTTTAAATTAAGTTATGATACATCT	960
Dp	901	TTATTTATGCTTGAATGCTTCACTTAAATGACATTTTAAATTAAGTTATGATACATCT	960
Qy	961	GAAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAGTGATGATTTTCACTGTTTTTAA	1020
Dp	961	GAAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAGTGATGATTTTCACTGTTTTTAA	1020
Qy	1021	ATCTAGCAATTAATCAATTTTGTGCTTCATCAAAAGTGSTTCAATATTTTATAGTTGGTT	1080
Dp	1021	ATCTAGCAATTAATCAATTTTGTGCTTCATCAAAAGTGSTTCAATATTTTATAGTTGGTT	1080
Qy	1081	AGAAATCTTTCTTCATAGTCAATTTCTCAACCTATATTTGGAATATGTGTGGTCT	1140
Dp	1081	AGAAATCTTTCTTCATAGTCAATTTCTCAACCTATATTTGGAATATGTGTGGTCT	1140
Qy	1141	TTTGTTTTTCTCTAAGTATAGCAATTTTAAATAAATAATTAAGATCAATCTTTGTAC	1200
Dp	1141	TTTGTTTTTCTCTAAGTATAGCAATTTTAAATAAATAATTAAGATCAATCTTTGTAC	1200

QY	1201 AATTGTGAATGTTAGAAATTTTTTATTATCGTAAATAAATAATATTCACACA	1257
Db	1201 AATTGTAAATGTTAGAATTTTTTTTAATCTGTTAAATAAAAATATTCACA	1257
 RESULT 35 US-10-175-740-365 ; Sequence 365, Application US/10175740 ; Publication No. US20030027268A1 ; GENERAL INFORMATION: ; APPLICANT: Baker, Kevin P. ; APPLICANT: Chen, Jian ; APPLICANT: Desnoyers, Luc ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Gurney, Austin L. ; APPLICANT: Pan, James ; APPLICANT: Smith, Victoria ; APPLICANT: Watanabe, Colin K. ; APPLICANT: Wood, William I. ; APPLICANT: Zhang, Zemin ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ; FILE REFERENCE: P3430R1C61 ; CURRENT APPLICATION NUMBER: US/10/175,740 ; PRIOR FILING DATE: 2002-06-18 ; NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 365 ; LENGTH: 1257 ; TYPE: DNA ; ORGANISM: Homo Sapien US-10-175-740-365		
 Query Match 100.0%; Score 1257; DB 14; Length 1257; Best Local Similarity 100.0%; Pred. No. 3,4e-271; Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 GGAGAGAGGGCGGCGGTGAAGGAGGCATTGATGAGCTCGGCGGCGCTTGAGCGCGG	60
Db	1 GGAGAGAGCGCGCGGTGAAGGAGGCATTATGAGCTCGGCGGCGCTTGAGCGCGG	60
QY	61 CGGAGCCAGACGCTGACCAGCTTCTCTCTCGATCTCTCGGCTTCAGCTCGCGCTG	120
Db	61 CGGAGCCAGACGCTGACCAGCTTCTCTCTCGATCTCTCGGCTTCAGCTCGCGCTG	120
QY	121 CCGCGCACGCCGAGACCATGGAACCCAGGCGCCCGCCTCCCGCAGCGGCTCGCG	180
Db	121 CCGCGCACGCCGAGACCATGGAACCCAGGCGCCCGCCTCCCGCAGCGGCTCGCG	180
QY	181 GCCTCTCTGCTCTCTGTGCTGACGACGCGCGCGCTGCAAGCGCCCTGAGATCCCA	240
Db	181 GCCTCTCTGCTCTCTGTGCTGACGACGCGCGCGCTGCAAGCGCCCTGAGATCCCA	240
QY	241 AGGGAGACAAAAGCGCAGCTCCGGCAGAGGAGGTGTGACCTGTATATGAAATGT	300
Db	241 AGGGAGACAAAAGCGCAGCTCCGGCAGAGGAGGTGTGACCTGTATATGAAATGT	300
QY	301 GCTTACAGAGGCGCAGCAGAGTGCCTGCTGAGACGGAGAGCCCTGGGCGCAAATGTTATTC	360
Db	301 GCTTACAGAGGCGCAGCAGAGTGCCTGCTGAGACGGAGAGCCCTGGGCGCAAATGTTATTC	360
QY	361 CGGGTACACCTGGGATCCAGGTGCGGATGGAATCAAGAGAAAAGGGGAGATGTCTGA	420
Db	361 CGGGTACACCTGGGATCCAGGTGCGGATGGAATCAAGAGAAAAGGGGAGATGTCTGA	420
QY	421 GGGAAAGCTTTGAGAGAGCTTGACACCCAATACAGCAATGTTCAATGAGATTCATTTGA	480
Db	421 GGGAAAGCTTTGAGAGAGCTTGACACCCAATACAGCAATGTTCAATGAGATTCATTTGA	480
QY	481 ATTATGCAATGATCTTGAGAAAATTTGCGAGTGTACTTATCAAAATAGCGTCAATA	540

Db 481 ATTATGCAATAGATCTTGGGAAAATTGCGAGTACATTTACAAAGATGCTTCAATA 540
Qy 541 GTCCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTGTC 600
Db 541 GTCCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTGTC 600
Qy 601 AGCGTGTATTTCAATTCATGAGAGTGAATGTTGAGGACCTCTTCCATTTGAAGCTA 660
Db 601 AGCGTGTATTTCAATTCATGAGAGTGAATGTTGAGGACCTCTTCCATTTGAAGCTA 660
Qy 661 TAATTTATTTGACCAAGGAGCCCTGAAATGAAATTCACAAATTAATTCATGCACTT 720
Db 661 TAATTTATTTGACCAAGGAGCCCTGAAATGAAATTCACAAATTAATTCATGCACTT 720
Qy 721 CTTCTGTGGAAGACCTTTGTGAAGAAATGCTGTGATTAAGTGAATGTTGCTATCTGGG 780
Db 721 CTTCTGTGGAAGACCTTTGTGAAGAAATGCTGTGATTAAGTGAATGTTGCTATCTGGG 780
Qy 781 TTGGCACTTGTGAGATTACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTCTC 840
Db 781 TTGGCACTTGTGAGATTACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTCTC 840
Qy 841 GCATCATTTATGGAAGACTACCAAAATAAATGCTTTAATTTTCATTTGCTACTCTTTT 900
Db 841 GCATCATTTATGGAAGACTACCAAAATAAATGCTTTAATTTTCATTTGCTACTCTTTT 900
Qy 901 TTTATTTGCTTGGAAATGCTTCACTTAATGACATTTTAATTAAGTTTATGATACATCT 960
Db 901 TTTATTTGCTTGGAAATGCTTCACTTAATGACATTTTAATTAAGTTTATGATACATCT 960
Qy 961 GAATGAAAGCAAGCTAAATATGTTTACAGCAAGAGTGTGATTTTCACTGTTTAA 1020
Db 961 GAATGAAAGCAAGCTAAATATGTTTACAGCAAGAGTGTGATTTTCACTGTTTAA 1020
Qy 1021 ATCTACATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTATTTTATTTAGTGT 1080
Db 1021 ATCTACATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTATTTTATTTAGTGT 1080
Qy 1081 AGAATCTTTCTTCATGATGACATTTCTCTCAACCTTATATTTGGAATTTGTTGGTCT 1140
Db 1081 AGAATCTTTCTTCATGATGACATTTCTCTCAACCTTATATTTGGAATTTGTTGGTCT 1140
Qy 1141 TTTGTTTTTCTCTTGTATGATGATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200
Db 1141 TTTGTTTTTCTCTTGTATGATGATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200
Qy 1201 AATTTGTAATGTTAAGATTTTATTTATATCTGTTAAATAAATTAATTTCCACA 1257
Db 1201 AATTTGTAATGTTAAGATTTTATTTATATCTGTTAAATAAATTAATTTCCACA 1257

RESULT 36
US-10-175-743-365
; Sequence 365, Application US/10175743
; Publication No. US20030027269A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C52
; CURRENT APPLICATION NUMBER: US/10175, 743
; CURRENT FILING DATE: 2002-06-16
; PRIOR APPLICATION NUMBER: 10/052586

;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063564
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063734
;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 60/063870
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066120
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/066466
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/06772
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/069335
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/069425
;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: 60/069870
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/068017
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/078886
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;; PRIOR APPLICATION NUMBER: 60/078939
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;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
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;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081070
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083495
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PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087098
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087208
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655

PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGGGGGAAGCGCATGATGACGCGCGCGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGCGGGGGAAGCGCATGATGACGCGCGCGCGCTCGAGGCGCG 60
QY 61 CGAGCCAGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGCCAGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGCGAGCGGGAGCGATGCAACCCAGAGGCGCGCGCTCTCTCTCTCTCTCT 180
DB 121 CCGGCGAGCGGGAGCGATGCAACCCAGAGGCGCGCGCTCTCTCTCTCTCTCT 180
QY 181 GCTCTGCTGCT 240
DB 181 GCTCTGCTGCT 240
QY 241 AGGGAAGCAAAAGCGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 AGGGAAGCAAAAGCGCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 GCTTACAAGGGCGAGCGAGGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 360
DB 301 GCTTACAAGGGCGAGCGAGGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 360
QY 361 CGGATACCTGGAGTCCAGGTCTGGATGATTTCAAGAGAAAGGGGAATGTCTGA 420
DB 361 CGGATACCTGGAGTCCAGGTCTGGAGTGTATTTCAAGAGAAAGGGGAATGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGTCTCTGACACCAACTACAGAGGTCTTATGAGTTCATTGA 480
DB 421 GGGAAAGCTTTGAGAGTCTCTGACACCAACTACAGAGGTCTTATGAGTTCATTGA 480
QY 481 ATTATGCGATGATCTTGGGAAATTTGGAGGTGATTTTCAAGAGTCTTCAATA 540
DB 481 ATTATGCGATGATCTTGGGAAATTTGGAGGTGATTTTCAAGAGTCTTCAATA 540

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Db      481 ATTATGCAATAGATCTTGGGAAATTCGGAGTGTACATTTACAAAGATCGTTCAAA 540
Qy      541 GTCCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTGTC 600
Db      541 GTGCTCAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTGTC 600
Qy      601 AGCGTTGATTTTCAATTCATGAGAGCTGATGTTTCAAGAGCTCTTCCATTTGAAGCTA 660
Db      601 AGCGTTGATTTTCAATTCATGAGAGCTGATGTTTCAAGAGCTCTTCCATTTGAAGCTA 660
Qy      661 TAAATTTATTTGACCAAGAGAGCCCTGAAATTAATTCACATTAATTAATTCATGCACTT 720
Db      661 TAAATTTATTTGACCAAGAGAGCCCTGAAATTAATTCACATTAATTAATTCATGCACTT 720
Qy      721 CTTCTGTGGAAGAGCTTTTGTGAAGAAATGTTGTTGATGATGATGATGATGATGATGATG 780
Db      721 CTTCTGTGGAAGAGCTTTTGTGAAGAAATGTTGTTGATGATGATGATGATGATGATGATG 780
Qy      781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACATGGAATTCAGTTTCTC 840
Db      781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACATGGAATTCAGTTTCTC 840
Qy      841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTTTT 900
Db      841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTTTT 900
Qy      901 TTATTTATGCTTGGAAATGCTTCACTTAATGACATTTTAAATGATTTAATGATTAATCATCT 960
Db      901 TTATTTATGCTTGGAAATGCTTCACTTAATGACATTTTAAATGATTTAATGATTAATCATCT 960
Qy      961 GAATGAAAAGCAAGCTTAATTAATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAA 1020
Db      961 GAATGAAAAGCAAGCTTAATTAATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAA 1020
Qy      1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTGTTCAATATTTTATTTTATGTTG 1080
Db      1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTGTTCAATATTTTATTTTATGTTG 1080
Qy      1081 AGAATCTTCTTCATGATGACATCTCTCAACCTAATTAATTTGGAATATTTGTTGCTCT 1140
Db      1081 AGAATCTTCTTCATGATGACATCTCTCAACCTAATTAATTTGGAATATTTGTTGCTCT 1140
Qy      1141 TTTGTTTTTCTCTAGTATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
Db      1141 TTTGTTTTTCTCTAGTATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
Qy      1201 AATTGTAAATGTTAAGAAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1257
Db      1201 AATTGTAAATGTTAAGAAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1257

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RESULT 37
US-10-176-488-365
; Sequence 365, Application US/10176488
; Publication No. US2003027271A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OR INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C119
; CURRENT APPLICATION NUMBER: US/10176,488
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-488-365

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGCGGCTCGAGCGCG 60
Db      1  GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGCGGCTCGAGCGCG 60
Qy      61  CGAGGCAAGACGCTGACACAGTTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db      61  CGAGGCAAGACGCTGACACAGTTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Qy      121  CCGGCGAGCGGGAGGCGATGACGACCCAGGGGCCCGCGCTCCCGGAGCGGCTCCGCG 180
Db      121  CCGGCGAGCGGGAGGCGATGACGACCCAGGGGCCCGCGCTCCCGGAGCGGCTCCGCG 180
Qy      181  GCCTCCCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db      181  GCCTCCCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy      241  AGGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGTGTGACCTGTATTAATGGAATGT 300
Db      241  AGGGGAAGCAAAAGCGCGAGCTCCGCGAGAGGAGTGTGACCTGTATTAATGGAATGT 300
Qy      301  GCTTCAAGGGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db      301  GCTTCAAGGGCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy      361  CGGGTACACCTGAGATGCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGT 420
Db      361  CGGGTACACCTGAGATGCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGT 420
Qy      421  GGGAAAGCTTTGAGAGAGTCTTGACACCCCACTACAGAGTGTTCATGAGATTCATGA 480
Db      421  GGGAAAGCTTTGAGAGAGTCTTGACACCCCACTACAGAGTGTTCATGAGATTCATGA 480
Qy      481  ATTATGCAATAGATCTTGGGAAATTTGGGAGTGTATTTTCAAAAGATGCGTTCAAA 540
Db      481  ATTATGCAATAGATCTTGGGAAATTTGGGAGTGTATTTTCAAAAGATGCGTTCAAA 540
Qy      541  GTGCTTAAGAGTTTGTTCAGTGGCTCACTTCCGCTAAATGCAAGAAATGCAATGCTGTC 600
Db      541  GTGCTTAAGAGTTTGTTCAGTGGCTCACTTCCGCTAAATGCAAGAAATGCAATGCTGTC 600
Qy      601  AGCGTTGATTTTCAATTCATGAGAGCTGATGTTTCAAGAGCTCTTCCATTTGAAGCTA 660
Db      601  AGCGTTGATTTTCAATTCATGAGAGCTGATGTTTCAAGAGCTCTTCCATTTGAAGCTA 660
Qy      661  TAAATTTATTTGACCAAGAGAGCCCTGAAATTAATTCACATTAATTAATTAATTAATTAATTAAT 720
Db      661  TAAATTTATTTGACCAAGAGAGCCCTGAAATTAATTCACATTAATTAATTAATTAATTAATTAAT 720
Qy      721  CTTCTGTGGAAGAGCTTTTGTGAAGAAATGTTGTTGATGATGATGATGATGATGATGATGATG 780
Db      721  CTTCTGTGGAAGAGCTTTTGTGAAGAAATGTTGTTGATGATGATGATGATGATGATGATGATG 780
Qy      781  TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACATGGAATTCAGTTTCTC 840
Db      781  TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACATGGAATTCAGTTTCTC 840
Qy      841  GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTTTT 900
Db      841  GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTTTT 900
Qy      901  TTATTTATGCTTGGAAATGCTTCACTTAATGACATTTTAAATGATTTAATGATTAATCATCT 960

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Db 901 TTATTATGCTTGGATGGTTCATTAAATGACATTTTAAATAGTTATGTATACATCT 960
Qy 961 GAATGAAAGCAAGCTAAATNGTTTACAGACCAAGTGTATTTTCACTGTCTTTTAA 1020
Db 961 GAATGAAAGCAAGCTAAATNGTTTACAGACCAAGTGTATTTTCACTGTCTTTTAA 1020
Qy 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGT 1080
Db 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGT 1080
Qy 1081 AGAATACCTTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAATATTTGTGTCT 1140
Db 1081 AGAATACCTTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAATATTTGTGTCT 1140
Qy 1141 TTGTGTTTTCTTCTAGTATAGCATTTTAAATAATATTAAGTACCAATCTTTGTAC 1200
Db 1141 TTGTGTTTTCTTCTAGTATAGCATTTTAAATAATATTAAGTACCAATCTTTGTAC 1200
Qy 1201 AATTTGTAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCAAACA 1257
Db 1201 AATTTGTAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCAAACA 1257

RESULT 38

US-10-176-492-365
; Sequence 365, Application US/10176492
; Publication No. US20030027272A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C107
; CURRENT APPLICATION NUMBER: US/10/176,492
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-492-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGAGCGCGCGGTGAAGGCGCATTTGATGAGCGTGGCGCGCTCGAGCGCGG 60
Db 1 GGAAGAGAGCGCGCGGTGAAGGCGCATTTGATGAGCGTGGCGCGCTCGAGCGCGG 60
Qy 61 CGAGAGCGAGCGTGAACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 61 CGAGAGCGAGCGTGAACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Qy 121 CCCGAGCGCGGAGGAGCAATGCAACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCT 180
Db 121 CCCGAGCGCGGAGGAGCAATGCAACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCT 180
Qy 181 GCT 240
Db 181 GCT 240
Qy 241 AGGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAAGCTGTATTAATGAATGT 300

Db 241 AGGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAAGCTGTATTAATGAATGT 300
Qy 301 GCTTACAAAGGCGAGAGAGTGGCTGTGTGAGAAGGAGCGCTGGGCGCAATGTATTC 360
Db 301 GCTTACAAAGGCGAGAGAGTGGCTGTGTGAGAAGGAGCGCTGGGCGCAATGTATTC 360
Qy 361 CGGGTACACCTGGGATCCCAAGTGGATGATTAATCAAGAGAAAGGGGAAATGTCTGA 420
Db 361 CGGGTACACCTGGGATCCCAAGTGGATGATTAATCAAGAGAAAGGGGAAATGTCTGA 420
Qy 421 GGGAAAGCTTTGAGAGTCTGAGACCACTCAAGCAAGTGTTCATGAGAGTTGATGA 480
Db 421 GGGAAAGCTTTGAGAGTCTGAGACCACTCAAGCAAGTGTTCATGAGAGTTGATGA 480
Qy 481 ATTATGCAATGATCTGGGAAATTTGGAGGTGTATTCATTAAGAGTGGTCAATAA 540
Db 481 ATTATGCAATGATCTGGGAAATTTGGAGGTGTATTCATTAAGAGTGGTCAATAA 540
Qy 541 GTGCTCTAGAGTGTGTGTGAGTGTCTCACTTGGCTTAAATGCAAAATGCAATGCTG 600
Db 541 GTGCTCTAGAGTGTGTGTGAGTGTCTCACTTGGCTTAAATGCAAAATGCAATGCTG 600
Qy 601 AGCGTTGGTATTTCAATTCAGTGAAGTGTGAGAGCTCTTCCATTTGAAGCTA 660
Db 601 AGCGTTGGTATTTCAATTCAGTGAAGTGTGAGAGCTCTTCCATTTGAAGCTA 660
Qy 661 TAATTTATTTGGACCAAGAGAGGCTTGAATTAATTAATTAATTTATTCATGCACT 720
Db 661 TAATTTATTTGGACCAAGAGAGGCTTGAATTAATTAATTAATTTATTCATGCACT 720
Qy 721 CTCTGTGGAAGACCTTTGTGAAGAAATGTGTGTGATTAAGTGAATGTGTGATCTG 780
Db 721 CTCTGTGGAAGACCTTTGTGAAGAAATGTGTGTGATTAAGTGAATGTGTGATCTG 780
Qy 781 TTGGCACTTGTTCAGATTTACCAAGAGAGATGCTTCTACGTGATGATTCAGTTCTC 840
Db 781 TTGGCACTTGTTCAGATTTACCAAGAGAGATGCTTCTACGTGATGATTCAGTTCTC 840
Qy 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAAATTTTCACTTCTCTCTCTTT 900
Db 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAAATTTTCACTTCTCTCTCTTT 900
Qy 901 TTATTATGCTTGAAGTGTCTTCAATTAATGATTAATTAATTTTATTTAGTTGT 960
Db 901 TTATTATGCTTGAAGTGTCTTCAATTAATGATTAATTAATTTTATTTAGTTGT 960
Qy 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTTAA 1020
Db 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTTAA 1020
Qy 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGT 1080
Db 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGT 1080
Qy 1081 AGAATACCTTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAATATTTGTGTCT 1140
Db 1081 AGAATACCTTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAATATTTGTGTCT 1140
Qy 1141 TTGTGTTTTCTTCTAGTATAGCATTTTAAATAATATTAAGTACCAATCTTTGTAC 1200
Db 1141 TTGTGTTTTCTTCTAGTATAGCATTTTAAATAATATTAAGTACCAATCTTTGTAC 1200
Qy 1201 AATTTGTAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCAAACA 1257
Db 1201 AATTTGTAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCAAACA 1257

RESULT 39

US-10-176-747-365
; Sequence 365, Application US/10176747
; Publication No. US20030027273A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C92
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-747-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGGCGCGGGGTGAAAGCGCATTTGATGACGCGCGCGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGGCGCGGGGTGAAAGCGCATTTGATGACGCGCGCGCGCTCGAGGCGCG 60
QY 61 CGAGAGCGAGCGCTGACGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCGAGCGCTGACGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGAGCGCGGGAGCGATGCGA CCGCAGGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCT 180
DB 121 CCGGAGCGCGGGAGCGATGCGA CCGCAGGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCT 180
QY 181 GCCT 240
DB 181 GCCT 240
QY 241 AGGAG 300
DB 241 AGGAG 300
QY 301 GCTTACAGGAG 360
DB 301 GCTTACAGGAG 360
QY 361 CGGAGTACCTGGAGATCCAGAGTCCGAGTGGATGATTTCAAGAGAGAGAGAGAGAGAG 420
DB 361 CGGAGTACCTGGAGATCCAGAGTCCGAGTGGATGATTTCAAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAG 480
DB 421 GGGAG 480
QY 481 ATTATGAGCATAGATCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATTATGAGCATAGATCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTCGGCTAAATGACAGAAATGACAGTGTTC 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTCGGCTAAATGACAGAAATGACAGTGTTC 600
QY 601 AGGAGTGTATTTTTCACATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 AGGAGTGTATTTTTCACATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TAATTTATTTTGACCAAG 720

DB 661 TAATTTATTTTGACCAAG 720
QY 721 CTTCTGTGAG 780
DB 721 CTTCTGTGAG 780
QY 781 TTGGAG 840
DB 781 TTGGAG 840
QY 841 GCATCATTTATGAG 900
DB 841 GCATCATTTATGAG 900
QY 901 TTATTTATGAG 960
DB 901 TTATTTATGAG 960
QY 961 GAATGAG 1020
DB 961 GAATGAG 1020
QY 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGGTTCAATTTTATTTTATTTTATTTT 1080
DB 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGGTTCAATTTTATTTTATTTTATTTT 1080
QY 1081 AGAATATCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AGAATATCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 TTTGTTTCTTCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TTTGTTTCTTCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1257
DB 1201 AATTTGTAATGTTAAGATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1257

RESULT 40
US-10-176-750-365
; Sequence 365, Application US/10176750
; Publication No. US20030027274A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C103
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-750-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY 1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACAGCTGCGCGGGCTCGGAGCGCG 60
DB 1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACAGCTGCGCGGGCTCGGAGCGCG 60
QY 61 CGGAGCGAAGCGCTGACACAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAAGCGCTGACACAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGCCCGCGCGCTCCCGCGAGCGCGCTCGG 180
DB 121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGCCCGCGCGCTCCCGCGAGCGCGCTCGG 180
QY 181 GCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGGAGGAAAAGCGGAGCTTCCGCGACAGGGAGGTGTGTGACCTGTATATGAAATGT 300
DB 241 AGGGGAGGAAAAGCGGAGCTTCCGCGACAGGGAGGTGTGTGACCTGTATATGAAATGT 300
QY 301 GCTTACAAGGCGCAGCAGAGTCCCTGATCGAGACGGAGCCCTGGGGCAATGTATTTC 360
DB 301 GCTTACAAGGCGCAGCAGAGTCCCTGATCGAGACGGAGCCCTGGGGCAATGTATTTC 360
QY 361 CGGGTACACTTGGGATCCCAAGTCCGAGTGAATTCAGAGGAAAAGGGGGAATGTCTGA 420
DB 361 CGGGTACACTTGGGATCCCAAGTCCGAGTGAATTCAGAGGAAAAGGGGGAATGTCTGA 420
QY 421 GGGAAAGCTTTGAGGAGTCTGAGACCCCACTACAAGAGGTTCATGAGATCTCTTGA 480
DB 421 GGGAAAGCTTTGAGGAGTCTGAGACCCCACTACAAGAGGTTCATGAGATCTCTTGA 480
QY 481 ATTATGCAATAGATCTTGGGAAAATTCGAGAGTGTACATTTACAAGATGCTTCAATA 540
DB 481 ATTATGCAATAGATCTTGGGAAAATTCGAGAGTGTACATTTACAAGATGCTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCTCTTCCGCTTAAATGCAAAATGCAATGCTGTC 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCTCTTCCGCTTAAATGCAAAATGCAATGCTGTC 600
QY 601 AGCGTTGGTATTTACATTCATGAGAGTGAATGTTCAAGACCTCTCCCATTTGAAGCTA 660
DB 601 AGCGTTGGTATTTACATTCATGAGAGTGAATGTTCAAGACCTCTCCCATTTGAAGCTA 660
QY 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGAATTCACAATTAATTTATTCACACT 720
DB 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGAATTCACAATTAATTTATTCACACT 720
QY 721 CTTCTGTGAGAGGACTTTGTGAGAAATTTGTGCTGATTAAGATGTGCTATCTGGG 780
DB 721 CTTCTGTGAGAGGACTTTGTGAGAAATTTGTGCTGATTAAGATGTGCTATCTGGG 780
QY 781 TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTC 840
DB 781 TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTC 840
QY 841 GCATCATTTATTTAGAGAACTACCAAAATAAATGCTTTAATTTTCAATTTGCTACTTTT 900
DB 841 GCATCATTTATTTAGAGAACTACCAAAATAAATGCTTTAATTTTCAATTTGCTACTTTT 900
QY 901 TTATTTATGCTTGGAAATGTTCACTTAATGCAATTTTAAATAATTTTATGATCACT 960
DB 901 TTATTTATGCTTGGAAATGTTCACTTAATGCAATTTTAAATAATTTTATGATCACT 960
QY 961 GAAATGAAAAGCAAGCTAATAATGTTTACAGCCAAATGTGATTTTCACTGTTTTTAA 1020
DB 961 GAAATGAAAAGCAAGCTAATAATGTTTACAGCCAAATGTGATTTTCACTGTTTTTAA 1020
QY 1021 ATCTAGCAATTTATCTTTTGTCTTCAATCAAAAGTGTTCATTAATTTTATTTTATGTTG 1080
DB 1021 ATCTAGCAATTTATCTTTTGTCTTCAATCAAAAGTGTTCATTAATTTTATTTTATGTTG 1080
QY 1081 AGAATACCTTTCTTATGATGACATTCCTGCAACCTAATAATTTGAAATATGTGTGCT 1140
```

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DB 1081 AGAATACCTTTCTTATGATGACATTCCTGCAACCTAATAATTTGAAATATGTGTGCT 1140
QY 1141 TTTGTTTTTCTTATGATGACATTTTAAATAATAAAGCTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTTCTTATGATGACATTTTAAATAATAAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGCTTAAGAAATTTTATATCTGTAAATTAATTAATTTATTTCCACA 1257
DB 1201 AATTTGTAATGCTTAAGAAATTTTATATCTGTAAATTAATTAATTTATTTCCACA 1257
```

RESULT 41

```
US-10-176-985-365
; Sequence 365, Application US/10176985
; Publication No. US2003002727A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C99
; CURRENT APPLICATION NUMBER: US/10/176,985
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-985-365
```

```
Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACAGCTGCGCGGGCTCGGAGCGCG 60
DB 1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACAGCTGCGCGGGCTCGGAGCGCG 60
QY 61 CGGAGCGAAGCGCTGACACAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAAGCGCTGACACAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGCCCGCGCGCTCCCGCGAGCGCGCTCGG 180
DB 121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGCCCGCGCGCTCCCGCGAGCGCGCTCGG 180
QY 181 GCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGGAGGAAAAGCGGAGCTTCCGCGACAGGGAGGTGTGTGACCTGTATATGAAATGT 300
DB 241 AGGGGAGGAAAAGCGGAGCTTCCGCGACAGGGAGGTGTGTGACCTGTATATGAAATGT 300
QY 301 GCTTACAAGGCGCAGCAGAGTCCCTGATCGAGACGGAGCCCTGGGGCAATGTATTTC 360
DB 301 GCTTACAAGGCGCAGCAGAGTCCCTGATCGAGACGGAGCCCTGGGGCAATGTATTTC 360
QY 361 CGGGTACACTTGGGATCCCAAGTCCGAGTGAATTCAGAGGAAAAGGGGGAATGTCTGA 420
DB 361 CGGGTACACTTGGGATCCCAAGTCCGAGTGAATTCAGAGGAAAAGGGGGAATGTCTGA 420
```

QY 421 GGGAAAGCTTTGAGAGCTCTGGAACCAACCACTACAAGAGTGTTCATGAGTTCATTA 480
| | | | |
DB 421 GGGAAAGCTTTGAGAGCTCTGGAACCAACCACTACAAGAGTGTTCATGAGTTCATTA 480
| | | | |
QY 481 ATTATGCGATGATCTTTGGGAAAATTGCGAGTGTACATTTACAAAGATGCGTTCAATA 540
| | | | |
DB 481 ATTATGCGATGATCTTTGGGAAAATTGCGAGTGTACATTTACAAAGATGCGTTCAATA 540
| | | | |
QY 541 GTGCTCTAAGAGTGTGTTCAGTGTGCTCACTTCGCTAAATATGCAAGATGATGTCTC 600
| | | | |
DB 541 GTGCTCTAAGAGTGTGTTCAGTGTGCTCACTTCGCTAAATATGCAAGATGATGTCTC 600
| | | | |
QY 601 AGCGTTGGATTTTCACTTCAATGAGCTGAATGTTCAGAGACCTCTTCCCATTTGAAGCTA 660
| | | | |
DB 601 AGCGTTGGATTTTCACTTCAATGAGCTGAATGTTCAGAGACCTCTTCCCATTTGAAGCTA 660
| | | | |
QY 661 TAATTTATTTGGACCAAGAGAGCCCTGAATATGATTCACATTTAATTTATTCATGCACTT 720
| | | | |
DB 661 TAATTTATTTGGACCAAGAGAGCCCTGAATATGATTCACATTTAATTTATTCATGCACTT 720
| | | | |
QY 721 CTTCTGTGAAGAGCTTTGTGAAGAAATTGCTGTGATTTAGTGAATGTTGCTATCTGGG 780
| | | | |
DB 721 CTTCTGTGAAGAGCTTTGTGAAGAAATTGCTGTGATTTAGTGAATGTTGCTATCTGGG 780
| | | | |
QY 781 TTGGGACCTTGTTCAGATTAACCAAGAGAGATGCTCTAAGTGAATGCAATTCAGTTCTC 840
| | | | |
DB 781 TTGGGACCTTGTTCAGATTAACCAAGAGAGATGCTCTAAGTGAATGCAATTCAGTTCTC 840
| | | | |
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
| | | | |
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900
| | | | |
QY 901 TTAATTAAGCTTGAATGCTTCACTTAATGATTTTAATTAATTAATTAATTAATTAAT 960
| | | | |
DB 901 TTAATTAAGCTTGAATGCTTCACTTAATGATTTTAATTAATTAATTAATTAATTAAT 960
| | | | |
QY 961 GAATGAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGTTTCAACGTTTAA 1020
| | | | |
DB 961 GAATGAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGTTTCAACGTTTAA 1020
| | | | |
QY 1021 ATCTAGCATTTATTCATTTTGTTCATTCATCAAAAGTGTTCATTAATTTTAAAGTGT 1080
| | | | |
DB 1021 ATCTAGCATTTATTCATTTTGTTCATTCATCAAAAGTGTTCATTAATTTTAAAGTGT 1080
| | | | |
QY 1081 AGAATATCTTCTTCATATGCACTTCTGCAACCTTAATTTGGAATTTGTTGCTCT 1140
| | | | |
DB 1081 AGAATATCTTCTTCATATGCACTTCTGCAACCTTAATTTGGAATTTGTTGCTCT 1140
| | | | |
QY 1141 TTTGTTTTTCTCTTGTATGATGATTTTAAATTAATTAATTAATTAATTAATTAAT 1200
| | | | |
DB 1141 TTTGTTTTTCTCTTGTATGATGATTTTAAATTAATTAATTAATTAATTAATTAAT 1200
| | | | |
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257
| | | | |
DB 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257
| | | | |
RESULT 42
US-10-176-987-365
; Sequence 365, Application US/10176987
; Publication No. US20030027278A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Aubert L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C93
; CURRENT APPLICATION NUMBER: US/10/176,987
; PRIOR APPLICATION: 2002-06-21
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-987-365
Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271; Mismatches 0; Indels 0; Gaps 0;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAAGAGAGCGCGCGGTAAGAGCGCATTTGATGAGCTGCGCGCGCTCCGAGCGCGG 60
| | | | |
DB 1 GGAAGAGAGCGCGCGGTAAGAGCGCATTTGATGAGCTGCGCGCGCTCCGAGCGCGG 60
| | | | |
QY 61 CGGAGCCAGAGCGGTGACCACTTCTTCTGCTGCTCTCTCCGCTCCAGCTCCGCGCTG 120
| | | | |
DB 61 CGGAGCCAGAGCGGTGACCACTTCTTCTGCTGCTCTCTCCGCTCCAGCTCCGCGCTG 120
| | | | |
QY 121 CCGGAGACCGGAGACCATTCGACCCCAAGGCGCGCGCTCCGCGAGCGCGCTCCGCGG 180
| | | | |
DB 121 CCGGAGACCGGAGACCATTCGACCCCAAGGCGCGCGCTCCGCGAGCGCGCTCCGCGG 180
| | | | |
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
| | | | |
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
| | | | |
QY 241 AGGAGAGCAAAAGCGGAGCTCCGCGAGAGGAGGTGTGAGCTGTATTAATGAATGT 300
| | | | |
DB 241 AGGAGAGCAAAAGCGGAGCTCCGCGAGAGGAGGTGTGAGCTGTATTAATGAATGT 300
| | | | |
QY 301 GCTTACAAAGGCGCACAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
| | | | |
DB 301 GCTTACAAAGGCGCACAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
| | | | |
QY 361 CGGATACCTGAGATCCAGGTCCGAGTGAATTAAGAGAGAGAGAGAGAGAGAGAGAG 420
| | | | |
DB 361 CGGATACCTGAGATCCAGGTCCGAGTGAATTAAGAGAGAGAGAGAGAGAGAGAGAG 420
| | | | |
QY 421 GGGAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGAGTGTTCATGAGTTCATTA 480
| | | | |
DB 421 GGGAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGAGTGTTCATGAGTTCATTA 480
| | | | |
QY 481 ATTATGCGATGATCTTTGGGAAAATTGCGAGTGTACATTTACAAAGATGCGTTCAATA 540
| | | | |
DB 481 ATTATGCGATGATCTTTGGGAAAATTGCGAGTGTACATTTACAAAGATGCGTTCAATA 540
| | | | |
QY 541 GTGCTCTAAGAGTGTGTTCAGTGTGCTCACTTCGCTAAATATGCAAGATGATGTCTC 600
| | | | |
DB 541 GTGCTCTAAGAGTGTGTTCAGTGTGCTCACTTCGCTAAATATGCAAGATGATGTCTC 600
| | | | |
QY 601 AGCGTTGGATTTTCACTTCAATGAGCTGAATGTTCAGAGACCTCTTCCCATTTGAAGCTA 660
| | | | |
DB 601 AGCGTTGGATTTTCACTTCAATGAGCTGAATGTTCAGAGACCTCTTCCCATTTGAAGCTA 660
| | | | |
QY 661 TAATTTATTTGGACCAAGAGAGCCCTGAATATGATTCACATTTAATTTATTCATGCACTT 720
| | | | |
DB 661 TAATTTATTTGGACCAAGAGAGCCCTGAATATGATTCACATTTAATTTATTCATGCACTT 720
| | | | |
QY 721 CTTCTGTGAAGAGCTTTGTGAAGAAATTGCTGTGATTTAGTGAATGTTGCTATCTGGG 780
| | | | |
DB 721 CTTCTGTGAAGAGCTTTGTGAAGAAATTGCTGTGATTTAGTGAATGTTGCTATCTGGG 780
| | | | |
QY 781 TTGGGACCTTGTTCAGATTAACCAAGAGAGATGCTCTAAGTGAATGCAATTCAGTTCTC 840
| | | | |
DB 781 TTGGGACCTTGTTCAGATTAACCAAGAGAGATGCTCTAAGTGAATGCAATTCAGTTCTC 840
| | | | |

QY	841	SCATCATATATGGAAGAACACCAAAATAATGCTTAATTTTCATTTGCTACCTCTTTT	900
Db	841	GCATATATATGGAAGAACTACCAAAATAATGCTTAATTTTCATTTGCTACCTCTTTT	900
QY	901	TTATATATGCTTGAATGTTCACTTAAATGACATTTTAAATAAGTTATATGATACATCT	960
Db	901	TTATATATGCTTGAATGTTCACTTAAATGACATTTTAAATAAGTTATATGATACATCT	960
QY	961	GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTCCACATGTTTTTAA	1020
Db	961	GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTCCACATGTTTTTAA	1020
QY	1021	ATCTAGCATATATTCATTTTGTGCTCAATCAAAAAGTGTTCAATATTTTTTTATGTGGT	1080
Db	1021	ATCTAGCATATATTCATTTTGTGCTCAATCAAAAAGTGTTCAATATTTTTTTATGTGGT	1080
QY	1081	AGAAATACCTTCTTCATATGACATATCTCTCAACCATATATTTGGAATATTTGTGTGCT	1140
Db	1081	AGAAATACCTTCTTCATATGACATATCTCTCAACCATATATTTGGAATATTTGTGTGCT	1140
QY	1141	TTTGTGTTTTCTCTTAGATAGCATTTTAAAAAAATATAAAGTACCAATCTTGTGAC	1200
Db	1141	TTTGTGTTTTCTCTTAGATAGCATTTTAAAAAAATATAAAGTACCAATCTTGTGAC	1200
QY	1201	AATTTGTAAATGTTAAGAAATTTTTTTTATATCTGTTAAATAAAATTTTCCACAA	1257
Db	1201	AATTTGTAAATGTTAAGAAATTTTTTTTATATCTGTTAAATAAAATTTTCCACAA	1257

```

RESULT 43
US-10-176-992-365
; Sequence 365, Application US/10176992
; Publication No. US20030027279A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCES: P943ORIC100
CURRENT APPLICATION NUMBER: US/10/176,992
PRIORITY FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-992-365

```

	Query Match	100.0%	Score 1257	DB 14	Length 1257
	Best Local Similarity	100.0%	Pred. No. 3,4e-271		
	Matches 1257	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	GGAGAGAGCGCGCGGTGAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGACGCGG	60		
Db	1	GGAGAGAGCGCGCGGTGAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGACGCGG	60		
QY	61	CGAAGCCAGAGAGCTGACCAAGTTCCTCTCTCGGTCTCTTCCTCGCTCGAGCTCGGCTG	120		
Db	61	CGAGCGCAGACGCTGACCAAGTTCCTCTCTCTCGGTCTCTTCCTCGCTCGAGCTCGGCTG	120		
QY	121	CCGCGCAGCGCGGAGCATGACCCCAAGGGGCCCGCGCGCTCCCGCGAGCGGCTTCGCGG	180		
Db	121	CCCGCGAGCCGGAGCCATGACCCCAAGGGGCCCGCGCGCTCCCGCGAGCGGCTTCGCGG	180		

QY	181	GGCTCTGTGTCCTCGTGTGACAGCTGCCCCGGCCGGCTCGAGGGCTCTGAGATCCCA	240
Db	181	GGCTCTGTGTCCTCTGCTGCTGCACTGCCCCGGCCGGCTCTGAGATCCCA	240
QY	241	AGGGGAAGCAAAAGCCGACGCTCGGCAAGAGGAGTGGTGACCTGTATAATGAAATGT	300
Db	241	AGGGGAAGCAAAAGCCGACGCTCGGCAAGAGGAGTGGTGACCTGTATAATGAAATGT	300
QY	301	GGTTTCAAGGGGCAACAGAGTCCCTGGTTCAGAGCGGAGCCCTGGGCAATGTTATTC	360
Db	301	GGTTTCAAGGGGCAACAGAGTCCCTGGTTCAGAGCGGAGCCCTGGGCAATGTTATTC	360
QY	361	CGGATACACCTGGGATGCCAGGTCCGAGTGAATTCAAAGAGAAAGGGAGATGTCTGA	420
Db	361	CGGATACACCTGGGATGCCAGGTCCGAGTGAATTCAAAGAGAAAGGGAGATGTCTGA	420
QY	421	GGGAAAGCTTTGAGAGATCTTGGAACCCACTACAGCAGTGTTCATGAGTTCAATGA	480
Db	421	GGGAAAGCTTTGAGAGATCTTGGAACCCACTACAGCAGTGTTCATGAGTTCAATGA	480
QY	481	ATTATGCAATGATCTTGGAAGAAATTTGGAGGTGACATTTACAAGAATGGATCAATA	540
Db	481	ATTATGCAATGATCTTGGAAGAAATTTGGAGGTGACATTTACAAGAATGGATCAATA	540
QY	541	GTGCTTAAGATTTTGTTCAGTGGCTCACTTCGGCTTAAAATGCAAAATGCATGCTGTC	600
Db	541	GTGCTTAAGATTTTGTTCAGTGGCTCACTTCGGCTTAAAATGCAAAATGCATGCTGTC	600
QY	601	AGCGTGGATTTTCAATTCATGAGGTGAATGTTCAAGACCTTCCTCCATGGAAGTA	660
Db	601	AGCGTGGATTTTCAATTCATGAGGTGAATGTTCAAGACCTTCCTCCATGGAAGTA	660
QY	661	TAAATTAATTTGAGACCAAGAAAGCCCTGAAATGAATTCACAATTAATTTATGCACTT	720
Db	661	TAAATTAATTTGAGACCAAGAAAGCCCTGAAATGAATTCACAATTAATTTATGCACTT	720
QY	721	CTTCTGTGGAAGACTTTGTGAAGAAATTTGGTCTGATTAATGAGATGTTGCTAATCTGGG	780
Db	721	CTTCTGTGGAAGACTTTGTGAAGAAATTTGGTCTGATTAATGAGATGTTGCTAATCTGGG	780
QY	781	TTGGCACTTGTTCAGATTAACCAAAAGAAATGCTTCACTGAGATGGAATTCATTTCTC	840
Db	781	TTGGCACTTGTTCAGATTAACCAAAAGAAATGCTTCACTGAGATGGAATTCATTTCTC	840
QY	841	GCATCATTAATGAAGAACTACCAAAATAAATGCTTAATTTTCAATTTGCTACTCTTTTT	900
Db	841	GCATCATTAATGAAGAACTACCAAAATAAATGCTTAATTTTCAATTTGCTACTCTTTTT	900
QY	901	TTATTAATGCGTTGGAATGCTTCACTTAATGACATTTTAAATAGTTATGATATACCT	960
Db	901	TTATTAATGCGTTGGAATGCTTCACTTAATGACATTTTAAATAGTTATGATATACCT	960
QY	961	GAAATGAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTCACTGTTTTTAA	1020
Db	961	GAAATGAAGCAAAAGCTAAATATGTTTACAGACCAAAAGTGTGATTTCACTGTTTTTAA	1020
QY	1021	ATCTAGCATTAATCAATTTTGCTCAATCAAAAGTGTTCATATATTTTTTTAGTGGTT	1080
Db	1021	ATCTAGCATTAATCAATTTTGCTCAATCAAAAGTGTTCATATATTTTTTTAGTGGTT	1080
QY	1081	AGATTAATCTTCAATGATGACATTCCTCACTTAATTAATTTGGAATATGTTGTGCT	1140
Db	1081	AGATTAATCTTCAATGATGACATTCCTCACTTAATTAATTTGGAATATGTTGTGCT	1140
QY	1141	TTTGTTTTTTCTCTTAGATAGCAATTTTAAAAAATATATAAAAGCTACCAATCTTTGTAC	1200
Db	1141	TTTGTTTTTTCTCTTAGATAGCAATTTTAAAAAATATATAAAAGCTACCAATCTTTGTAC	1200
QY	1201	AATTTGTAATGTAATAAATTTTTTTTATATCTGTTAAATATAAATATTTTCCAACTA	1257
Db	1201	AATTTGTAATGTAATAAATTTTTTTTATATCTGTTAAATATAAATATTTTCCAACTA	1257

```
RESULT 44
US-10-176-993-365
; Sequence 365, Application US/10176993
; Publication No. US20030027280A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C89
; CURRENT APPLICATION NUMBER: US/10/176,993
; PRIOR FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-993-365

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCTCGGCGCGCTCGAGCGCGG 60
DB 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCTCGGCGCGCTCGAGCGCGG 60
QY 61 CGAGGCGAAGCGCTGACGACGCTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTG 120
DB 61 CGAGGCGAAGCGCTGACGACGCTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTG 120
QY 121 CCGGCGAGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 180
DB 121 CCGGCGAGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 180
QY 181 GCCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GCCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AGGCGAAGCGAAGCGGCGAGCTCCGCGAGAGGAGGTGTGAAGCTGTATATGAAATGT 300
DB 241 AGGCGAAGCGAAGCGGCGAGCTCCGCGAGAGGAGGTGTGAAGCTGTATATGAAATGT 300
QY 301 GCTTACAAGGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 360
DB 301 GCTTACAAGGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 360
QY 361 CGGCTACCTCTGGAGTCCAGGCTCGGAGTGAATTAAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CGGCTACCTCTGGAGTCCAGGCTCGGAGTGAATTAAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAAAGCTTTGAGAGTCTCTGAGACCCAACTACAGAGCTGTTCATGAGTTCAATGA 480
DB 421 GGGAAAGCTTTGAGAGTCTCTGAGACCCAACTACAGAGCTGTTCATGAGTTCAATGA 480
QY 481 AATTAGGCAATAGATCTTTGGAGAAATGGGAGGTGATCATTTAAGAGATGCGTTCAAA 540
DB 481 AATTAGGCAATAGATCTTTGGAGAAATGGGAGGTGATCATTTAAGAGATGCGTTCAAA 540
QY 541 GTGCTCTAAGAGATTTGTTGTCAGTGTGCTCACTTCGCTAAATGACAGAAATGATGCTG 600
DB 541 GTGCTCTAAGAGATTTGTTGTCAGTGTGCTCACTTCGCTAAATGACAGAAATGATGCTG 600
```

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QY 601 AGGTTGGATTTTCAATTCATGAGAGCGAATGTTTCAGAGACCTCTCCCATTTGAAGCTA 660
DB 601 AGGTTGGATTTTCAATTCATGAGAGCGAATGTTTCAGAGACCTCTCCCATTTGAAGCTA 660
QY 661 TAATTTATTTGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TAATTTATTTGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTTCTGTGAGAGAGCTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CTTCTGTGAGAGAGCTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TTGGGACCTTTGACATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TTGGGACCTTTGACATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TTATTTATGCTTGAATGCTTCAATTAATGACATTTTAAATGATTTATGATACATCT 960
DB 901 TTATTTATGCTTGAATGCTTCAATTAATGACATTTTAAATGATTTATGATACATCT 960
QY 961 GAATGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 ACTAGCATTTATGATTTTGTCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 ACTAGCATTTATGATTTTGTCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 AGAATATCTTTCTTCAATGACATTTCTCAACCTATATTTGGAATATGTTGTGCTCT 1140
DB 1081 AGAATATCTTTCTTCAATGACATTTCTCAACCTATATTTGGAATATGTTGTGCTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATACATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 TTTGTTTTTCTCTAGTATACATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 AATTGTAAATGATTAAGATTTTATATCTGTTAATATAATTAATTTATTTCCACA 1257
DB 1201 AATTGTAAATGATTAAGATTTTATATCTGTTAATATAATTAATTTATTTCCACA 1257

RESULT 45
US-10-184-658-365
; Sequence 365, Application US/10184658
; Publication No. US20030027281A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C228
; CURRENT APPLICATION NUMBER: US/10/184,658
; PRIOR FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
```

US-10-184-658-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTGATGACGCTGCGCGCGCTCGAGAGCGCG 60
 Db 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTGATGACGCTGCGCGCGCTCGAGAGCGCG 60
 QY 61 CGGAGCGAGCGCTGACCAAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 Db 61 CGGAGCGAGCGCTGACCAAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 121 CCGGCGAGCGCGGAGCGCATGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 Db 121 CCGGCGAGCGCGGAGCGCATGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 QY 181 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 301 GCTTACAAAGGCGCGAG 360
 Db 301 GCTTACAAAGGCGCGAG 360
 QY 361 CGGAG 420
 Db 361 CGGAG 420
 QY 421 GGGAG 480
 Db 421 GGGAG 480
 QY 481 ATTATGAGATGATCTTGAG 540
 Db 481 ATTATGAGATGATCTTGAG 540
 QY 541 GTGCTCTAAG 600
 Db 541 GTGCTCTAAG 600
 QY 601 AGCGTGTATTTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660
 Db 601 AGCGTGTATTTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660
 QY 661 TAAATTTATTTGAG 720
 Db 661 TAAATTTATTTGAG 720
 QY 721 CTTCTGAG 780
 Db 721 CTTCTGAG 780
 QY 781 TTGGCAGCTTGTTCAGATTCACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 781 TTGGCAGCTTGTTCAGATTCACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 841 GCATCATTTATGAG 900
 Db 841 GCATCATTTATGAG 900
 QY 901 TTATTTAGCTTGAAG 960
 Db 901 TTATTTAGCTTGAAG 960
 QY 961 GAATGAG 1020
 Db 961 GAATGAG 1020

QY 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGAGAGAGAGAGAGAGAGAGAGAG 1080
 Db 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAAAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1081 AGAATATCTTTCTTCAATGACATTCATTCATTCATTCATTCATTCATTCATTCATTC 1140
 Db 1081 AGAATATCTTTCTTCAATGACATTCATTCATTCATTCATTCATTCATTCATTCATTC 1140
 QY 1141 TTTGTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
 Db 1141 TTTGTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
 QY 1201 AATTGTAATGTAAG 1257
 Db 1201 AATTGTAATGTAAG 1257

RESULT 46

US-10-176-991-365
 ; Sequence 365, Application US/10176991
 ; Publication No. US20030027324A1

GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Guiney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C122
 ; CURRENT APPLICATION NUMBER: US/10/176, 991
 ; PRIORITY FILING DATE: 2002-06-21
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 365
 ; LENGTH: 1257
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-176-991-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTCATTCATTCATTCATTCATTCATTCATTCATTC 60
 Db 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTCATTCATTCATTCATTCATTCATTCATTCATTC 60
 QY 61 CGGAGCGAGAGCGTGAACAGTTCTCTCTCGATCTCTCTCGATCTCTCGATCTCTCGATCT 120
 Db 61 CGGAGCGAGAGCGTGAACAGTTCTCTCTCGATCTCTCTCGATCTCTCTCGATCTCTCGATCT 120
 QY 121 CCGGCGAGCGCGGAGAGCATGCGACCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 Db 121 CCGGCGAGCGCGGAGAGCATGCGACCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 QY 181 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 181 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 301 GCTTACAGGCGCGAG 360
 Db 301 GCTTACAGGCGCGAG 360

```
Db 301 GCTTACAGGCGCCAGAGAGTCTGTCTGAGACGCGAGCCCTGGGCGCAATGTTATTC 360
Qy 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420
Db 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420
Qy 421 GGGAAAGCTTTGAGAGTCTGAGACACCACTACAGAGAGTGTTCAGAGTTCATTTGA 480
Db 421 GGGAAAGCTTTGAGAGTCTGAGACACCACTACAGAGAGTGTTCAGAGTTCATTTGA 480
Qy 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCATA 540
Db 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCATA 540
Qy 541 GTGCTCTAAGAGTGTTCAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 GTGCTCTAAGAGTGTTCAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 AGCGTGTGATTTACATTCATGAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTC 660
Db 601 AGCGTGTGATTTACATTCATGAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTC 660
Qy 661 TAAATTTATTTGACCAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 661 TAAATTTATTTGACCAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAAT 720
Qy 721 CTTCCTGTGAGAGAGCTTTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 721 CTTCCTGTGAGAGAGCTTTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Qy 781 TTGGCACTTGTGAGATTTACCAAAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 781 TTGGCACTTGTGAGATTTACCAAAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy 841 GCATCATTTATTTGAGAGAGCTTCAAAATTAATTAATTTATTTATTTATTTATTTAT 900
Db 841 GCATCATTTATTTGAGAGAGCTTCAAAATTAATTTATTTATTTATTTATTTATTTAT 900
Qy 901 TTTATTTGCTTGTGAGAGTGTTCATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Db 901 TTTATTTGCTTGTGAGAGTGTTCATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Qy 961 GAATGAAAGCAAGAGCTTAAATTAATTTATTAAGAGAGTGTTCATTAATTTATTTAT 1020
Db 961 GAATGAAAGCAAGAGCTTAAATTAATTTATTAAGAGAGTGTTCATTAATTTATTTAT 1020
Qy 1021 ATCTAGCATTTATTTATTTGCTTCAATCAAAAGTGTTCATTAATTTATTTATTTAT 1080
Db 1021 ATCTAGCATTTATTTATTTGCTTCAATCAAAAGTGTTCATTAATTTATTTATTTAT 1080
Qy 1081 AGAATACCTTCTTCATTAATTAATTTATTAATTTATTAATTTATTAATTTATTAAT 1140
Db 1081 AGAATACCTTCTTCATTAATTAATTTATTAATTTATTAATTTATTAATTTATTAAT 1140
Qy 1141 TTTGTTTTTCTCTTGTATAGATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200
Db 1141 TTTGTTTTTCTCTTGTATAGATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200
Qy 1201 AATTTGTAATGTTAAGAAATTTTATTAATTTATTAATTAATTAATTAATTTATTA 1257
Db 1201 AATTTGTAATGTTAAGAAATTTTATTAATTTATTAATTAATTAATTAATTTATTA 1257
```

RESULT 47

US-10-063-549-121
; Sequence 121, Application US/10063549
; Publication No. US20030027986A1; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary B.; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,549  
; PRIORITY FILING DATE: 2002-05-02  
; PRIORITY APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 121  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-549-121  
  
Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGAGAGGCGCGCGGCTGAAAGCGCATTTGATGAGAGCTGGGCGGCGCTCGAGGCGG 60  
Db 1 GAGAGAGGCGCGCGGCTGAAAGCGCATTTGATGAGAGCTGGGCGGCGCTCGAGGCGG 60  
Qy 61 CGAGGCGAGAGCTGACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 61 CGAGGCGAGAGCTGACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Qy 121 CCGGAGCGCGGAGAGCATGAGAGCCGAGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
Db 121 CCGGAGCGCGGAGAGCATGAGAGCCGAGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
Qy 181 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Db 181 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Qy 241 AGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGTGAGACCTGATTAATGAAATGT 300  
Db 241 AGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGTGAGACCTGATTAATGAAATGT 300  
Qy 301 GCTTACAGGCGCCAGAGAGTGTCTGTGAGACGAGAGCCCTGGGCGCAATGTTATTC 360  
Db 301 GCTTACAGGCGCCAGAGAGTGTCTGTGAGACGAGAGCCCTGGGCGCAATGTTATTC 360  
Qy 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420  
Db 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420  
Qy 421 GGGAAAGCTTTGAGAGTCTTGGAGAGAGCTTCAAGAGAGTGTTCATTAATTTATTTAT 480  
Db 421 GGGAAAGCTTTGAGAGTCTTGGAGAGAGCTTCAAGAGAGTGTTCATTAATTTATTTAT 480  
Qy 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCATA 540  
Db 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCATA 540  
Qy 541 GTGCTCTAAGAGTGTTCAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 GTGCTCTAAGAGTGTTCAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Qy 601 AGCGTGTGATTTACATTCATGAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTC 660  
Db 601 AGCGTGTGATTTACATTCATGAGAGTGTTCAGAGTGTTCAGAGTGTTCAGAGTGTTC 660  
Qy 661 TAAATTTATTTGACCAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAAT 720  
Db 661 TAAATTTATTTGACCAAGAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAAT 720  
Qy 721 CTTCCTGTGAGAGAGCTTTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
Db 721 CTTCCTGTGAGAGAGCTTTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
```


QY 781 TTGGCACTTTGTCAGATTACCCAAAAGAGATGCTTCTAATGATGAAATTCAGTTTCTC 840
DB 781 TTGGCACTTTGTCAGATTACCCAAAAGAGATGCTTCTAATGATGAAATTCAGTTTCTC 840
QY 841 GCATCATTTATGAAACCTAACCAAAATTAATGCTTTAATTTTCACTTGTCTCTCTTTT 900
DB 841 GCATCATTTATGAAACCTAACCAAAATTAATGCTTTAATTTTCACTTGTCTCTCTTTT 900
QY 901 TTATTAATGCTTTGAAATGCTTCACTTAATGACATTTTAATTAATGATTAATGATACATC 960
DB 901 TTATTAATGCTTTGAAATGCTTCACTTAATGACATTTTAATTAATGATTAATGATACATC 960
QY 961 GAATGAAAAGCAAACTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTAA 1020
DB 961 GAATGAAAAGCAAACTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTAA 1020
QY 1021 ATCTAGCAATTAATGCTTTGCTCAATGCAAAAGTGCTTCAATTTTATTTTATGTTGCT 1080
DB 1021 ATCTAGCAATTAATGCTTTGCTCAATGCAAAAGTGCTTCAATTTTATTTTATGTTGCT 1080
QY 1081 AGAATACTTTCTTCACTAGTCACTCTCAACCTTAATTTGAAATATGTTGCTCT 1140
DB 1081 AGAATACTTTCTTCACTAGTCACTCTCAACCTTAATTTGAAATATGTTGCTCT 1140
QY 1141 TTTGTTTTTCTCTTAGTATGCAATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTTCTCTTAGTATGCAATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGAAATTTTATCTGTTAAATTAATTTATTTTCAACA 1257
DB 1201 AATTTGTAATGTTAAGAAATTTTATCTGTTAAATTAATTTATTTTCAACA 1257

RESULT 48

US-10-173-695-365

; Sequence 365, Application US/10173695

; Publication No. US20030032101A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Deenoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Paul J.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C3

; CURRENT APPLICATION NUMBER: US/10/173,695

; PRIORITY FILING DATE: 2002-06-17

; PRIORITY APPLICATION REMOVED - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 365

; LENGTH: 1257

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-10-173-695-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best local Similarity 100.0%; Pred. No. 3,48-271;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCGCGGCGGGAAGGCGCATTTGATGAGCGCTGGCGGCGCTCGAGCGCGG 60
DB 1 GGAAGAGGCGCGCGGCGGGAAGGCGCATTTGATGAGCGCTGGCGGCGCTCGAGCGCGG 60
QY 61 CGAGAGCAGAGCGCTGACCAAGCTTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCAGAGCGCTGACCAAGCTTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 120

QY 121 CCCGACCGGAGAGCCATGCGACCCCGAGGCGCCCGCGCTCCCGCAGCGGCTCCGG 180
DB 121 CCCGACCGGAGAGCCATGCGACCCCGAGGCGCCCGCGCTCCCGCAGCGGCTCCGG 180
QY 181 GCTCTCTGCTCTCTGCTGAGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCA 240
DB 181 GCTCTCTGCTCTCTGCTGAGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCA 240
QY 241 AGGGAGCAAAAGCGAGCTCCGCGAGAGAGGTGCGAGCTTATTAATGGAATGT 300
DB 241 AGGGAGCAAAAGCGAGCTCCGCGAGAGAGGTGCGAGCTTATTAATGGAATGT 300
QY 301 GCTTCAAGGCGCAGAGAGTGCCTGCTGAGAGCGGAGCGCTGGGCGCAATGTTATTC 360
DB 301 GCTTCAAGGCGCAGAGAGTGCCTGCTGAGAGCGGAGCGCTGGGCGCAATGTTATTC 360
QY 361 CGGCTACCTGCGATCCAGGCTGGGATGGAATTCAGAGAAAGGGGGAATGCTGGA 420
DB 361 CGGCTACCTGCGATCCAGGCTGGGATGGAATTCAGAGAAAGGGGGAATGCTGGA 420
QY 421 GGGAAAGCTTTGAGGAGCTGGAACCCAACTACAGAGAGTTCATGAGTTCAATGA 480
DB 421 GGGAAAGCTTTGAGGAGCTGGAACCCAACTACAGAGAGTTCATGAGTTCAATGA 480
QY 481 ATTATGCAATGATCTTGGGAAAATGCGAGTGTACATTTACAAAGATCGTTCAATA 540
DB 481 ATTATGCAATGATCTTGGGAAAATGCGAGTGTACATTTACAAAGATCGTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTCTAGTGTCTGCTCACTTGGGCTTAAATGCAAGATGCTGTC 600
DB 541 GTGCTCTAAGAGTTTGTCTAGTGTCTGCTCACTTGGGCTTAAATGCAAGATGCTGTC 600
QY 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTCAGAGCGCTCCCATGGAAGCTA 660
DB 601 AGCGTTGATTTTCACTTCAATGAGAGTGAATGTCAGAGCGCTCCCATGGAAGCTA 660
QY 661 TAAATTTATTTGAGCAAGAGAGCGCTGAAATGAAATTCACAAATTAATTTATTCGCACTT 720
DB 661 TAAATTTATTTGAGCAAGAGAGCGCTGAAATGAAATTCACAAATTAATTTATTCGCACTT 720
QY 721 CTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAATGAGATGTTGCTATCTGGG 780
DB 721 CTCTGTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAATGAGATGTTGCTATCTGGG 780
QY 781 TTGGCACTTTGTCAGATTACCCAAAAGAGATGCTTCTAATGATGAAATTCAGTTTCTC 840
DB 781 TTGGCACTTTGTCAGATTACCCAAAAGAGATGCTTCTAATGATGAAATTCAGTTTCTC 840
QY 841 GCATCATTTATGAAACCTAACCAAAATTAATGCTTTAATTTTCACTTGTCTCTCTTTT 900
DB 841 GCATCATTTATGAAACCTAACCAAAATTAATGCTTTAATTTTCACTTGTCTCTCTTTT 900
QY 901 TTATTAATGCTTTGAAATGCTTCACTTAATGACATTTTAATTAATGATTAATGATACATC 960
DB 901 TTATTAATGCTTTGAAATGCTTCACTTAATGACATTTTAATTAATGATTAATGATACATC 960
QY 961 GAATGAAAAGCAAACTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTAA 1020
DB 961 GAATGAAAAGCAAACTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTAA 1020
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DB 1021 ATCTAGCAATTAATGCTTTGCTCAATGCAAAAGTGCTTCAATTTTATTTTATGTTGCT 1080
QY 1081 AGAATACTTTCTTCACTAGTCACTCTCAACCTTAATTTGAAATATGTTGCTCTCT 1140
DB 1081 AGAATACTTTCTTCACTAGTCACTCTCAACCTTAATTTGAAATATGTTGCTCTCT 1140
QY 1141 TTTGTTTTTCTCTTAGATGCAATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTTCTCTTAGATGCAATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200


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; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-705-365
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Query Match	100.0%;	Score 1257;	DB 14;	Length 1257;
Best Local Similarity	100.0%;	Pred. No. 3.4e-271;		
Matches 1257; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	GGAGAGAGGCGCGCGGGTAAAGGCCATTTGATGCAAGCTGCGCGGCGCTCGAGCGCGG	60
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QY	61	CGAGCCAGACGCTGACCAAGTTCCTCTCTCTCGAGTCTCTCGGCTTCAGACTCCGCGCTG	120
Db	61	CGAGCCAGACGCTGACCAAGTTCCTCTCTCTCGAGTCTCTCGGCTTCAGACTCCGCGCTG	120
QY	121	CCCCGACGCCCCGAGGCGCATGCCACCCCAAGGCCCCCGCGCTCCCGCAGCGGCTCCGGC	180
Db	121	CCCCGACGCCCCGAGGCGCATGCCACCCCAAGGCCCCCGCGCTCCCGCAGCGGCTCCGGC	180
QY	181	GCCTCTGTGTCCTCGTCTGCTGACAGTGCCTCGCGCGCTGAGAGGCTCTGAGATCCCA	240
Db	181	GCCTCTGTGTCCTCGTCTGCTGACAGTGCCTCGCGCGCTGAGAGGCTCTGAGATCCCA	240
QY	241	AGGGGAAGCAAAAGCGCGACGCTCCGCGAGAGGAGGTGTGACCTGTATTAATGAATGT	300
Db	241	AGGGGAAGCAAAAGCGCGACGCTCCGCGAGAGGAGGTGTGACCTGTATTAATGAATGT	300
QY	301	GCTTCAAGGGCGCAGAGAGATGSCCTGCTGAGAACGGGAGCCCTGGGGCCAAATGTAATC	360
Db	301	GCTTCAAGGGCGCAGAGAGATGSCCTGCTGAGAACGGGAGCCCTGGGGCCAAATGTAATC	360
QY	361	CGGATACACCTGSGAATCCAGGTCGCGGATGGAATTCAAAGAGAAAAGGGGGAATGTCTGA	420
Db	361	CGGATACACCTGSGAATCCAGGTCGCGGATGGAATTCAAAGAGAAAAGGGGGAATGTCTGA	420
QY	421	GGGAAGCTTTGAGAGAGTCTGTGACACCCCACTPACAGAGTGTTCATGAGATTGATGA	480
Db	421	GGGAAGCTTTGAGAGAGTCTGTGACACCCCACTPACAGAGTGTTCATGAGATTGATGA	480
QY	481	ATTATGGCATTAATCTTGGGAAAATTGCGGAGGTATCATTTACAAAAGATGCGTTCAATA	540
Db	481	ATTATGGCATTAATCTTGGGAAAATTGCGGAGGTATCATTTACAAAAGATGCGTTCAATA	540
QY	541	GTGCTCTAAGAGTTTGTTCAGTGGGCTCACTTGGGCTTAAATGAGAAATGATGCTGTGTC	600
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QY	601	AGCGTTGGTATTTCACTTCAATGAGAGCTGAATGTTGAGGACCTCTTCCCATTTGAAGCTA	660
Db	601	AGCGTTGGTATTTCACTTCAATGAGAGCTGAATGTTGAGGACCTCTTCCCATTTGAAGCTA	660
QY	661	TAAATTTATTTGAGCAAGAGAGCCCTGGAATGAATTCACAAATTAATTAATTCATGCACTT	720
Db	661	TAAATTTATTTGAGCAAGAGAGCCCTGGAATGAATTCACAAATTAATTAATTCATGCACTT	720
QY	721	CTTCTGTGAGAGACTTTGAGAAAGAAATGGTGTCTGATAAGTGAATGTTGCTATCTGGG	780
Db	721	CTTCTGTGAGAGACTTTGAGAAAGAAATGGTGTCTGATAAGTGAATGTTGCTATCTGGG	780
QY	781	TTGGCACTTGTTCAAGATTAACCAAAAGAGAGTCTTACTGATGAGATTCAGTTCTC	840
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Db	841	GCATCATTTATGAGAACTACCAAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT	900
QY	901	TTATTAATGCTTGAATGGTTCCTTAATAGACATTTAATAGTAAATAGTTATGTAATACATC	960
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Qy	961	GAATGAAGAAGCAAAATTAATGTTATACAGACCAAGTGGATTTACACTGTTTTTAA	1020
Dp	961	GAATGAAGAAGCAAAATTAATGTTATACAGACCAAGTGGATTTACACTGTTTTTAA	1020
Qy	1021	ATCTAGCATTAATTCATTTTGCTTCATCAACAAAGTGGTTCCATATATTTTTTTAGTTGCTT	1080
Dp	1021	ATCTAGCATTAATTCATTTTGCTTCATCAACAAAGTGGTTCCATATATTTTTTTAGTTGCTT	1080
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Dp	1081	AGAAATACCTTTCATATAGTACATCTCTCAACCTATAATTTGGAAATATGTTGTGCT	1140
Qy	1141	TTTGTTTTTCTCTTAAGTATGACATTTTTTAAAAAATATTAAGCTACCAATCTTTGTAC	1200
Dp	1141	TTTGTTTTTCTCTTAAGTATGACATTTTTTAAAAAATATTAAGCTACCAATCTTTGTAC	1200
Qy	1201	AATTTGTAATNGTAAAGATTTTTTTTATATATCGTTAAATTAATAATATTTCACACA	1257
Dp	1201	AATTTGTAATNGTAAAGATTTTTTTTATATATCGTTAAATTAATAATATTTCACACA	1257

Search completed: December 25, 2004, 02:12:42
Job time : 743 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 22:01:19 ; Search time 4401 Seconds

(without alignments)
10407.803 Million cell updates/sec

Title: US-10-063-734-121

Perfect score: 1257

Sequence: 1 ggaagagagcgcgcgcggtga.....aataaaattattccacaa 1257

Scoring table: IDENTITY NUC

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 100 summaries

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252.2	99.6	1288	3	BC021025 Homo sapi
2	1202.2	95.6	1207	3	CR605392 full-length
3	1184.2	94.2	1189	3	CR596030
4	1106.2	88.0	1111	3	CR612318 full-length
5	1098.2	87.4	1103	3	CR594803 full-length
6	999	79.5	1098	1	AL532456
7	951.6	75.7	1102	1	AL575307
8	941	74.9	1064	1	AL564395
9	914.2	72.7	1100	1	AL551834
10	861.6	68.5	986	5	BM560093
11	842.2	67.0	1073	5	BM560093
12	842.2	67.0	1132	4	BM560093
13	815.2	64.9	903	4	BM560093
14	811.2	64.5	827	1	AL544722
15	739.4	58.8	851	1	BM560093
16	727.2	57.9	922	9	BM560093
17	716.4	56.8	922	9	BM560093
18	714.4	56.1	1037	4	BM560093
19	705.2	56.1	1037	4	BM560093
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21	700.4	55.7	747	6	BM560093
22	695.6	55.3	796	5	BM560093
23	693.2	55.1	734	5	BM560093
24	691	55.0	723	6	BM560093

25	690	54.9	724	5	BM009009
26	685.8	54.6	700	6	BM009009
27	682.2	54.3	716	7	BM009009
28	682	54.3	702	5	BM009009
29	681.4	54.2	683	2	BM009009
30	681.4	54.2	683	2	BM009009
31	679.8	54.1	836	1	BM009009
32	679.6	54.1	709	1	BM009009
33	679	54.0	730	5	BM009009
34	678.2	54.0	1099	4	BM009009
35	678.2	54.0	986	5	BM009009
36	672.4	53.5	707	5	BM009009
37	672.2	53.5	902	5	BM009009
38	658.2	52.4	1161	3	BM009009
39	655.4	52.1	723	5	BM009009
40	651.6	51.8	1168	3	BM009009
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44	636.4	50.6	670	5	BM009009
45	633.8	50.4	654	5	BM009009
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50	581.4	46.3	610	5	BM009009
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53	569.6	45.3	617	5	BM009009
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57	561.4	44.7	567	6	BM009009
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63	523.4	41.6	583	2	BM009009
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85	456.8	36.3	644	7	BM009009
86	453	36.0	453	2	BM009009
87	450.6	35.8	590	6	BM009009
88	448	35.6	455	2	BM009009
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90	445.4	35.4	476	1	BM009009
91	444	35.3	472	1	BM009009
92	439.4	35.0	473	2	BM009009
93	436	34.7	1159	5	BM009009
94	435.6	34.6	454	1	BM009009
95	434	34.5	435	2	BM009009
96	434	34.5	448	1	BM009009
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C 99	431	34.3	436	1	A1380885	A1380885
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						DG11-96p2

ALIGNMENTS

RESULT 1	BC021025	1288 bp	mRNA	linear	HTC 04-AUG-2004
LOCUS	BC021025				
DEFINITION	Homo sapiens collagen triple helix repeat containing 1, mRNA (CDNA clone IMAGE:3517332).				
ACCESSION	BC021025				
VERSION	BC021025.1	GI:18045042			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 1288)				
AUTHORS	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,				

TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16839-16903 (2002)
PIRMEID	12477932

JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)
PUBMED	12477932				
REFERENCE	2	(bases 1 to 1288)			
AUTHORS	Director MGC Project.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-JAN-2002)	National Institutes of Health, Mammalian			

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	Contact: MGC help desk

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 24 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1992398
This clone has the following problem: no cloning site / microdeletion.

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FEATURES      Location/Qualifiers
source        1. .1288
              /organism="Homo sapiens"
              /mol_type="mRNA"
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ORIGIN

Query Match	99.6%;	Score 1253.2;	DB 3;	Length 1288;
Best Local Similarity	99.8%;	Pred. No. 4,4e-258;		
Matches 1254;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

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[illegible]

[illegible]

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Db	121	CCGCGAGGCGCTCCGGGCTCTCTGCTGCTCTCTGCTGAGCTGCCGCGCTCGAGC	180
Qy	225	GCCCTGAGATCCCGAAGGGGAAGCAAAAGCCGAGTCCGGCAGAGGAGTGTGTGAC	284
Db	181	GCCCTGAGATCCCGAAGGGGAAGCAAAAGCCGAGTCCGGCAGAGGAGTGTGTGAC	240
Qy	285	CTGATATATGGAATGTGCTTACAAAGGCGACAGAGAGTGCCTGGTCCAGACGGAGCCCT	344
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Qy	345	GGGGCCAAATGTTATTCGGGTTACACTTGGGATCCGAGTCCGGATTCGAAAGGAA	404
Db	301	GGGGCCAAATGTTATTCGGGTTACACTTGGGATTCGAAAGGAA	360
Qy	405	AAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTCTCTGACACCCACTACAGAGTGT	464
Db	361	AAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTCTCTGACACCCACTACAGAGTGT	420
Qy	465	TCATGGAATCAATGAATTAATGCAATGATCTTGGGAAATTTGGGAGTGTACATTTACA	524
Db	421	TCATGGAATCAATGAATTAATGCAATGATCTTGGGAAATTTGGGAGTGTACATTTACA	480
Qy	525	AAGATGGCTCAAAATAGTGTCTTAAGAGTTTGTTCAGTGGCTACTTCGGCTAAAATGC	584
Db	481	AAGATGGCTCAAAATAGTGTCTTAAGAGTTTGTTCAGTGGCTACTTCGGCTAAAATGC	540
Qy	585	AGAAATGATGCTGTACAGCTTGGTATTTCAATTCAATGAGCTGAATGTTCCAGAGCT	644
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Qy	645	CTTCCCAATGAAGCTAATATTTAATTTGGACCAAGAGAGCCCTGAATGAATTCACAACTT	704
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Qy	825	TGGAATTCAGTTTCTCGCATTCATTAATGGAAGACTACCAAAATTAAGCTTTAATTTTCA	884
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Qy	1005	TTTCACTGTTTTTAAATCTAGCATTAATCTATTGCTTCAATGAAAAGTGTTCATA	1064
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Qy	1065	TTTTTTTTAGTGTGTAATACCTTCTCTAGTACATTTCTGTCAACCTAATTTTGG	1124
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Db	1081	AATATGTGTGTGCTTTTGTTTTCTCTAGTATGACATTTTAAAAAAATATTAAG	1140
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Db 1141 CTACCAATCTTGTGCAATTTGTAAATGTTAAAGATTTTTTATATCTGTAAATMAA 1200
QY 1245 ATTATTT 1251
Db 1201 ATTATTT 1207

RESULT 3
CR596030
LOCUS full-length cDNA clone CS0D1061YA20 of Placenta Cot 25-normalized
DEFINITION 1189 bp mRNA linear HTC 21-JUL-2004
ACCESSION CR596030
VERSION CR596030.1 GI:50476837
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1189)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1189)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen
FEATURES
source Location/Qualifiers
1..1189
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1061YA20"
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ORIGIN
Query Match 94.2% Score 1184.2; DB 3; Length 1189;
Best Local Similarity 99.7% Pred. No. 1.7e-243;
Matches 1186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 105 CTCAGCTCCGCGCTCCCGGCGAGCGGAGCCATCGACCCCGAGGCGCCGCGCTTC 164
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Db 301 GGGGCCAATGCGATTCGGGTACACTGTGAGATCCAGGTCGGAGTGAATCAAGAGAA 360
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QY 465 TCATGAGTTCATGAAATTAATGATAGATCTTGGGAAATTTGGGAGTGTACATTTACA 524
Db 421 TCATGAGTTCATGAAATTAATGATAGATCTTGGGAAATTTGGGAGTGTACATTTACA 480
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Db 481 AAGATGCTTCAATATGATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGC 540
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Db 661 AATATTCATGCCACTTCTCTGTCGAGAGACTTTGAGAGAAATGGTGTGATTAATG 720
QY 765 GATGTGCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAGAGTCTTACTGGA 824
Db 721 GATGTGCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAGAGTCTTACTGGA 780
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Db 781 TGAATTCAGTTTCTGCACTATTTATTTGAGAACTACCAAAATTAATGCTTTAATTTGA 840
QY 885 TTTCCTACCTCTTTTATTTATTTAGCCCTGGAATGCTTCAATTAAGACATTTAATA 944
Db 841 TTTCCTACCTCTTTTATTTATTTAGCCCTGGAATGCTTCAATTAAGACATTTAATA 900
QY 945 GTTATGTATATCATCTGATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTAT 1004
Db 901 GTTATGTATATCATCTGATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTAT 960
QY 1005 TTACACTGTTTAAATTTAGCATTAATTTGCTTCAATCAAAAGTGTTCATATA 1064
Db 961 TTACACTGTTTAAATTTAGCATTAATTTGCTTCAATCAAAAGTGTTCATATA 1020
QY 1065 TTTTATTTAGTGTGAAATTAATCTTCTTCAATGTCATATCTCAACTATTAATTTGG 1124
Db 1021 TTTTATTTAGTGTGAAATTAATCTTCTTCAATGTCATATCTCAACTATTAATTTGG 1080
QY 1125 AATATGTGTGCTTTTGTGTTTCTCTTATATAGCAATTTTAAATAATATPAAAG 1184
Db 1081 AATATGTGTGCTTTTGTGTTTCTCTTATATAGCAATTTTAAATAATATPAAAG 1140
QY 1185 CTACCAATCTTTGTACAAATTTGTAATGTTAAGAAATTTTAAATCT 1233
Db 1141 CTACCAATCTTTGTACAAATTTGTAATGTTAAGAAATTTTAAATCT 1189

RESULT 4
CR612318
LOCUS 1111 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D014YN20 of Fetal liver of Homo sapiens
(human).
ACCESSION CR612318
VERSION CR612318.1 GI:50493125
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1111)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1111)

REFERENCE
AUTHORS Genoscope.
TITLE Direct Submision
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DM014YN20"
/issue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 88.0%; Score 1106.2; DB 3; Length 1111;
Best Local Similarity 99.7%; Pred. No. 9.5e-227;
Matches 1108; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

140 GGCACCCCAAGGCGCGCGCGCTCCCGAGCGCGCTCCGCGCGCTCTGCTGCT 199
1 GGCACCCCAAGGCGCGCGCGCTCCCGAGCGCGCTCCGCGCGCTCTGCTGCT 60

200 GCTGACGCTGCCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGCGCA 259
61 GCTGACGCTGCCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGCGCA 120

260 GCTCCGCGAGAGGAGAGTGTGTGACCTGTATATGAAATGCTTCAAGGGCGACAG 319
121 GCTCCGCGAGAGGAGAGTGTGTGACCTGTATATGAAATGCTTCAAGGGCGACAG 180

320 AGTGCTGTGCGAGAGGAGCGCTGGGCGCAATGTTATCCGGGTACACCTGGATCCC 379
181 AGTGCTGTGCGAGAGGAGCGCTGGGCGCAATGCGGTACACCTGGATCCC 240

380 AGGTGCGGATGATTCAGAGGAGAAAGGGGGAATGTCTGAGGGAAGCTTTGAGGAGTC 439
241 AGGTGCGGATGATTCAGAGGAGAAAGGGGGAATGTCTGAGGGAAGCTTTGAGGAGTC 300

440 CTGGACACCCACTACAGAGAGTGTTCATGAGATTCATGAATTATGCGATAGATCTTGG 499
301 CTGGACACCCACTACAGAGAGTGTTCATGAGATTCATGAATTATGCGATAGATCTTGG 360

500 GAAATTTGGCGAGTGTACATTTACAAAGATGCGTCAATAGCTCTAAGATTTGTT 559
361 GAAATTTGGCGAGTGTACATTTACAAAGATGCGTCAATAGCTCTAAGATTTGTT 420

560 CAGTGTCTCACTTCGGCTAAATATGCAAGAAATGATGCTGTGATTTTCAATT 619
421 CAGTGTCTCACTTCGGCTAAATATGCAAGAAATGATGCTGTGATTTTCAATT 480

620 CATGAGAGTGTATGTTTCAGAGACTCTTCCCATTTGAAGCTATATTTATTTGACCAAG 679
481 CATGAGAGTGTATGTTTCAGAGACTCTTCCCATTTGAAGCTATATTTATTTGACCAAG 540

680 AACCCCTGAAATGAATTCACCAATTAATATTCAGCACTTCTCTGGAAGGACTTGG 739
541 AACCCCTGAAATGAATTCACCAATTAATATTCAGCACTTCTCTGGAAGGACTTGG 600

740 TGAAGGAATTTGCTGTGATTTAGTGTATCTGTGATCTGGGTTGCACTTTGTCAGATTA 799
601 TGAAGGAATTTGCTGTGATTTAGTGTATCTGTGATCTGGGTTGTCAGATTA 660

800 CCCAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTGCGATCATTTATGAAGACT 859
661 CCCAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTGCGATCATTTATGAAGACT 720

860 ACCAAATTAATGCTTAAATTTTCAATTTGCTACTCTTTTATTAATGCTTGAATG 919
721 ACCAAATTAATGCTTAAATTTTCAATTTGCTACTCTTTTATTAATGCTTGAATG 780

920 TTCACCTTAATGACATTTTAAATTAAGTTTAACTATACATCGAAGAAAGCAAGCTTA 979
781 TTCACCTTAATGACATTTTAAATTAAGTTTAACTATACATCGAAGAAAGCAAGCTTA 840

980 ATATGTTTACAGACCAAGATGATTTCACTGTTTTTAAATCTAGCATTTATTCATTT 1039
841 ATATGTTTACAGACCAAGATGATTTCACTGTTTTTAAATCTAGCATTTATTCATTT 900

1040 GCTTCATCAAAAAGTGTTCAAATTTTATTTAGTTGTTAGAAATCTTCTCATAGT 1099
901 GCTTCATCAAAAAGTGTTCAAATTTTATTTAGTTGTTAGAAATCTTCTCATAGT 960

1100 CACATTTCTCAACCTATATATTTGGAATATTTGTGTGCTTTTGTCTTCTTACATA 1159
961 CACATTTCTCAACCTATATATTTGGAATATTTGTGTGCTTTTGTCTTCTTACATA 1020

1160 TAGCATTTTAAATAATTAAGCTACCAATCTTTGACAAATTTGTAATGTTAAGAA 1219
1021 TAGCATTTTAAATAATTAAGCTACCAATCTTTGACAAATTTGTAATGTTAAGAA 1080

1220 TTTTATATCTGTATTAATTAATTAATTT 1250
1081 TTTTATATCTGTATTAATTAATTAATTT 1111

RESULT 5
CR594803 1103 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DI022YF04 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR594803
VERSION CR594803.1 GI:50475610
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1103)

REFERENCE
AUTHORS Genoscope.
TITLE Direct Submision
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI022YF04"
/issue_type="Placenta Cot 25-normalized"
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ORIGIN

Query Match	87.4%	Score 1098.2	DB 3	Length 1103
Best Local Similarity	99.7%	Pred. No. 5e-225		
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DB	1	GAGCTGACCACTTCTCTCTCTGCTCTCTCTGCTCTCTGCTCCAGCTCCGCGTGC	CCGCGAC	60
QY	129	CCGGAGGCGCATGAGACCCCAAGGGGCCCCCGGCTTCCCCGAGCGGCTCTCTG	188	
DB	61	CCGGAGGCGCATGAGACCCCAAGGGGCCCCCGGCTTCCCCGAGCGGCTCTCTG	120	
QY	189	CTGCTCTCTGCTGCTGAGCTGCTCCGCGCTGAGCGCTCTGAGATCCCCAAGGGAG	248	
DB	121	CTGCTCTCTGCTGCTGAGCTGCTCCGCGCTGAGCGCTCTGAGATCCCCAAGGGAG	180	
QY	249	CAAAAGCGCAGCTCCGCGCAGAGGAGTGTGACCTGTATAAGATGTCTTACA	308	
DB	181	CAAAAGCGCAGCTCCGCGCAGAGGAGTGTGACCTGTATAAGATGTCTTACA	240	
QY	309	GGGCGCAGAGAGTGCCTGGTGCAGACGGGAGCCCTGGGGCCAAATGTATTCGGGTAC	368	
DB	241	GGGCGCAGAGAGTGCCTGGTGCAGACGGGAGCCCTGGGGCCAAATGTATTCGGGTAC	300	
QY	369	CCTGGGATCCAGAGTCGGGATGGAATTCAAAGAGAAAGGGGAGATGCTGAGGAGAGC	428	
DB	301	CCTGGGATCCAGAGTCGGGATGGAATTCAAAGAGAAAGGGGAGATGCTGAGGAGAGC	360	
QY	429	TTTGAGAGTCCCTGAGCACCCCACTACAGACTGTTCATGAGTTCATTGAATTGGC	488	
DB	361	TTTGAGAGTCCCTGAGCACCCCACTACAGACTGTTCATGAGTTCATTGAATTGGC	420	
QY	489	ATAGATCTTGAGAGAAATTCGGAGTGTACATTACAAAGATGGCTCAATAGTGTCTA	548	
DB	421	ATAGATCTTGAGAGAAATTCGGAGTGTACATTACAAAGATGGCTCAATAGTGTCTA	480	
QY	549	AGAGTTTGTTCAGTGGCTCACTTGGCTTAAATGCAAGATGCATGCTGCGCGTGG	608	
DB	481	AGAGTTTGTTCAGTGGCTCACTTGGCTTAAATGCAAGATGCATGCTGCGCGTGG	540	
QY	609	TATTCACATTCAGTGAAGTGTTCAGACCTCTTCCATTCAGTAAAGTAAATTTAT	668	
DB	541	TATTCACATTCAGTGAAGTGTTCAGACCTCTTCCATTCAGTAAAGTAAATTTAT	600	
QY	669	TTGACCAAGAGAGCCCTGAATGAATTCACAATTAATATTCATGCACTTCTCTGTG	728	
DB	601	TTGACCAAGAGAGCCCTGAATGAATTCACAATTAATATTCATGCACTTCTCTGTG	660	
QY	729	GAAAGCTTTGGAAGGAATTCGTGTGATTAAGTGAATGTGTCTATCTGGGTGGCACT	788	
DB	661	GAAAGCTTTGGAAGGAATTCGTGTGATTAAGTGAATGTGTCTATCTGGGTGGCACT	720	
QY	789	TGTTGAGATTACCAAAAGAGATGTTCTACTGATGAGAAATTCAGTTCCTGCACTAT	848	
DB	721	TGTTGAGATTACCAAAAGAGATGTTCTACTGATGAGAAATTCAGTTCCTGCACTAT	780	
QY	849	ATTGAAGACTACCAAAATTAATTCCTTAATTTCTATTTGCTACTCTTTTATTAATG	908	
DB	781	ATTGAAGACTACCAAAATTAATTCCTTAATTTCTATTTGCTACTCTTTTATTAATG	840	
QY	909	CTTGGAATGTCTCACTTAATGACATTTTAATAAGTTATGATATCATCTGGAATGAA	968	
DB	841	CTTGGAATGTCTCACTTAATGACATTTTAATAAGTTATGATATCATCTGGAATGAA	900	
QY	969	AGCAAGCTAAATATGTTTACAGCCAAAGTGATTCACACTGTTTTAATCTAGAG	1028	
DB	901	AGCAAGCTAAATATGTTTACAGCCAAAGTGATTCACACTGTTTTAATCTAGAG	960	
QY	1029	TTATTCATTTGCTCAATCAAAAGTGTTTCAATTTTTTTTATGTTGGTTAGTAATCT	1088	
DB	961	TTATTCATTTGCTCAATCAAAAGTGTTTCAATTTTTTTTATGTTGGTTAGTAATCT	1020	

QY	DB	QY	DB	RESULT 6	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT			
1089	1081	1149	1081	AL532456	AL532456	1098 bp mRNA 11near EST 24-MAR-2004	AL532456	CS00M014YMN20 5-prime, mRNA sequence.	AL532456	AL532456.3 GI:45707373	EST	Human sapiens (human)	Human sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1098)	Li, W.B., Gruber, C., Jesses, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	On Feb 13, 2001 this sequence version replaced gi:31070288.

Contact: genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segefre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 4941.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CSDMD014D310QPI&c=4941.f>.
 Location/Qualifiers
 1..1098
 source

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/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

Query Match	79.5%;	Score 999;	DB 1;	Length 1098;
Best Local Similarity	96.2%;	Pred. No. 9,9e-204;		
Matches 1059;	Conservative 15;	Mismatches 20;	Indels 7;	Gaps 5;

[illegible]

Qy	380	AGGTCGGGATGGAATTTCAAGAGAAAGAGGGGAAATGTCGAGGAAACCTTTGAGAGTC	433
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Qy	440	CTGGACACCCAACTACAGACAGTGTTCATGGAGTCAATTGAATATAGGCATAGACTTTGG	499
Db	300	CTGGACACCCAACTACAGACAGTGTTCATGGAGTCAATTGAATATAGGCATAGACTTTGG	359
Qy	500	GAAATATGCGGAGTGTACATTTACAMAGTSCGTTCAATATAGTGTCTAGAGTTCGTT	559
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Qy	560	CAGTGGCTCACTTGGGCTAAAATGCAAAATGCATCTGTCAAGCTTGGATTTCACTT	619
Db	420	CAGTGGCTCACTTGGGCTAAAATGCAAAATGCATCTGTCAAGCTTGGATTTCACTT	479
Qy	620	CAATGGAGCTGAATGTTGAGGACCTCTCCCATTTGAAAGCTATATTTATTTGAGCAAG	679
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Qy	680	AAGCCCTGAAATGAAATCAACAATTAATATTCATGCACTTCTCTGGAAGACTTTG	739
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Qy	740	TGAAGGAATGTCGTGTGATAGTGAGATGTTCTATCTGGGTTGGCACTTGTTCAGATTA	799
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Qy	800	CCCCAAAAGGAATGCTTCTACTGATGGAATTCAGTTCTGGCATCATTTATGGAAGACT	859
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Qy	860	ACCAAAATPAAATGCTTAAATTTTCAATTTGCTACCCCTTTTTTATATAGCCCTGGAAAG	919
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Qy	980	ATATGTTTACGACCAAGTGTGATTTCACTGTTTTTTAAATCTAGCATTAATCATTTT	1039
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Qy	1040	GCTTCAATCAAAAGTGTTCAAATTTTATTTTATAGTGTAGATACCTTCTTCATAGT	1099
Db	900	GCTTCAATCAAAAGTGTTCAAATTTTATTTTATAGTGTGTGWRGACCTTCTTCATAGT	959
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Db	960	CACATTCCTCAACCTATATATTTGGAAATATGTTGTGCTTTGTTTCTCTTAGTA	1016
Qy	1160	TAGCATTTTAAAAAATATATAAGCTAACCAATCTTGTAGCAATTTGTAAATGTTAAGAA	1219
Db	1017	TAGCATTTTAAAAAATATATAAGC-WCAATCTTTKACA--TTTGAATGTTAAGAT	1072
Qy	1220	TTTTTTTTATATCTGTAAAT	1240
Db	1074	TTTTTTTTTTTTTAAAAAAT	1094

RESULT 7	1102 bp	mRNA	EST 06-APR-2000
AL575307/c			
LOCUS	AL575307		linear
DEFINITION	AL575307 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS01061YA20.3-PRIME, mRNA sequence.		
ACCESSION	AL575307		
VERSION	AL575307.3	GI:46248266	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;		

REFERENCE	1 (bases 1 to 1102)
AUTHORS	Li, W. B., Gruber, C., Jeese, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On Feb 16, 2001 this sequence version replaced gi:31313615 .

BP 191 91006 EVRY cedex - France
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
end enriched, double-stranded cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/s=CS01D01B1A10NP1&c=4941.f>.

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (drr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	Similarity	75.7%:	Score	95.1.6:	DB	1:	Length	1102:
Best Local	Similarity	95.7%:	Pred.	No.1.5e-193:				
Matches	992:	Conservative	4:	Mismatches	38:	Indels	3:	Gaps
QY	199	TGCTGCAAGCTCCCGCGCCGTGAGCGCTTCGATGATCCCGAAGGGAGCAAAAGCGC	258					
Db	1036	TTCTGTYTSTGCASTGCCCGGCGCTTTCGAGCTTCCCAAGGGAGCAAAAGCGC	977					
QY	259	AGCTTCGGCAGAGGAGGTGTGACCTGTATTAATGCAATGCTCTACAGGGCCAGAG	318					
Db	976	AGCTTCGGCAGAGGAGGTGTGT-CACCTGTATTAATGCAATGCTCTACAGGGCCAGAG	918					
QY	319	GAGTGCCCTGTCGAGAGCGGGAGCCCTGGGGCCAAATGTTATTCGGGGTACACTGGGATCC	378					
Db	917	GAGTGCCCTGTCGAGAGCGGGAGCCCTGGGGCCAAATGGCATTCGGGGTACACTGGGATCC	858					
QY	379	CAGGTCCGGATGATATTCAAAGAGAAAAAGGGGATGTCTGAGGGAAAGCTTTGAGAGGT	438					
Db	857	CAGGTCCGGATGATATTCAAAGAGAAAAAGGGGATGTCTGAGGGAAAGCTTTGAGAGGT	798					
QY	439	CCTGGACACCCAACTACAGCAGTGTTCATGAGTTCATTGCAATTAATGCAATAGATCTTG	498					
Db	797	CCTGGACACCCAACTACAGCAGTGTTCATGAGTTCATTGCAATTAATGCAATAGATCTTG	738					
QY	499	GGAAATTTGGCGAGGTGATCTTTCAAAGATGCGTTCAAATAGTCTTAAGATTTTGT	558					
Db	737	GGAAATTTGGCGAGGTGATCTTTCAAAGATGCGTTCAAATAGTCTTCGAAAGATTTTGT	678					
QY	559	TCAGTGGCTCACTTCGCTTAATAATGCAAAATGCAATGCTGTCAAGCGTGTGATTTTCACAT	618					
Db	677	TCAGTGGCTCACTTCGCTTAATAATGCAAAATGCAATGCTGTCAAGCGTGTGATTTTCACAT	618					
QY	619	TCATATGAGCTGAATGTTCAAGACTCTTCCCATTTGAAGCTATATATTTATTTGACCAAG	678					
Db	617	TCATATGAGCTGAATGTTCAAGACTCTTCCCATTTGAAGCTATATATTTATTTGACCAAG	558					
QY	679	GAAGCCCTGGAATAAATTCACACATTTAATTCATTCGACTCTCTGCTGGAGGAATCTT	738					
Db	557	GAAGCCCTGGAATAAATTCACACATTTAATTCATTCGACTCTCTCTGGAAGGAATCTT	498					
QY	739	GTTGAGGAAATGTGTCTGATTAATGATGATGTGCTATCTGGATTGGACATTTGTCAGATT	798					

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799 ACCCAAGAGAGATGCTTCTACGTGAGTGAATTCAGTTCTCCGATCATTTGAAGAAC 858
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437 ACCCAAGAGAGATGCTTCTACGTGAGTGAATTCAGTTCTCCGATCATTTGAAGAAC 378
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859 TACCAAAATAAATGCTTAAATTTTCACTTGTGCTACTCTTTTATTAATGCTTGAATG 918
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317 GTTCACTTAATGACATTTTAAATAGTTATGATATACATCTGAATGAAAGCAAGCTA 258
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1039 TGCCTCAATCAAAAGTGTTCATATTTTATTTAGTTGATGAATACCTTCTTCATAG 1098
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QY 1217 GAATTTTATTTATCT 1233
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Db 17 AATTTTATTTATCT 1
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RESULT 8
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LOCUS AL564395 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM014YN20 3-PRIME, mRNA sequence.
ACCESSION AL564395
VERSION AL564395.3 GI:46231315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1064)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31288373.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0DM014DGLONPL&c=4941.f.
FEATURES
source
1..1064
location/Qualifiers
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/db_xref="caon:9606"
/clone="CS0DM014YN20"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"

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/clone_11b="Homo sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dt) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN
Query Match 74.9%; Score 941; DB 1; Length 1064;
Best Local Similarity 95.6%; Pred. No. 2,8e-191;
Matches 1022; Conservative 8; Mismatches 33; Indels 6; Gaps 6;
153 CCGCGCGCTCCCGCAGCGGCTCGCGGCTCTGCGTCTCGTGCAGCTGCC 212
|||
1064 CCCAGGCCCCCSCGCCCCGACGGGCGGCGCTCTGCTCTTGTGCTCTTGTGACGCT-CCC 1006
|||
QY 213 GCGCGGTGAGCGCCTGAGATCCCAAGGGGAGCAAAAGCGCAGCTCCGCGAGAG 272
|||
Db 1005 GCGCGGTGAGCS-CTTTGAGATCCCA-CCGAGCAAAAGCGCAGCTCCGCGAGAG 948
|||
QY 273 GAGGTGTTGACCTGTATTAATGGAATGCTTTACAAGGCGCAGAGAGTGCCTGTGCA 332
|||
Db 947 GAGGT-GTGACCTGTATTAATGGAATGCTTTACAAGGCGCAGAGAGTGCCTGTGCA 889
|||
QY 333 GACGGGAGCCCTGGGGCCCAATGTTATTCGGGGTACACTGAGATCCCAAGGTGGGATGGA 392
|||
Db 888 GACGGGAGCCCTGGGGCCCAATGTTATTCGGGGTACACTGAGATCCCAAGGTGGGATGGA 829
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QY 393 TTCAAGGAGAAAGGGGGAAATGCTGTAGGAAAGCTTTGAGAGTCTGTGACACCCAAAC 452
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Db 828 TTCAAGGAGAAAGGGGGAAATGCTGTAGGAAAGCTTTGAGAGTCTGTGACACCCAAAC 769
|||
QY 453 TACAAGGAGTGTATGAGGTTCATGAATTAATGAGCAATACTTGGGAAATTTGGGAG 512
|||
Db 768 TACAAGGAGTGTATGAGGTTCATGAATTAATGAGCAATACTTGGGAAATTTGGGAG 709
|||
QY 513 TGTACATTTTACAAGAGTCCGTTCAATATAGTCTCTAGAGTTTGTTCAGTGCCTCACTT 572
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Db 708 TGTACATTTTACAAGAGTCCGTTCAATATAGTCTCTAGAGTTTGTTCAGTGCCTCACTT 649
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QY 573 CG-GCTAAATGCAAAATGCAATGCTGTCAAGCTGTGATTTTCAATTCATGAGCTGA 631
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Db 648 CGGCTAAATGCAAAATGCAATGCTGTCAAGCTGTGATTTTCAATTCATGAGCTGA 589
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QY 632 ATGTTCAAGGAGCTTCCCAATGAAGCTATTAATTTATGAGCAAGAGCCCTGAAAT 691
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Db 588 ATGTTCAAGGAGCTTCCCAATGAAGCTATTAATTTATGAGCAAGAGCCCTGAAAT 529
|||
QY 692 GAATTCACAATTAATATTCATGCACTTCTCTGTGAGAGCACTTGTGAGGAATGG 751
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Db 528 GAATTCACAATTAATATTCATGCACTTCTCTGTGAGAGCACTTGTGAGGAATGG 469
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QY 752 TGTGTGATTAATGAGATGTTGCTATCTGGGTGCACTTGTTCAGATTTCCCAAGAGAGA 811
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Db 468 TGTGTGATTAATGAGATGTTGCTATCTGGGTGCACTTGTTCAGATTTCCCAAGAGAGA 409
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QY 812 TGTCTTACAGTGAATGAATCAGTTCTGCGATCATTTAATGAAGCAATCCAAATAAT 871
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Db 408 TGTCTTACAGTGAATGAATCAGTTCTGCGATCATTTAATGAAGCAATCCAAATAAT 349
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QY 872 GCTTAAATTTTCACTTGTCTCTTTTATTAATGCTTGAATGTTCTCACTTAATG 931
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Db 348 GCTTAAATTTTCACTTGTCTCTCTTTTATTAATGCTTGAATGTTCTCACTTAATG 289
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QY 932 ACATTTTAAATTAATTTATGATATACATCTGAATGAAAGCAAGTAAATATGTTTACAG 991
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Db 288 ACATTTTAAATTAATGTTATGATATACATCTGAATGAAAGCAAGTAAATATGTTTACAG 229
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QY 992 ACCAAAGTGTGATTTCACTGTTTAAATCTAGATTAATTCATTTGCTTCATTCAAA 1051
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Db 228 ACCAAAGTGTGATTTCACTGTTTAAATCTAGATTAATTCATTTGCTTCATTCAAA 169
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QY 1052 AGTGGTTCAATATTTTATTTTATGTTGTTAGATTAAGTATCTTCAATGACATTCCTCA 1111
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|||||
Db 168 AGGTGTTCAATATTTTATTTAGTTAGTACATCTTCTCAATGTCACATTCCTCA 109
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Qy 1112 ACCTTAATTTGGATATTTGTTGTTGTTCTTTGTTCTTCTAGTATAGCATTTTAA 1171
Db 108 ACCCTAATTTGGATATTTGTTGTTGTTCTTTGTTCTTCTAGTATAGCATTTTAA 49
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Qy 1172 AAAATATATAAGCTACCAATCTTTGTACAAATTTGTAATTTAAGAT 1220
Db 48 AAAATATATAAGCTACCAATCTTTGTACAA-TWGTAAAGTTAAGAT 1
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RESULT 9
AL551834 1100 bp mRNA linear EST 30-MAR-2004
LOCUS AL551834 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CS0D1061YA20 5-PRIME, mRNA sequence.
ACCESSION AL551834
VERSION AL551834.3 GI:45856624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1100)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31273650.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1061YA20&c=4941.f.
FEATURES
source
1. 1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1061YA20"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 72.7%; Score 914.2; DB 1; Length 1100;
Best Local Similarity 94.8%; Pred. No. 1,6e-185;
Matches 983; Conservative 5; Mismatches 40; Indels 9; Gaps 4;
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Qy 45 CGGCTCGGAGCGCGGAGCGAGACGATGACCAAGTCTCTCTCGGTCCTCCGC 104
Db 1 CGGATCGAGCGCGCGGAGCGAGACGATGACCAAGTCTCTCTCGGTCCTCCGC 60
|||
Qy 105 CTCACAGCTCCGCGCTCCCGGAGCGCGGAGCGAGCCGAGCCGAGCGCGCTCC 164
Db 61 CTCACAGCTCCGCGCTCCCGGAGCGCGGAGCGAGCCGAGCCGAGCGCGCTCC 120
|||
Qy 165 CGCAGCGGCTCCGCGCTCCCGGAGCGCGGAGCGAGCCGAGCCGAGCGCGCTCC 224
Db 121 CGCAGCGGCTCCGCGCTCCCGGAGCGCGGAGCGAGCCGAGCCGAGCGCGCTCC 180
Qy 225 GCCTTGAGATCCCAAGGGAAGCAAAAGCGCAGCTCCGAGAGGAGGTGTGAC 284
|||

Db 181 GCCTTGAGATCCCAAGGGAAGCAAAAGCGCA-CTCCGAGAGGAGGTGTGAC 239
Qy 285 CTGTATTAATGAATGCTTACAAGGCGCAGAGAGTCCGTGTCAGACGGAGCCCT 344
Db 240 CTGTATTAATGAATGCTTACAAGGCGCAGAGAGTCCGTGTCAGACGGAGCCCT 299
|||
Qy 345 GGGGCAATGTTATTCGCGGTACACCTGAGATCCAGGTGCGGATGATTTCAAGAGAA 404
Db 300 GGGGCAATGAGATTCGCGGTACACCTGAGATCCAGGTGCGGATGATTTCAAGAGAA 359
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Qy 405 AAGGGGAATGTTCTGAGGAAAAGCTTTGAGAGTCTTGACACCCCACTACAGAGTGT 464
Db 360 AAGGGGAATGTTCTGAGGAAAAGCTTTGAGAGTCTTGACACCCCACTACAGAGTGT 419
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Qy 465 TCATGAGATTCATTAATTAATGCAATCTTTGGAAAATTCGGAGATGATTTCA 524
Db 420 TCATGAGATTCATTAATTAATGCAATCTTTGGAAAATTCGGAGATGATTTCA 479
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Qy 525 AAGATGCGTTCAATAGTCTCTAAGAGTCTTCAAGTCTCACTTCCGCTAAATGC 584
Db 480 AAGATGCGTTCAATAGTCTCTAAGAGTCTTCAAGTCTCACTTCCGCTAAATGC 539
|||
Qy 585 AGAAATGCAATGCTGTCAGGCTGATTTTACATTCATGAGTGAATGTTCCAGACCT 644
Db 540 AGAAATGCAATGCTGTCAGGCTGATTTTACATTCATGAGTGAATGTTCCAGACCT 599
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Qy 645 CTTCCTCATGAGCTATTAATTTTGGACCAAGAGCCCTGGAATGAAATTCACAAAT 704
Db 600 CTTCCTCATGAGCTATTAATTTTGGACCAAGAGCCCTGGAATGAAATTCACAAAT 659
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Qy 705 AATATTCATGCACTCTCTCTGAGAGGACTTTTGAAGAAATGCTGATTTAGT 764
Db 660 AATATTCATGCACTCTCTCTGAGAGGACTTTTGAAGAAATGCTGATTTAGT 719
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Qy 765 GATGTTGCTATGCTGCTGAGGACTTTTGAAGAAATGCTGATTTAGT 824
Db 720 GATGTTGCTATGCTGCTGAGGACTTTTGAAGAAATGCTGATTTAGT 779
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Qy 825 TGGATTCATGCTGCTGAGGACTTTTGAAGAAATGCTGATTTAGT 884
Db 780 TGGATTCATGCTGCTGAGGACTTTTGAAGAAATGCTGATTTAGT 839
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Qy 885 TTTGCTACCTCTTTTATTAATGCTTGAAGTCTTCAATTAATGATTTAAATA 944
Db 840 TTTGCTACCTCTTTTATTAATGCTTGAAGTCTTCAATTAATGATTTAAATA 899
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Qy 945 GTTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
Db 900 GTTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
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Qy 1005 TTACACAGCTTTTATTAATGATGATGATGATGATGATGATGATGATGAT 1064
Db 956 ATTTCACAGCTTTTATTAATGATGATGATGATGATGATGATGATGATGAT 1011
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Qy 1065 TTTTATGATGATGAT 1081
Db 1012 TTTTATGATGATGAT 1028
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RESULT 10
BX387691 986 bp mRNA linear EST 29-APR-2004
LOCUS BX387691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CS0D1037YD19 5-PRIME, mRNA sequence.
ACCESSION BX387691
VERSION BX387691.2 GI:46875049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 986)
Li W.B., Gruber C., Jessee J. and Polayes D.


```

QY 412 AATGCTGAGGAAAGCTTTGAGAGCTCTGAGACCCCACTAACAAGAGTTCATGGA 471
DB 361 AATGCTGAGGAAAGCTTTGAGAGCTCTGAGACCCCACTAACAAGAGTTCATGGA 420
QY 472 GTTCAATGGAATATGCGATATGATCTTTGGGAAAATTCGGAGTGTACATTTACAAAGATGC 531
DB 421 GTTCAATGGAATATGCGATATGATCTTTGGGAAAATTCGGAGTGTACATTTACAAAGATGC 480
QY 532 GTTCAATGGAATATGCGATATGATCTTTGGGAAAATTCGGAGTGTACATTTACAAAGATGC 591
DB 481 GTTCAATGGAATATGCGATATGATCTTTGGGAAAATTCGGAGTGTACATTTACAAAGATGC 540
QY 552 CATGCTGTACAGCTGTGATATTTCACTCAATGAGCTGAATGTTTCAGAGCTCTTCCCA 651
DB 541 CATGCTGTACAGCTGTGATATTTCACTCAATGAGCTGAATGTTTCAGAGCTCTTCCCA 600
QY 652 TTGAGCTATATATTTATTTGACCAAGAAAGCCCTGAAATGAAATTTCAATTAATATTC 711
DB 601 TTGAGCTATATATTTATTTGACCAAGAAAGCCCTGAAATGAAATTTCAATTAATATTC 660
QY 712 ATGCACTCTCTCTGTGAAAGAGCTTTGAAAGAAATGTGCTGATTAAGATGTTG 771
DB 661 ATGCACTCTCTCTGTGAAAGAGCTTTGAAAGAAATGTGCTGATTAAGATGTTG 720
QY 772 CTATCTGAGG-TTGCACTTGTTCAGATTAACCAAAAAGAGATGCTTCTAAGATGAAAT 830
DB 721 CTATCTGAGG-TTGCACTTGTTCAGATTAACCAAAAAGAGATGCTTCTAAGATGAAAT 780
QY 831 TCAGTTTCTGCGATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCT 890
DB 781 TCAGTTTCTGCGATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCT 840
QY 891 ACCT-CTTTTTTATTAATGCTTGAAT-GGTTCACTTAATGACATTTTAATAATGTT 948
DB 841 ACCTCTTTTTTATTAATGAGCCCTGGAATGGGTTCACTTAAGAGCTTTTAATAATGTT 900
QY 949 ATGTAATACATCTGAATGAAAAGCAAGCTTA 979
DB 901 TATGAAATACCTCCGGAATGAAAAGGCAAA 931

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RESULT 13
LOCUS B1763295 903 bp mRNA linear EST 25-SEP-2001
DEFINITION 603047656P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188069 5',
mRNA sequence.
ACCESSION B1763295
VERSION B1763295.1 GI:15754873
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 903)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: L14M11469 row: 0 column: 14
High quality sequence stop: 875.

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FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"

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ORIGIN

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Query Match 64.9%; Score 815.2; DB 4; Length 903;
Best Local Similarity 96.4%; Pred. No. 2.8e-164;
Matches 855; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

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/clone="IMAGE:5188069"
/lab_host="DH10B"
/clone_11b="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

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QY 362 GGTACACCTGGATCCCAAGTCCGATGATTAAGAGAAAGGGGATGTCTGAG 421
DB 1 GGTACACCTGGATCCCAAGTCCGATGATTAAGAGAAAGGGGATGTCTGAG 60
QY 422 GAAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGACAGTTCATGAGTTCATGAA 481
DB 61 GAAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGACAGTTCATGAGTTCATGAA 120
QY 482 TTATGCGATATCTTGGAAAATTTGGGAGTGTACATTTCAAAAGATGCTCAAAATG 541
DB 121 TTATGCGATATCTTGGAAAATTTGGGAGTGTACATTTCAAAAGATGCTCAAAATG 180
QY 542 TGTCTAAGAGTTTGTTCAGTGTCTCACTTGGCTTAATGAGAAATGATGCTGTGA 601
DB 181 TGTCTAAGAGTTTGTTCAGTGTCTCACTTGGCTTAATGAGAAATGATGCTGTGA 240
QY 602 GCGTGTATTTCACTCAATGAGTGTGATGTCAGACCTCTTCCATGGAAGCTAT 661
DB 241 GCGTGTATTTCACTCAATGAGTGTGATGTCAGACCTCTTCCATGGAAGCTAT 300
QY 662 AATTTATTTGGAACCAAGAAAGCCCTGAATGAATTCACAAATTAATTAATTCATGCACTTC 721
DB 301 AATTTATTTGGAACCAAGAAAGCCCTGAATGAATTCACAAATTAATTAATTCATGCACTTC 360
QY 722 TTCTGTGAAAGAGCTTTGTAAGAAATGTGCTGATTAAGAGTGTGATGCTATGCTGT 781
DB 361 TTCTGTGAAAGAGCTTTGTAAGAAATGTGCTGATTAAGAGTGTGATGCTATGCTGT 420
QY 782 TGGCACTTGTTCAGATTAACCAAGAGATGCTTCTACATGATGATTCAGTTCCTG 841
DB 421 TGGCACTTGTTCAGATTAACCAAGAGATGCTTCTACATGATGATTCAGTTCCTG 480
QY 842 CATCATTAATGGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 901
DB 481 CATCATTAATGGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 540
QY 902 TATTAATGCTTGAATGCTTCATTAATGATTTAATTAATGATTTAATTAATGATTCG 961
DB 541 TATTAATGCTTGAATGCTTCATTAATGATTTAATTAATGATTTAATTAATGATTCG 600
QY 962 AATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTCACACTGTTTTTAA 1021
DB 601 AATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTCACACTGTTTTTAA 660
QY 1022 TCTAGCATTAATTAATTTGCTTTAATCAAAAGTGTTCATTAAT-TTTTTTAAAGTGT 1080
DB 661 TCTAGCATTAATTAATTTGCTTTAATCAAAAGTGTTCATTAAT-TTTTTTAAAGTGT 720
QY 1081 AGAATCTTCTTCATATGCACTTCTCAACTATATTTGGAATATGTTGAGTCT 1140
DB 721 AGAATCTTCTTCATATGCACTTCTCAACTATATTTGGAATATGTTGAGTCT 780
QY 1141 TTGTGTTTTTCTTATGATATGATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200

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Db      781 TTAG--TTATCTCTAGTATGCAATTTTTTAATAAAATTAAAGCTACCATCTTCGCAC   838
Cy      1201 AATTGTGAATGTTAAGAATTTTTTTTATATCGTTAAATAAAAAATT    1247
          AACCTGTAAGCTTAAGAAATTTTTTTTATATCTGTTAAATAATATATTT    885

RESULT_14
AL544722
LOCUS       AL544722
DEFINITION clone CSODI022YR04 5-PRIME, mRNA sequence.
ACCESSION  AL544722
VERSION     AL544722.3  GI:45745219
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 827)
AUTHORS     Li,W.B., Gruber,C., Jeesee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31265563.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by life technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            4941.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?ts=CSODI022DCO2QP1&c=4941.f.

FEATURES             source
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                                digested with Not I and cloned into the Not I and EcoR V
                                sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match               64.5%; Score 811.2; DB 1; Length 827;
Best Local Similarity     99.5%; Pred. No. 2e-163;
Matches 824; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Cy      69 GACGCTGACCA CGTTCCTCTCTCCTCGGCTCTCTCCGCTTCAGACTCCGCGTCCCGGAG   128
          1 GATGTCGACCACGGTTCCTCTCCTCGGATCTCTCCGCTTCAGGCTCCGGGCTGCCGCGAG   60

Db      129 CCGGGAGCATGCGAACCCCAAGGGCCCCGCGCTCTCCCGACGCGCTCCGGGCTCTG   188
          61 CCGGAGACCATGCAACCCCAAGGGCCCCGCGCTCTCCCGACGCGCTCCGGGCTCTG   120

Cy      189 CTGCTCTCGAGCTGCGACGTGCGCGCGCGCTCGAGCGGCTCTGAGATCCCAAGGGAG   248
          121 CTGCTCTCTGCTGCGACGTGCGCGCGCGCTCGAGCGGCTCTGAGATCCCAAGGGAG   180

Cy      249 CAAGAAGCGACGCTCCGGCAGAGGAGTGATGCACTGTATTAATGATGTGCTTACA   308
          181 CAAGAAGCGCAG-TCCGCAAGAGGAGTGATGCACTGTATTAATGATGTGCTTACA   239

Cy      309 GGCGCAGAGGAGTGTGCTGTGCAAGCGGAGCCCTGGGCGCAATGTTATTCGGGTACA   368
          111 GGCGCAGAGGAGTGTGCTGTGCAAGCGGAGCCCTGGGCGCAATGTTATTCGGGTACA   368

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D	b		240	GGGCAGACAGAAAGTGCCTGATCGAGACGGGAGCCCTG369GCAATTGGCATTTCCGGGTACA	299
Oy			369	CTGGGATCCCAGGTCGGGATTGGAATTCAAAGGAGAAAAGGGGAAATGTTCTGAGGGAAAAGC	428
D	b		300	CTGGGATCCCAGGTCGGGATTGGAATTCAAAGGAGAAAAGGGGAAATGTTCTGAGGGAAAAGC	359
Oy			429	TTTTGAGAAGTCCTGGGACACCCAACTACAGAGAGTTTCATGAGTTGATTAATTAATGAGC	488
D	b		360	TTTGAAGAGTCCTGGGACACCCAACTACAGAGAGTTTCATGAGTTGATTAATTAATGAGC	419
Oy			489	ATAGATCTTGGGAAAATTTGGCGAGTGTACTTTAACAAGAATGCCGTTCAAAATAGTCTCTA	548
D	b		420	ATAGATCTTGGGAAAATTTGGCGAGTGTACTTTAACAAGAATGCCGTTCAAAATAGTCTCTA	479
Oy			549	AGAGTTTGTTCAGTGGCTCACTTCGGCTAAATTCGAAAATGCATGCTGTACAGCGTTGG	608
D	b		480	AGAGTTTGTTCAGTGGCTCACTTCGGCTAAATTCGAAAATGCATGCTGTACAGCGTTGG	539
Oy			609	TATTTCACTTCAATGAGCGTGAATGTTTCAGAGCCTCTCCCATGGAAGCTATAATTAAT	668
D	b		540	TATTTCACTTCAATGAGCGTGAATGTTTCAGAGCCTCTCTCCCATGGAAGCTATAATTAAT	599
Oy			669	TTGGACCAGGAAGAGCCCTGAAATGAATTCACAATTAATTAATTCATGCGACCTTCTTGCTG	728
D	b		600	TTGGACCAGGAAGAGCCCTGAAATGAATTCACAATTAATTAATTCATGCGACCTTCTTGCTG	659
Oy			729	GAAGGACTTTGTGAGGAATTTGTGCTGATTTAGTGAGATGTTGCTATCTGGGTTGGCACT	788
D	b		660	GAAGGACTTTGTGAGGAATTTGTGCTGATTTAGTGAGATGTTGCTATCTGGGTTGGCACT	719
Oy			789	TGTTCAAGTATCCCAAAAGGAGATGCTTCTACTGAGATGGAATTAAGTTTCTCGATCATTT	848
D	b		720	TGTTCAAGTATCCCAAAAGGAGATGCTTCTACTGAGATGGAATTAAGTTTCTCGATCATTT	779
Oy			849	ATTGAACAACCTACCAAAATTAATGCTTTAATTTTCATTTGGTACTCCT	896
D	b		780	ATTGAACAACCTACCAAAATTAATGCTTTAATTTTCATTTGGTACTCCT	827
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R	E	S	U	L	T
RESULT_15					
BQ425266					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
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REFERENCES					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
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AGENCY	COURT_7912803 NIH_MGC_72 Homo sapiens cdna clone IMAGE:6150166				
5', mRNA sequence.					
BQ425266					
BQ425266.1 GI:21120581					
EST.					
Homo sapiens (human)					
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
1 (bases 1 to 851)					
NIH-MGC http://mgc.nci.nih.gov/.					
National Institutes of Health, Mammalian Gene Collection (MGC)					
Unpublished (1999)					
Contact: Robert Strausberg, Ph.D.					
Email: cgabs-remail.nih.gov					
Tissue Procurement: ATCC/DCTP					
CDNA Library Preparation: Life Technologies, Inc.					
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
DNA Sequencing by: Agencourt Bioscience Corporation					
clone distribution: MGC clone distribution information can be					
found through the I.M.A.G.E. Consortium/LNL at:					
http://image.llnl.gov					
plate: LAM13484 row: f column: 23					
High quality sequence stop: 670.					
Location/Qualifiers					
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/organism="Homo sapiens"					
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/clone="IMAGE:6150166"					
/tissue_type="melanotic melanoma"					
<hr/>					
FEATURES					
source					

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/lab_host="VDH10B (phage-resistant)"
/clone_lib="NTM_MCC_72"
/notes="Organ: skin; Vector: PCMV-SPORE6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt
Average insert size 2 kb. Library constructed by Life
Technologies."

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ORIGIN

Query Match	58.8%;	Score 739.4;	DB 5;	Length 851;
Best Local Similarity	99.1%;	Pred. No. 5.2e-148;		
Matches 754; Conservative	0;	Mismatches 6;	Indels 1;	Gaps 1

QY	6	GAGGGCCCGGGTGAAGGCGCATTTGATGCAGCTCGGGCGGCGTGGAGCGCGGCGAG	65
Db	36	GAGGGCCCGGGTGAAGGCGCATTTGATGCAGCTCGGGCGGCGTGGAGCGCGGCGAG	95
QY	66	CCAGACGGTGACCAAGTTCTCTCTCGGTCTCTCCGCTCCAGCTCCGCGCTCCGAG	125
Db	96	CCAGACGGTGACCAAGTTCTCTCTCGGTCTCTCTCGGCTCCAGCTCCGCGCTCCGAG	155
QY	126	CAGCCGGGAGCCATCGGACCCCAAGGAGCCCGCGCTCCCGCAAGGAGCTCGCGGCTC	185
Db	156	CAGCCGGGAGCCATCGACCCCAAGGAGCCCGCGCTCCCGCAAGGAGCTCGCGGCTC	215
QY	186	CTGCTGCTCTGCTGCTGAGCTGCGCGCGGCTGAGGCGCTTGAGATCCCCCAAGGAG	245
Db	216	CTGCTGCTCTGCTGCTGAGCTGCGCGCGGCTGAGGCGCTTGAGATCCCCCAAGGAG	275
QY	246	AAGCAAAAGGCGCAGCTCCGCGCAGAGGAGTGTGTGACCTGTATATATGAAATGTACTTA	305
Db	276	AAGCAAAAGGCGCAGCTCCGCGCAGAGGAGTGTGTGACCTGTATATATGAAATGTACTTA	335
QY	306	CAAGGGCCAGCAGAGGTGCTGTGTGAGACGGGAGCCTTGSGGCGAATGTATATTCGGGT	365
Db	336	CAAGGGCCAGCAGAGGTGCTGTGTGAGACGGGAGCCTTGSGGCGAATGTATATTCGGGT	395
QY	366	ACACCTGGGATGCCAGGTCCGAGTGGATTTCAAAGGAAAGAGGGGAAATGTCGTAGGGA	425
Db	396	ACACCTGGGATGCCAGGTCCGAGTGGATTTCAAAGGAAAGAGGGGAAATGTCGTAGGGA	455
QY	426	AGCTTTGAGAGTCCGTGACACCCCAACTCAAGAAGTGTCTCAGAGTTCAATTGAATAT	485
Db	456	AGCTTTGAGAGTCCGTGACACCCCAACTCAAGAAGTGTCTCAGAGTTCAATTGAATAT	515
QY	486	GGCATTAGATCTTTGGGAAAATTGCGGAGTGTACATTTAACAAAGATCGTTCAATAGTCT	545
Db	516	GGCATTAGATCTTTGGGAAAATTGCGGAGTGTACATTTAACAAAGATCGTTCAATAGTCT	575
QY	546	CTAAGAGTTTGTTCAGTGGCTCAATTTGGGCTTAAATGCAAAATGCACTGCTCAGCGT	605
Db	576	CTAAGAGTTTGTTCAGTGGCTCAATTTGGGCTTAAATGCAAAATGCACTGCTCAGCGT	635
QY	606	TGTATTTTCAATTTCAATGAGCTGAATGTTCAAGACCTTCCCATTTGAAGCTATATTT	665
Db	636	TGTATTTTCAATTTCAATGAGCTGAATGTTCAAGACCTTCCCATTTGAAGCTATATTT	695
QY	666	TATTTGACCAAGGAAGCCCTGAATGATTTCAACATTTAATATTATCATGCACTTCTCT	725
Db	696	TATTTGACCAAGGAAGCCCTGAATGATTTCAACATTTAATATTATCATGCACTTCTCT	755
QY	726	GTGGAAGGACTTTGTG-AAAGAAATTTGCTGTGATTAAGTGG	765
Db	756	GTGGAAGGACTTTGTGAAAGAAATTTGCTGTGATTAATTTG	796

RESULT 16		
AJ399084		
Locus		
Definition	732 bp DNA linear GSS 15-DEC-2003 Homo sapiens CTNRC1 gene, VIRUTAL TRANSCRIPT, partial sequence,	
Accession	AJ399084	
Version	G genomic survey sequence.	
Keywords	AJ399084.1 GI:39755073 GSS.	

SOURCE

ORGANISM

REFERENCES

REFERENCE

ADDITION

TITLE

FORM 1

JOURNAL
DITMERS

REFERENCE

REFERENCES

• • • • •

TITL

JOURNAL,

COMMENT

CONCLUSION

FEATURES

Source:

2030

gerne

ORIGIN

Query Mat

Best Local

Matches

2

27

Db

ORIGIN

Query Match	57.9%	Score 727.2;	DB 9;	Length 732;
Best Local Similarity	99.6%;	Pred. No. 2.1e-145;		
Matches 729; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	136	ATGCAACCCCAAGGGGCCCCCGCGCTCCCGGAGGGGCTCCGCGGCTCTGCTGCTCTG	197
QY	1	ATGCAACCCCAAGGGGCCCCCGCGCTCCCGGAGGGGCTCCGCGGCTCTGCTGCTCTG	60
QY	198	CTGCTGCAAGTCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAGCAAAAGCG	257
Db	61	CTGCTGCAAGTCTCCCGCGCGCTCGAGGGCTCTGAGATCCCAAGGGGAAGCAAAAGCG	120
QY	258	CAGCTCCGCGAGAGGAGAGTGTGGACCTGTATATGGAATGACTTAACAGGGGCAAGA	317
Db	121	CAGCTCCGCGAGAGGAGAGTGTGGACCTGTATATGGAATGTGCTTACAAAGGGCAAGA	180
QY	318	GGAGTGCCTGCTCGAGACGGGAGCCTCTGGGGCCAAATGTTATTCCGGGTACACTGGGAATC	377
Db	181	GGAGTGCCTGCTCGAGACGGGAGCCTCTGGGGCCAAATGGAATTCGGGTACACTGGGAATC	240
QY	378	CCAGGTGGGAGTGGATTCAAAAGGAGAAAGGGGAAATGTCTAGGGAAAGCTTTAGAG	437
Db	241	CCAGGTGGGAGTGGATTCAAAAGGAGAAAGGGGAAATGTCTAGGGAAAGCTTTAGAG	300
QY	438	TCCTGGACACCACTACAGCAGGTGTCTATGAGTTCAATGAATTAATGCAATAGATCTT	497
Db	301	TCCTGGACACCACTACAGCAGGTGTCTATGAGTTCAATGAATTAATGCAATAGATCTT	360
QY	498	GGGAAATTTGGGGAGTGAATTTTACAAAGATAGCTTCAATATGTGCTCTAAGAGTTTG	557
Db	361	GGGAAATTTGGGGAGTGAATTTTACAAAGATAGCTTCAATATGTGCTCTAAGAGTTTG	420
QY	558	TTCAATGCTCACTTCGGCTAAATGACAAATGCATGCTCAGCGTGTGATATTTCACA	617
Db	421	TTCAATGCTCACTTCGGCTAAATGACAAATGCATGCTCAGCGTGTGATATTTCACA	480
QY	618	TTCAATGAGCTGAATGTTTACGAGACTCTTCCCATTTGAAGCTATATTAATTGGACCA	677
Db	481	TTCAATGAGCTGAATGTTTACGAGACTCTTCCCATTTGAAGCTATATTAATTGGACCA	540

QY 678 GGAAGCCCTGAATGATCAATTAATATTCATCGACTTCTGTGAGAGACTT 737
DB 541 GGAAGCCCTGAATGATCAATTAATATTCATCGACTTCTGTGAGAGACTT 600
QY 738 TGTGAAGGATTTGCTGCTGATTTAGTGAATGTTGCTATCTGGTGGCACTTGTTCAGAT 797
DB 601 TGTGAAGGATTTGCTGCTGATTTAGTGAATGTTGCTATCTGGTGGTGTCTGTTTTCAGAT 660
QY 798 TACCCAAAGAGAGAGCTTCTACTGATGGAATTCAGTTCTCGCATCTTATTTAGAGAA 857
DB 661 TACCCAAAGAGAGAGCTTCTACTGATGGAATTCAGTTCTCGCATCTTATTTAGAGAA 720
QY 858 CTACCAAAATTA 869
DB 721 CTACCAAAATTA 732

RESULT 17
BQ425098 922 bp -mRNA linear EST 23-MAY-2002
LOCUS BQ425098
DEFINITION AGENCOURT_7902947 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157844
5', mRNA sequence.
ACCESSION BQ425098
VERSION BQ425098.1 GI:21120413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 922)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DC/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13504 row: f column: 21
High quality sequence stop: 714.
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/clone="IMAGE:6157844"
/feature_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 57.0%; Score 716.4; DB 5; Length 922;
Best Local Similarity 89.4%; Pred. No. 4.5e-143;
Matches 816; Conservative 0; Mismatches 92; Indels 5; Gaps 4;

QY 25 CGCATTGATGACCTGCGCGGCTTCGAGCGCGGAGCAAGACCTGACCACTTC 84
DB 10 CGCATTGATGACCTGCGCGGCTTCGAGCGCGGAGCAAGACCTGACCACTTC 69
QY 85 CTCTCTCGGTCCTCCGCTCCGCTCCGCTCCGCTCCGCGGAGCGGAGGACCATGAGC 144
DB 70 CTCTCTCGGTCCTCCGCTCCGCTCCGCTCCGCGGAGCGGAGGACCATGAGC 129
QY 145 CCCAGGCGCGCGCTCCGCGGAGCGGCTCCGCGGCTCTGCTCTGCTGCTGCTGC 204

DB 130 CCCAGGCGCGCGCTCCGCGGAGCGGCTCCGCGGCTCTGCTGCTCTGCTGCTGC 189
QY 205 AGCTGCGCGCGCTCCGCGGAGCGGCTCCGAGATCCCAAGGAGGAGAAAGGCGAGCTCC 264
DB 190 AGCTGCGCGCGCTCCGCGGAGCGGCTCCGAGATCCCAAGGAGGAGAAAGGCGAGCTCC 249
QY 265 GGCAGAGGAGAGTGTGAGCCTGTATTAATGAAATGTGCTTACAAAGGCGCAGAGAGTGC 324
DB 250 GGCAGAGGAGAGTGTGAGCCTGTATTAATGAAATGTGCTTACAAAGGCGCAGAGAGTGC 309
QY 325 CTGTGTGAGAGCGGAGCGCTGGGGCCAAATGTTATTCCTGGGATACCTGGAGATCCAGGTC 384
DB 310 CTGTGTGAGAGCGGAGCGCTGGGGCCAAATGCGATTCGGGGTACACTGGGATCCAGGTC 369
QY 385 GGGATGATTCAAAGAGAGAAAGGGGGAATGCTGAGGGAAGCTTGGAGAGCTGTGA 444
DB 370 GGGATGATTCAAAGAGAGAAAGGGGGAATGCTGAGGGAAGCTTGGAGAGCTGTGA 429
QY 445 CACCAACTACAGAGAGTTCATGAGATTCATTAATGATGAGATCTTGGGAGAA 504
DB 430 CACCAACTACAGAGAGTTCATGAGATTCATTAATGATGAGATCTTGGGAGAA 489
QY 505 TTGCGAGATGACATTTACAAAGATGCGTTCAATATGATGCTTAAGAGTTTGTTCAGTG 564
DB 490 TTGCGAGATGACATTTACAAAGATGCGTTCAATATGATGCTTAAGAGTTTGTTCAGTG 549
QY 565 GCTCACTTCGCTAAAGAGAGAAATGATGCTGACGCTGATTTACATTCAGT 624
DB 550 GCTCACTTCGCTAAAGAGAGAAATGATGCTGACGCTGATTTACATTCAGT 609
QY 625 GAGCTGAATGTCAGAGACTCTTCCCATTTGAAGCTATTAATTTTGGACCAAGAGAGCC 684
DB 610 GAGCTGAATGTCAGAGACTCTTCCCATTTGAAGCTATTAATTTTGGACCAAGAGAGCC 669
QY 685 CTGAATGATTAACAATTAATTAATTCATGCACTT-CTTCTGCGAAGAGCTTGTG-A 742
DB 670 CTGAATGATTAACAATTAATTAATTCATGCACTTCTTGTGGAAGAGACTTGTGAA 729
QY 743 AGGAATGATGCT-AGATTAAGGATGTTGC--TATCTGCTTGGACATTTTTCAGATTA 799
DB 730 AGGAATGATGCTGGAATTAATGATGTTGCTTATCTGGGATGACACTGTTTCCAAAT 789
QY 800 CCCAAAGAGAGATGCTTACTGATGAGATTCAGTTTCTGSCATCATATTAAGAGACT 859
DB 790 ACCCAAAGGAGAGATGCTTACTGATGAGAGATTCAGTTTCTGSCATCATATTA 849
QY 860 ACCAAATTAATGCTTAATTTTCAATTTGCTACTCTTTTTTATTAATGCTTGAATG 919
DB 850 TTGGAAGAACTAACCAAAATTAATTAATGCTTAATTTTTCATTTGCTGACCTTACC 909
QY 920 TTCACTTAATGA 932
DB 910 TTCTTTGAATTA 922

RESULT 18
AY399085 732 bp DNA linear GSS 15-DEC-2003
LOCUS AY399085
DEFINITION Pan troglodytes CTHRC1 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY399085
VERSION AY399085.1 GI:39755074
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
1 (bases 1 to 732)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
Fierliera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL Science 302 (5652), 1960-1963 (2003)
 REFERENCE 14671302
 AUTHORS 2 (bases 1 to 732)
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.W., Civello, D.R., Lu, F., Murphy, B.,
 Ferritera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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 /db_xref="taxon:9598"
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gene

ORIGIN

Query Match 56.8%; Score 714.4; DB 9; Length 732;
 Best Local Similarity 98.1%; Pred. No. 1.2e-142;
 Matches 718; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

138 ATGCGACCCCAAGGCGCCGCGCTCCCGCAGCGGCTCCGCGGCTCTGCTGCTCCG 197
 1 ATGCGACCCCAAGGCGCCGCGCTCCCGCAGCGGCTCCGCGGCTCTGCTGCTCCG 60
 198 CTGCTGCACTGCGCGCGCGCTGCAAGCGCTCTGAGATCCCAAGGGAAGCAAGCG 257
 61 CTGCTGCACTGCGCGCGCGCATGAGCGCTCTGAGATCCCAAGGGAAGCAAGCG 120
 258 CAGCTCCGCGCAGGAGGAGTGTGAGCTCTGATTAATGAAATGCTTACAAAGGCGCAG 317
 121 CAGCTCCGCGCAGGAGGAGTGTGAGCTCTGATTAATGAAATGCTTACAAAGGCGCAG 180
 318 GAGATGCTGTGTCAGACGCGGAGCCCTGGGCGCAATGTTATCCGAGTACACTGAGATC 377
 181 GAGATGCTGTGTCAGACGCGGAGCCCTGGGCGCAATGTTATCCGAGTACACTGAGATC 240
 378 CCAGCTCGGAGTGCATTAAGAGAGAAAGGGGAAATGTTCTGAGGGAAGCTTTGAGAG 437
 241 CCAGCTCGGAGTGCATTAAGAGAGAAAGGGGAAATGTTCTGAGGGAAGCTTTGAGAG 300
 438 TCCTGAGACCACTACAGAGAGTTCATGAGATTCATTAATGATGCTTATGATCTT 497
 301 TCCTGAGACCACTACAGAGAGTTCATGAGATTCATTAATGATGCTTATGATCTT 360
 498 GGGAAATTCGGAATGATACATTAACAAAGATGCTTCAAAATGCTCTAAGATTTTG 557
 361 GGGAAATTCGGAATGATACATTAACAAAGATGCTTCAAAATGCTCTAAGATTTTG 420
 558 TTGAGTGGCTACTTCGCTAAATGCAAGAAATGCTGCTGAGCTGTTGATTTTCA 617
 421 TTGAGTGGCTACTTCGCTAAATGCAAGAAATGCTGCTGAGCTGTTGATTTTCA 480
 618 TTCAATGAGAGTGAATGTTCAAGACCTCTCCCATTTGAGGATTAATTAATTTTGA 677
 481 TTCAATGAGAGTGAATGTTCAAGACCTCTCCCATTTGAGGATTAATTAATTTTGA 540
 678 GGAAGCCCTGAATGAATTAACAATTAATTAATTCACACTTCTTCTGAGAGAGCTT 737
 541 GGAAGCCCTGAATGAATTAACAATTAATTAATTCACACTTCTTCTGAGAGAGCTT 600
 738 TGTGAAAGAAATGCTGCTGAGATTAGTGAATGCTGCTGCTGCTGCTGCTGCTGCT 797
 601 TGTGAAAGAAATGCTGCTGAGATTAGTGAATGCTGCTGCTGCTGCTGCTGCTGCT 660
 798 TACCAAAAGAGATGCTTCTACTGAGATGAATCAGTTTCTCGATTAATTAAGAA 857

Db 661 TACCAAAAGAGATGCTTCTACTGAGATGAATCAGTTTCTCGATTAATTAAGAA 720
 Qy 858 CTACCAAAATTA 869
 Db 721 CTACCAAAATTA 732

RESULT 19
 BM915926
 LOCUS DEFINITION
 BM915926 1037 bp mRNA linear EST 12-MAR-2002
 AGENCOURT 6639781 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482196
 5', mRNA sequence.
 BM915926
 BM915926.1 GI:19366305
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1037)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.llnl.gov
 Plate: L1CM2007 row: n column: 21
 High quality sequence stop: 482.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5482196"
 /issue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_41"
 /note="Organ: skin; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
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 GGCAACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 56.1%; Score 705.4; DB 4; Length 1037;
 Best Local Similarity 91.7%; Pred. No. 1.1e-140;
 Matches 791; Conservative 0; Mismatches 66; Indels 6; Gaps 4;

53 GAGCGCGCGGAGCAGACGTCAGCAAGTCTCTCTCGCTGCTGCTGCTGCTGCTGCT 112
 1 GAGCGCGCGGAGCAGACGTCAGCAAGTCTCTCTCGCTGCTGCTGCTGCTGCTGCT 60
 113 CCGGCTGCGCGCGGAGCAGACGTCAGCAAGTCTCTCTCGCTGCTGCTGCTGCTGCT 172
 61 CCGGCTGCGCGCGGAGCAGACGTCAGCAAGTCTCTCTCGCTGCTGCTGCTGCTGCT 120
 173 GCTGCGGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 232
 121 GCTGCGGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 233 GATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 292
 181 GATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

Qy	293	TGGAATGCGCTTACAAAGGCCAGAGAGATGCTCGTGTGAAACGGAGAGCCCTGGGGCCAA	352
Db	241	TGGATGATGCTTACCAAGGCCAGCAGAGATGCTCGTGTGAAACGGAGAGCCCTGGGGCCAA	300
Qy	353	TGTATATCCGGGTACACCTGGGATCCCAAGCTCGGGATAGTATTCAAAGAGAAAAGGGGGA	412
Db	301	TGGCATTCGGGGTACACTGGGATCCCAAGTCCGGATGGAATTCAAAGAGAAAAGGGGGA	360
Qy	413	ATGTCGAGGAAAGCTTTGAGAGTCTGGACACCCACTACAGACAGTTCATGGAG	472
Db	361	ATGTCGAGGAAAGCTTTGAGAGTCTGGACACCCACTACAGACAGTTCATGGAG	420
Qy	473	TTCAATTAATTAATGCAATAGATCTTTGGGAAAATTCGGAGTGCATTTAAAGATGCG	532
Db	421	TTCAATTAATTAATGCAATAGATCTTTGGGAAAATTCGGAGTGCATTTAAAGATGCG	480
Qy	533	TTCAATTAATGCTCTAAGAGTCTTTGTTCAAGTGCCTCACTTGGGCTAAATGACAGAAATGC	592
Db	481	TTCAATTAATGCTCTAAGAGTCTTTGTTCAAGTGCCTCACTTGGGCTAAATGACAGAAATGC	540
Qy	593	ATGCTGTACGCGTTGTATTTTCAATTCATGAGCTGAATGTTCAAGACCTTTCCAT	652
Db	541	ATGCTGTACGCGTTGTATTTTCAATTCATGAGCTGAATGTTCAAGACCTTTCCAT	600
Qy	653	TGAAGCTATATTTATTTTGAACCAAGAGCCCT-GAAATGAATTCACAAATTAATATTC	711
Db	601	TGAAGCTATATTTATTTTGAACCAAGAGCCCTGAATGAATTAATTCACAAATTAATATTC	660
Qy	712	ATC-GCACCTTCTGCTGAGAGGACCTTGTGAAGGAATGTGTGCTGATTAATGATGATGTT	770
Db	661	ATCGGCACCTTCTGCTGAGAGGACCTTGTGAAGGAATGTGTGCTGATTAATGATGATGTT	720
Qy	771	GCTATCTGGGTT--GGCATTGTTCAATTAACCCAAAGAGATGCTTCTAC--TGATG	826
Db	721	GCTATCGGGGTGGGGAATTTGTTCACTTACCCCAAGAAATGCTTCCACCTGGCCGG	780
Qy	827	GAATTCAGTCTTCGTCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTCTAT	886
Db	781	AATGTCGCGCCCTCTCTCCGAGTGACGAATCCCAAACTCACGCTTTAATGCTACT	840
Qy	887	TGCTACCTCTTTTATTATATGTC	909
Db	841	TGGCAGACCTCTCTTCGGAGGC	863
RESULT 20			
CR592899			
LOCUS			
DEFINITION	CR592899	710 bp	mRNA linear
ACCESSION	CR592899		full-length cDNA clone CS00107YB01 of Placenta Cot 25-normalized
VERSION	CR592899.1		of Homo sapiens (human).
KEYWORDS	HTC; cNSLT; cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1. (bases 1 to 710)		
JOURNAL	L.J.W.B., Gruber, C., Jeesee, J. and Polayes, D.		
REMARK	Full-length cDNA libraries and normalization		
	Unpublished		
	Contact : Feng Liang Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
	Paradise Avenue		
REFERENCE	2. (bases 1 to 710)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :		
	BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
COMMENT			

was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1. 710

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/db_xref="taxon:9606"

/clone="CS0D1077YB01"

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/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 56.1%; Score 705.2; DB 3; Length 710;

Best Local Similarity 99.6%; Pred. No. 1,1e-140;

Matches 707; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

175 TCCGCGGCGCTCTCTCTGCTCTCTGCTGACAGTCCCGCGCCGTGACGCGCTGTAGA 234

1 TCCCGGCGCTCTCTCTCTCTCTCTGCTGACAGTCCCGCGCCGTGACGCGCTGTAGA 60

235 TCCCAAGGGGAGCAAAAGGCGAGCTCCGGCAGAGGGAGTGTGTGACTGTATATG 294

61 TCCCAAGGGGAGCAAAAGGCGAGCTCCGGCAGAGGGAGTGTGACTGTATATG 120

295 GAATGTGCTTCAAGGGCCACAGAGATGCTGTGACAGAGGAGCCCTGGGCCAATG 354

121 GAATGTGCTTCAAGGGCCACAGAGATGCTGTGACAGAGGAGCCCTGGGCCAATG 180

355 TTATTTCCGGGAGACCTGGGATCCCAAGTGGGATGATTCAAGAGAGAAAGGGGAA 414

181 GCATTTCCGGGAGACCTGGGATCCCAAGTGGGATGATTCAAGAGAGAAAGGGGAA 240

415 GTCTGAGGAAAGCTTTGAGGAGTCTTGACACCCTACACAGAGTTCATGAGTT 474

241 GTCTGAGGAAAGCTTTGAGGAGTCTTGACACCCTACACAGAGTTCATGAGTT 300

475 CATTTGAATTTATGCAATGATCTTTGGGAAATTTGGGAGTGTACATTTACAAAGTGC 534

301 CATTTGAATTTATGCAATGATCTTTGGGAAATTTGGGAGTGTACATTTACAAAGTGC 360

535 CAATTTAGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGGCTTAATTTGACGAATGAT 594

361 CAATTTAGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGGCTTAATTTGACGAATGAT 420

595 GCTGTCAAGCGTTGATTTCACTTCAATGAGCTGATGTTTCAAGACCTTCCCATTTG 654

421 GCTGTCAAGCGTTGATTTCACTTCAATGAGCTGATGTTTCAAGACCTTCCCATTTG 480

655 AAGCTATATTTATTTGGACCAAGAGACCTCTGAATGATTTCAACATTTATATTCATC 714

481 AAGCTATATTTATTTGGACCAAGAGACCTCTGAATGATTTCAACATTTATATTCATC 540

715 GCATTTCTTCGTGAGAGCACTTTGTGAAGAAATTTGTGTGATGATGATGATGATG 774

541 GCATTTCTTCGTGAGAGCACTTTGTGAAGAAATTTGTGTGATGATGATGATGATG 600

775 TCTGGGTTGGCACTTTGACAGATTAACCAAGAGAGATGCTTCACTGAGATGAAATTCAG 834

601 TCTGGGTTGGCACTTTGACAGATTAACCAAGAGAGATGCTTCACTGAGATGAAATTCAG 660

835 TTCTTCGATCATTTATGAGAGACTACCAATAATATGCTTTAATTTTCA 884

661 TTCTTCGATCATTTATGAGAGACTACCAATAATATGCTTTAATTTTCA 710

RESULT 21

CA415410/c

LOCUS

DEFINITION

UI-H-B20-baw-n-12-0-UI_s1 NCI CGAP Ch1 Homo sapiens cDNA clone

UI-H-B20-baw-n-12-0-UI 3', mRNA sequence.

ACCESSION

CA415410

VERSION

CA415410.1

GI:24778061

EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 747)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 TITLE Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Steven Gitcells/ Rush Presbyterian, Dept. of Orthopedics
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this CDNA sequence: 1-60, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
 source
 Location/Qualifiers
 1..747
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E20-Daw-n-12-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_11b="NCI CGAP Ch1"
 /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ch1 is a CDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldi, Lemon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TAGTACGCGCT.
 TAG_TISSUE=grade-2-chondrosarcoma
 TAG_LIB=UI-H-E20
 TAG_SEQ=ATCTAATATG"

ORIGIN
 Query Match 55.7%; Score 700.4; DB 6; Length 747;
 Best Local Similarity 98.9%; Pred. No. 1.2e-139;
 Matches 716; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

534 TCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTACTTCGGCTAAATGCAAAATGCA 593
 742 TCAAAATAGTCTTAAGAGTTT--GTTCAAGTCTCACTTCGGCTAAATGCAAAATGCA 685
 594 TGCTGTGAGCGTTGATTTACATTCATTAAGAGCTGAATGTTGAGAGCTCTCCCAT 653
 684 TGCTGTGAGCGTTGATTTACATTCATTAAGAGCTGAATGTTGAGAGCTCTCCCAT 625
 654 GAAAGCTAATTAATTTTGGACCAAGAAAGCCCTGAATGAATTCACAAATTAATTCAT 713
 624 GAAAGCTAATTAATTTTGGACCAAGAAAGCCCTGAATGAATTCACAAATTAATTCAT 565
 714 GGAAGCTCTCTCTGGAAGAGCTTTGTAAGAAATGCTGCTGATTTAGTGAATGCT 773
 564 GGAAGCTCTCTCTGGAAGAGCTTTGTAAGAAATGCTGCTGATTTAGTGAATGCT 505
 774 ATCTGGGTTGGAAGCTTGTTCAGATTACCAAAAGAGAGTCTTCACTGATGAATTC 833

Db 504 ATCTGGGTTGGAAGCTTGTTCAGATTACCAAAAGAGAGTCTTCTACTGATGAATTC 445
 Qy 834 GTTTCGCAATCATTAATTAAGAACTACCAAAATTAATGCTTAATTTGATTTGCTACC 893
 Db 444 GTTTCGCAATCATTAATTAAGAACTACCAAAATTAATGCTTAATTTGATTTGCTACC 385
 Qy 894 TCTTTTATTAATGAGCTGGAAGTGTCTACTTAAGACATTTAATTAAGTTATGTA 953
 Db 384 TCTTTTATTAATGAGCTGGAAGTGTCTACTTAAGACATTTAATTAAGTTATGTA 325
 Qy 954 TACATCTGAATGAAGCAAGCAAGCTTAATTAATGTTTACAGACCAAGTGTGATTCACACTG 1013
 Db 324 TACATCTGAATGAAGCAAGCAAGCTTAATTAATGTTTACAGACCAAGTGTGATTCACACTG 265
 Qy 1014 TTTTAAATCTGACATTTATTTATTTGCTTCATCAAAAGTGTTCATATTTTATTA 1073
 Db 264 TTTTAAATCTGACATTTATTTATTTGCTTCATCAAAAGTGTTCATATTTTATTA 205
 Qy 1074 GTTGTGGAATTAATCTTCTCATAGTCAATCTCTCAACCTAATTTGGAATTTGTT 1133
 Db 204 GTTGTGGAATTAATCTTCTCATAGTCAATCTCTCAACCTAATTTGGAATTTGTT 145
 Qy 1134 GTTGTCTTTGTTTCTCTTCTAGTATAGCATTTTAAATTAATTAAGCTTACATC 1193
 Db 144 GTTGTCTTTGTTTCTCTTCTAGTATAGCATTTTAAATTAATTAAGCTTACATC 85
 Qy 1194 TTTGTACATTTGTAATGTTAAGAAATTTTATATCTGTTAATTAATTAATTTTCC 1253
 Db 84 TTTGTACATTTGTAATGTTAAGAAATTTTATATCTGTTAATTAATTAATTTTCC 25
 Qy 1254 AACA 1257
 Db 24 AACA 21

RESULT 22
 BQ008675/C 796 bp mRNA linear EST 26-MAR-2002
 DEFINITION UI-H-E10-ay1-c-24-0-UI.s1 NCI CGAP_E10 Homo sapiens cDNA clone
 IMAGE:5840207 3', mRNA sequence.
 BQ008675 BQ008675.1 GI:19733576
 VERSION BQ008675.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 796)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 TITLE Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/URL at: http://image.llnl.gov
 The following repetitive elements were found in this CDNA sequence: 24-57, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
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 Location/Qualifiers
 1..796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5840207"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"

/clone.lib="NCI CGAP E10"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP E10 is a cDNA library containing the following
 tissue(s): Chondrosarcoma. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is AACTTGCAC.
 TAG TISSUE=chondrosarcoma
 TAG_LIB=UT-H-E10
 TAG_SEQ=AACTTGCAC"

ORIGIN

Query Match 55.3%; Score 695.6; DB 5; Length 796;
 Best Local Similarity 100.0%; Pred. No. 1.3e-138; Mismatches 0; Indels 0; Gaps 0;
 Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 565 GCTCACTTGGCTAAATGCAAGAAATGCTGTCAGCGTTGTAATTCACATTCAGT 624
DB 710 GCTCACTTGGCTAAATGCAAGAAATGCTGTCAGCGTTGTAATTCACATTCAGT 651
QY 625 GAGCTGAATGTCAGAGCTCTTCCCATGAAAGCTAATTTATTTGGACCAAGAGCC 684
DB 650 GAGCTGAATGTCAGAGCTCTTCCCATGAAAGCTAATTTATTTGGACCAAGAGCC 591
QY 685 CTGAATGTAATCAATTAATTAATTCATGCGACTCTCTGGAAGAGCACTTTGGAAG 744
DB 590 CTGAATGTAATCAATTAATTAATTCATGCGACTCTCTGGAAGAGCACTTTGGAAG 531
QY 745 GAATGTCGTCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
DB 530 GAATGTCGTCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
QY 805 AAGGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 864
DB 470 AAGGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
QY 865 AATAATGCTTAATTTTCACTCTTTTATTAATTAATTAATTAATTAATTAATTAAT 924
DB 410 AATAATGCTTAATTTTCACTCTTTTATTAATTAATTAATTAATTAATTAATTAAT 351
QY 925 TTAATGATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 984
DB 350 TTAATGATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 291
QY 985 TTTACAGACCAAGTGTGATTTCACTGTTTTTAATTAATTAATTAATTAATTAATTA 1044
DB 230 TTTACAGACCAAGTGTGATTTCACTGTTTTTAATTAATTAATTAATTAATTAATTA 231
QY 1045 AATCAAAAGTGTGATTTCACTGTTTTTAATTAATTAATTAATTAATTAATTAATTA 1104
DB 230 AATCAAAAGTGTGATTTCACTGTTTTTAATTAATTAATTAATTAATTAATTAATTA 171
QY 1105 TCTCTCAACCTTAATTTGGAATATGTTGGTCTTTTGTGTTTCTTGTAGTATGCA 1164
DB 170 TCTCTCAACCTTAATTTGGAATATGTTGGTCTTTTGTGTTTCTTGTAGTATGCA 111
QY 1165 TTTTAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1224
DB 110 TTTTAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 51
QY 1225 TTTATATGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1257
DB 50 TTTATATGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 18

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RESULT 23

EX114800
 LOCUS 734 bp mRNA linear EST 07-FEB-2003
 DEFINITION BX114800 Soares NhhMPU_S1 Homo sapiens cDNA clone IMAGE753428 ;
 IMAGE:753428, mRNA sequence.
 ACCESSION BX114800
 VERSION BX114800.1 GI:27879811
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 734)
 Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radloff, U., Schneider, D. and Korn, B.
 TITLE Human Unigeneset - RZPD3
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAG998F211852.
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 ML3r, primer sequence: TTTACACAGAAACACTATGAC.
 Location/Qualifiers
 1..734
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAG998F211852 ; IMAGE:753428"
 /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_host="DH10B"
 /clone.lib="Soares NhhMPU_S1"
 /note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBH, pregnant uterus 2NBHPU, and fetal heart 2NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

FEATURES

source

ORIGIN

Query Match 55.1%; Score 693.2; DB 5; Length 734;
 Best Local Similarity 98.5%; Pred. No. 4.2e-138; Mismatches 10; Indels 1; Gaps 1;
 Matches 706; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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QY 540 AGTGCCTAAGAGTTTGTGTCAGTGCCTCACTGCGCTAAATGAGAATGATGATGCTGT 599
DB 1 AGTGCCTAAGAGTTTGTGTCAGTGCCTCACTGCGCTAAATGAGAATGATGATGCTGT 60
QY 600 CAGCGTGTGATTTTCACTTCAATGAGCTGATGATGATGATGATGATGATGATGATGAT 659
DB 61 CAGCGTGTGATTTTCACTTCAATGAGCTGATGATGATGATGATGATGATGATGATGAT 120
QY 660 ATTAATTTTGGACCAAGAGCCCTGAATGATTTCAACAATTAATTAATTTGATGCTACT 719
DB 121 ATTAATTTTGGACCAAGAGCCCTGAATGATTTCAACAATTAATTAATTTGATGCTACT 180
QY 720 TCTTCTGGAAGGACTTTGTAAGGAATGATGATGATGATGATGATGATGATGATGATGAT 779

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Db 181 TCTCTGTGAGAGACTTTGGAAGAAATGTGTGATTAAGATGATTTGCTATCTGG 240
Qy 780 GTTGGGACTTGTTCAGATTACCCAAAGAGATGCTTACTGATGGAATTCAGTTCT 839
Db 241 GTTGGGACTTGTTCAGATTACCCAAAGAGATGCTTACTGATGGAATTCAGTTCT 300
Qy 840 CGCATCTATTGGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTT 899
Db 301 CGCATCTATTGGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTT 360
Qy 900 TTTATTAATGCTTGAATGTTGCTCACTTAATGACATTTTAAATTAATGTTATGATAC 959
Db 361 TTTATTAATGCTTGAATGTTGCTCACTTAATGACATTTTAAATTAATGTTATGATAC 420
Qy 960 TGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGGTGATTTCACTGTTTAA 1019
Db 421 TGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGGTGATTTCACTGTTTAA 480
Qy 1020 AATCTAGCATTAATTCATTTGCTTCATCAATCAAAAGTGTTCATAA-TTTTTTTAGTTGG 1078
Db 481 AATCTAGCATTAATTCATTTGCTTCATCAATCAAAAGTGTTCATAA-TTTTTTTAGTTGG 540
Qy 1079 TTAAGATTAATCTTCTTCATAGTCAATCTCTCAACTATTAATTTGGAATTTGTTGGT 1138
Db 541 TTAAGATTAATCTTCTTCATAGTCAATCTCTCAACTATTAATTTGGAATTTGTTGGT 600
Qy 1139 CTTTGTGTTTTCTCTTGTATGATGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1198
Db 601 CTTTGTGTTTTCTCTTGTATGATGATTTTAAATTAATTAATTAATTAATTAATTAATTA 660
Qy 1199 ACAATTTGTAATGTTAAAGATTTTATTAATCTGTTAAATTAATTAATTTTCCAA 1255
Db 661 ACAATTTGTAATGTTAAAGATTTTATTAATCTGTTAAATTAATTAATTTTCCAA 717
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RESULT 24 CA431413 723 bp mRNA linear EST 07-NOV-2002
CA431413/c LOCUS
DEFINITION UI-H-FG1-bgp-g-18-0-UI-s1 NCI CGAP FGI Homo sapiens cDNA clone
UI-H-FG1-bgp-g-18-0-UI 3', mRNA sequence.
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ACCESSION CA431413.1 GI:24794139
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 723)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
```

```
COMMENT Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Cloning Distribution: Cloning distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-57, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLY-A=yes.
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FEATURES
Source Location/Qualifiers
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1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FG1-bgp-g-18-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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/clone_lib="NCI CGAP FGI"
/notes="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR 1; Site 2: Not I;
NCI CGAP FGI is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG_TISSUE=Enchondroma cell line (Max of EN1 and EN2)
TAG_LIB=UI-H-FGI
TAG_SEQ=CGGTCACTC"
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ORIGIN

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Query Match 55.0%; Score 691; DB 6; Length 723;
Best Local Similarity 99.7%; Pred. No. 1.2e-137; Indels 1; Gaps 1;
Matches 702; Conservative 0; Mismatches 1;
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Qy 554 TTTGTCAGTGGCTCAGCTTGGCTAAATGCAAGATGATGCTGACGGTTGATTT 613
Db 720 TTTGTCAGTGG-TCAGTCGGCTAAATGCAAGATGATGCTGACGGTTGATTT 662
Qy 614 CACATTCATAGAGCTGATAGTTTCAAGACCTCTTCCATGAGCATATATTTATTTGA 673
Db 661 CACATTCATAGAGCTGATAGTTTCAAGACCTCTTCCATGAGCATATATTTATTTGA 602
Qy 674 CCAAGGAAGCCCTGAATGATTCACATTAATTAATTCATGCACTCTCTGTGGAAG 733
Db 601 CCAAGGAAGCCCTGAATGATTCACATTAATTAATTCATGCACTCTCTGTGGAAG 542
Qy 734 ACTTGTGAAGAAATGTTGCTGATTAAGTATGATGTTGCTATCTGGTTGCACTGTTTC 793
Db 541 ACTTGTGAAGAAATGTTGCTGATTAAGTATGATGTTGCTATCTGGTTGCACTGTTTC 482
Qy 794 AGATTAACCCAAAGAGAGTCTTCTACTGATGGAATTCAGTTTCTCGCATCTTAATGA 853
Db 481 AGATTAACCCAAAGAGAGTCTTCTACTGATGGAATTCAGTTTCTCGCATCTTAATGA 422
Qy 854 AGAATACCAAAATTAATGCTTTAATTTTCACTTCTTTTATTTATGCTTG 913
Db 421 AGAATACCAAAATTAATGCTTTAATTTTCACTTCTTTTATTTATGCTTG 362
Qy 914 GAATGTTCACTTAATGACATTTTAAATTAAGTTATGATTAATCTGAATGAAGCAA 973
Db 361 GAATGTTCACTTAATGACATTTTAAATTAAGTTATGATTAATCTGAATGAAGCAA 302
Qy 974 AGCTTAATATGTTTACAGACCAAGTGTGATTTACACCTGTTTAAATCTACATTAAT 1033
Db 301 AGCTTAATATGTTTACAGACCAAGTGTGATTTACACCTGTTTAAATCTACATTAAT 242
Qy 1034 CATTGTCCTCAATCAAAAGGTTTCAATATTTTATAGTTAGTTAGTAATCTTCT 1093
Db 241 CATTGTCCTCAATCAAAAGGTTTCAATATTTTATAGTTAGTTAGTAATCTTCT 182
Qy 1094 CATAGTCACATTTCTCAACCTTAATTAATTTGGAATATGTTGTGCTTTTGTTC 1153
Db 181 CATAGTCACATTTCTCAACCTTAATTAATTTGGAATATGTTGTGCTTTTGTTC 122
Qy 1154 TTAAGTATGCAATTTTAAATTAATTAAGCTACCAATCTTGTCAATTTGAATGT 1213
Db 121 TTAAGTATGCAATTTTAAATTAATTAAGCTACCAATCTTGTCAATTTGAATGT 62
Qy 1214 TTAAGATTTTATTAATCTGTTAAATTAATTAATTTTCCACA 1257
Db 61 TTAAGATTTTATTAATCTGTTAAATTAATTAATTTTCCACA 18
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RESULT 25
 BQ009009/c 724 bp mRNA linear EST 26-MAR-2002
 LOCUS UI-H-E10-aym-e-16-0-UI.s1 NCI_CGAP_E10 Homo sapiens cDNA clone
 DEFINITION IMAGE:5840631 3', mRNA sequence.
 BQ009009
 ACCESSION BQ009009.1 GI:19733903
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 724)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LIN at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 30-63, SAT_Fich#Low_complexity (matched complement)
 Seg primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source
 1..724
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5840631"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_E10"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP E10 is a cDNA library containing the following
 tissue(s): Chondrosarcoma. The library was constructed
 according to Bonaldi, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is ACACCTGCAC.
 TAG_TISSUE=chondrosarcoma
 TAG_LIB=UI-H-E10
 TAG_SEQ=ACACCTGCAC"

ORIGIN
 Query Match 54.9%; Score 690; DB 5; Length 724;
 Best Local Similarity 99.9%; Pred. No. 2e-137;
 Matches 701; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 736 TTGTGAAGGAATGTGTGTGATTAGTAGATGTTGCTATCTGGGTGGCACTTGTTCAG 795
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 Db 544 TTGTGAAGGAATGTGTGTGATTAGTAGATGTTGCTATCTGGGTGGCACTTGTTCAG 485
 |||||
 QY 796 ATTACCCAAAGAGATGCTTCTACTGTAGTAGAATTCAGTTTCTGCATCATTAATGAAG 855
 |||||
 Db 484 ATTACCCAAAGAGATGCTTCTACTGTAGTAGAATTCAGTTTCTGCATCATTAATGAAG 425
 |||||
 QY 856 AACTACCAAAATTAATGCTTTAATTTTCACTTTGCTACCTCTTTTATATAGCCTTGGCA 915
 |||||
 Db 424 AACTACCAAAATTAATGCTTTAATTTTCACTTTGCTACCTC-TTTTATATAGCCTTGGCA 366
 |||||
 QY 916 ATGGTTCACCTTAATAGACATTTAAATAGATTATGATPACATCGAATGAAGAAAG 975
 |||||
 Db 365 ATGGTTCACCTTAATAGACATTTAAATAGATTATGATPACATCGAATGAAGAAAG 306
 |||||
 QY 976 CTAAATATGTATTACAGACCAAGTGTGATTCACATGTTTAAATCTAGCATTATTCGA 1035
 |||||
 Db 305 CTAAATATGTATTACAGACCAAGTGTGATTCACATGTTTAAATCTAGCATTATTCGA 246
 |||||
 QY 1036 TTTTGCTTCATCAAAAGTGTTCATATTTTGTAGTGTGATTAATCTTCTTCA 1095
 |||||
 Db 245 TTTTGCTTCATCAAAAGTGTTCATATTTTGTAGTGTGATTAATCTTCTTCA 186
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 QY 1096 TAGTCACATCTCTCAACCTAATATTTGGAAATATGTTGGTCTTTGTTTCTCTT 1155
 |||||
 Db 185 TAGTCACATCTCTCAACCTAATATTTGGAAATATGTTGGTCTTTGTTTCTCTT 126
 |||||
 QY 1156 AGTATAGACATTTTAAATAATATTAAGCTACCATCTTTGTAGCAATTTGTAAATGTGA 1215
 |||||
 Db 125 AGTATAGACATTTTAAATAATATTAAGCTACCATCTTTGTAGCAATTTGTAAATGTGA 66
 |||||
 QY 1216 AGAATTTTATATATCTGTTAATTAATTAATTAATTTTCCACA 1257
 |||||
 Db 65 AGAATTTTATATATCTGTTAATTAATTAATTAATTTTCCACA 24
 |||||

RESULT 26
 CN394776 700 bp mRNA linear EST 16-MAY-2004
 LOCUS CN394776
 DEFINITION 1700042453311 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN394776
 VERSION CN394776.1 GI:47382371
 KEYWORDS EST.
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 700)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M.S., Mandalam, R.,
 Liebowski, J. and Stanton, L.W.
 Transcriptionome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 CONTACT: Brandenberger R
 JOURNAL Contact: Brandenberger R
 COMMENT Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert Length: 700 Std Error: 0.00.
 Location/Qualifiers
 1..700
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, embryoid bodies
 derived from H1, H7 and H9 cells"
 /clone_lib="GRN EB"
 /note="Oligo dT primed, full-length enriched cDNA library

ORIGIN

from embryoid body outgrowths derived from hbs cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

Query Match 54.6%; Score 685.8; DB 7; Length 700;
Best Local Similarity 99.7%; Pred. No. 1.6e-136;
Matches 687; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GCGCGCGGTTGAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGGAGCGCGCGGAGGC 67
DB 12 GCGCGCGGTTGAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGGAGCGCGCGGAGGC 71

QY 68 AGAGCGTTGACCAAGTTCT 127
DB 72 AGAGCGTTGACCAAGTTCT 131

QY 128 GCGCGGACCATTCGACATCCGAGGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 187
DB 132 GCGCGGACCATTCGACATCCGAGGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 191

QY 188 GCTGCT 247
DB 192 GCTGCT 251

QY 248 GCAAAAGCGGAGCT 307
DB 252 GCAAAAGCGGAGCT 311

QY 308 AGGGCGACAGAGGCT 367
DB 312 AGGGCGACAGAGGCT 371

QY 368 ACTCGGATCCGAGCTCGGAGTGAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 372 ACTCGGATCCGAGCTCGGAGTGAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431

QY 428 CTTTGAAGAGTCTGGAACCCCACTACAGCAGTGTTCATGAGATTCATGAAATTAATG 487
DB 432 CTTTGAAGAGTCTGGAACCCCACTACAGCAGTGTTCATGAGATTCATGAAATTAATG 491

QY 488 CATAGATCTTGGGAAATTTGGGAGTGAATTCATTTCAAAAGAGCTTCAAAATGAGCT 547
DB 492 CATAGATCTTGGGAAATTTGGGAGTGAATTCATTTCAAAAGAGCTTCAAAATGAGCT 551

QY 548 AAGAGTTTGTTCAGTGTCTCACTTGGCTAAATGAGAAATGATGATGTCAGCGTTG 607
DB 552 AAGAGTTTGTTCAGTGTCTCACTTGGCTAAATGAGAAATGATGATGTCAGCGTTG 611

QY 608 GTATTTCAATTCATGAGCTGAATGTTTCAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 667
DB 612 GTATTTCAATTCATGAGCTGAATGTTTCAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 671

QY 668 TTTGACCAAGAGAGCTTGAATGATTT 696
DB 672 TTTGACCAAGAGAGCTTGAATGATTT 700

RESULT 27
CA413294 716 bp mRNA linear EST 07-NOV-2002
LOCUS UI-H-E20-bap-h-20-0-UI s1 NCI CGAP Chl Homo sapiens cDNA clone
DEFINITION UI-H-E20-bap-h-20-0-UI 3', mRNA sequence.
ACCESSION CA413294
VERSION CA413294.1 GI:24775945
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 716)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contract: Robert Stransberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLY-A=Yes.

FEATURES
source

Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E20-bap-h-20-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="MDH10B (Life Technologies)"
/clone_lib="NCI CGAP Chl"
/note="Organ: Left Pelvis; Vector: pTR73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Chl is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pTR73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCGT.
TAG TISSUE=grade-2-chondrosarcoma
TAG LIB=UI-H-E20
TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 54.3%; Score 682.2; DB 6; Length 716;
Best Local Similarity 99.3%; Pred. No. 9.6e-136;
Matches 695; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 193 TCCGCTGCTGCACTCCGCGCGCGCGCTCTGAGATCCCCAAGGGAACAA 252
DB 716 TCCGCTGCTGCACTCCGCGCGCGCGCTCTGAGATCCCCAAGGGAACAA 657

QY 253 AGGCGAGCTCCGCGAGAGAGGTGTGAGCTGTATATGAAATGTCTTCAAGGCG 312
DB 656 AGGCGAGCTCCGCGAGAGAGGTGTGAGCTGTATATGAAATGTCTTCAAGGCG 597

QY 313 CAGCAGAGTCTCTGTGAGACGGAGCCCTGCGGCAATGTTATCCGGGTACACTG 372
DB 596 CAGCAGAGTCTCTGTGAGACGGAGCCCTGCGGCAATGTTATCCGGGTACACTG 537

QY 373 GGATCCAGGTCCGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
DB 536 GGATCCAGGTCCGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477

QY 433 AGGAGTCTTGAGACCCCACTACAGAGAGTTCATGAGATTCATGAGATTCATGAGATTC 492
DB 476 AGGAGTCTTGAGACCCCACTACAGAGAGTTCATGAGATTCATGAGATTCATGAGATTC 417

QY 493 ATCTTGGGAAATTTGGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
DB 416 ATCTTGGGAAATTTGGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357

QY 553 TTTTGTTCAGTGTCTCACTTGGCTAAATGAGAAATGATGATGATGATGATGATGATGAT 612
DB 356 TTTTGTTCAGTGTCTCACTTGGCTAAATGAGAAATGATGATGATGATGATGATGATGAT 297

QY 613 TCACATTCATGAGAGCTGATGTTGAGACCTCTCCATGAGCTATATATTTTGG 672
 DB 296 TCACATTCATGAGAGCTGATGTTGAGACCTCTCCATGAGCTATATATTTTGG 237
 QY 673 ACCAAGAAAGCCCTGAATGAATCAACATTAATATTCATGACCTCTCTGTTGAG 732
 DB 236 ACCAAGAAAGCCCTGAATGAATCAACATTAATATTCATGACCTCTCTGTTGAG 177
 QY 733 GACTTTGTAAGAAATGTTGCTGATTTAGTATGTTGCTATCTGGTTGGCACTTGT 792
 DB 176 GACTTTGTAAGAAATGTTGCTGATTTAGTATGTTGCTATCTGGTTGGCACTTGT 117
 QY 793 CAGATTACCCAAAGAGATGCTTCTACATGAGATGAGATTCAGTTCTCCGATCATTTAT 852
 DB 116 CAGATTACCCAAAGAGATGCTTCTACATGAGATGAGATTCAGTTCTCCGATCATTTAT 57
 QY 853 AAGAACTA-CCAAATTAATGCTTTAATTTTCAATTTGCTA 891
 DB 56 AAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTA 17
 RESULT 28
 LOCUS BQ010155/c 702 bp mRNA linear EST 26-MAR-2002
 DEFINITION UI-H-ED0-axz-f-23-0-UI.81 NCI_CGAP_ED0 Homo sapiens cDNA clone
 IMAGE:5835670 3', mRNA sequence.
 ACCESSION BQ010155
 VERSION BQ010155.1 GI:19735056
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 702)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/BLN at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 27-60, >AT rich#Low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=tes.
 FEATURES
 source Location/Qualifiers
 1..702
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5835670"
 /issue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP ED0"
 /note="Organ: Left Pubic Bone; Vector: pTT73-Pac
 (Pharmacia) with a modified polylinker; Site 1: Scov I;
 Site 2: Not I; NCI_CGAP_ED0 is a cDNA library containing
 the following tissue(s): Chondrosarcoma cell line C55. The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pTT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I

ORIGIN
 Query Match 54.3%; Score 682; DB 5; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1.1e-135; Mismatches 0; Indels 0; Gaps 0;
 Matches 682; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TAG_LIB=UI-H-ED0
 TAG_SEQ=CGTCAGGCT"
 site and the (d)18 tail. The sequence tag for this
 library is GCTCAGGCT.
 TAG_TISSUE=chondrosarcoma
 QY 576 CTAAATGAGAAATGCAATGCTGTGAGCGTTGGATTTTCAATTCATGAGCTGATGT 635
 DB 702 CTAAATGAGAAATGCAATGCTGTGAGCGTTGGATTTTCAATTCATGAGCTGATGT 643
 QY 636 TAGAGACCTCTCCATGAGACTAATTTATTTTGGACCAAGAAAGCCCTGAATGAT 695
 DB 642 TCAGACCTCTCCATGAGACTAATTTATTTTGGACCAAGAAAGCCCTGAATGAT 583
 QY 696 TCAGACCTCTCCATGAGACTAATTTATTTTGGACCAAGAAAGCCCTGAATGAT 755
 DB 582 TCAGACCTCTCCATGAGACTAATTTATTTTGGACCAAGAAAGCCCTGAATGAT 523
 QY 756 GGATTAGTGAATGCTATCTGATGCTGGTGGCACTGTTGATGATTCACCAAGAGATGCT 815
 DB 522 GGATTAGTGAATGCTATCTGATGCTGGTGGCACTGTTGATGATTCACCAAGAGATGCT 463
 QY 816 TCTACTGATGGAATTCAGTTTCTGCAATCATTTATGAAAGCTAACCAATTAATGCTT 875
 DB 462 TCTACTGATGGAATTCAGTTTCTGCAATCATTTATGAAAGCTAACCAATTAATGCTT 403
 QY 876 TTAATTTCAATTTGCTACCTCTTTTATTTATGCTGGAATGCTTCAATTAATGAT 935
 DB 402 TTAATTTCAATTTGCTACCTCTTTTATTTATGCTGGAATGCTTCAATTAATGAT 343
 QY 936 TTTAATTAAGTTTATGATATCATGATGAAAGCAAGCTAATATGTTTACAGACCA 995
 DB 342 TTTAATTAAGTTTATGATATCATGATGAAAGCAAGCTAATATGTTTACAGACCA 283
 QY 996 AAGTGTGATTCACACGTGTTTAAATCTAGCATTTATCTTTGCTTCATCAAAAGTG 1055
 DB 282 AAGTGTGATTCACACGTGTTTAAATCTAGCATTTATCTTTGCTTCATCAAAAGTG 223
 QY 1056 GTTTCATTAATTTTGTGTTGTTGTTAGAAATCTTCTCATGATGATCTCTCAACT 1115
 DB 222 GTTTCATTAATTTTGTGTTGTTGTTAGAAATCTTCTCATGATGATCTCTCAACT 163
 QY 1116 ATAAATTTGGAATATGTTGTTGTTGTTTCTTTCTTATGATGATGATTTTAAAAA 1175
 DB 162 ATAAATTTGGAATATGTTGTTGTTGTTTCTTTCTTATGATGATGATTTTAAAAA 103
 QY 1176 ATATTAAGCTACCAATCTTTGTACATTTGTAATGTTAAGAAATTTTATATCTGT 1235
 DB 102 ATATTAAGCTACCAATCTTTGTACATTTGTAATGTTAAGAAATTTTATATCTGT 43
 QY 1236 TTAATTAATTAATTTTCCACA 1257
 DB 42 TTAATTAATTAATTTTCCACA 21
 RESULT 29
 LOCUS BE607413/c 683 bp mRNA linear EST 25-FEB-2001
 DEFINITION COLONEST0306c04 colon carcinoma tissue cDNA library Homo sapiens
 CDNA, mRNA sequence.
 ACCESSION BE607413
 VERSION BE607413.1 GI:13123454
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 683)

AUTHORS Huang, Y.W., Wang, K., Zhang, J.Zh., Li, X.Y., Li, Y., Huang, D.O.,
Xie, Y., Mao, Y.M., Bao, L. and Sun, Zh.R.
TITLE Identification of genes differentially over-expressed in human
colon carcinoma using combination of SSH and cDNA microarray
analysis
JOURNAL Unpublished (2000)
COMMENT Contact: Huang Y.W.
Department of Experimental Medicine
Beijing 306 hospital, Beijing
No.9, Anxiang Beilei Road, Beijing, 100101, P.R.China
Tel: 8610-66356111
Fax: +86-10-66356111
Email: hywboy@sina.com.

FEATURES
source
1. .683
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="colon carcinoma tissue cDNA library"
/note="Organ: colon; Vector: pT Adv; Site_1: EcorI;
Site_2: EcorI"

ORIGIN
Query Match 54.2%; Score 681.4; DB 2; Length 683;
Best Local Similarity 99.9%; Pred. No. 1.4e-135;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
DB 683 ACATTACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 576 CTAATATGCAAGATGATGCTGTCAGCGTTGATTTTCACATTCATGAGCTGAATGT 635
DB 623 CTAATATGCAAGATGATGCTGTCAGCGTTGATTTTCACATTCATGAGCTGAATGT 564
QY 636 TCAGAGCCTCTCCCATTTGAAGCTATATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695
DB 563 TCAGAGCCTCTCCCATTTGAAGCTATATTTATTTGGACCAAGAAAGCCCTGAATGAAT 504
QY 696 TCAACAATTAATATTCATGCGACTTCTCTGGAAGAGACTTGGAAAGGAATGTGTCT 755
DB 503 TCAACAATTAATATTCATGCGACTTCTCTGGAAGAGACTTGGAAAGGAATGTGTCT 444
QY 756 GGATTAGATGATGTTGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGATGCT 815
DB 443 GGATTAGATGATGTTGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTTCTGCAATCATTTATTTGAAGAACTACCAAAATTAATGCTT 875
DB 383 TCTACTGATGGAATTCAGTTTCTGCAATCATTTATTTGAAGAACTACCAAAATTAATGCTT 324
QY 876 TAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAAGATGTTCACTTAATAGACAT 935
DB 323 TAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAAGATGTTCACTTAATAGACAT 264
QY 936 TTAATAATGATTATGATATCATCTGAATGAAGCAAGCTAAATATGTTTACAGACA 995
DB 263 TTAATAATGATTATGATATCATCTGAATGAAGCAAGCTAAATATGTTTACAGACA 204
QY 996 AAGGTGATTTTCAACCTGTTTAAATCTAGCATTTATTCATTTGCTTCAATCAAAAGTG 1055
DB 203 AAGGTGATTTTCAACCTGTTTAAATCTAGCATTTATTCATTTGCTTCAATCAAAAGTG 144
QY 1056 GTTTCATATTTTATTTAGTTAGTAAATCTTCTCATAGTACATTCCTCAACT 1115
DB 143 GTTTCATATTTTATTTAGTTAGTAAATCTTCTCATAGTACATTCCTCAACT 84
QY 1116 ATAATTTGGAATATGTTGCTGTTTGTGTTTCTCTTAGATATAGCAATTTTAAAAA 1175
DB 83 ATAATTTGGAATATGTTGCTGTTTGTGTTTCTCTTAGATATAGCAATTTTAAAAA 24
QY 1176 ATAATAAGCTACCAATCTTGT 1198
|||||

DB 23 ATATAAAGCTACCAATCTTGT 1

RESULT 30
BE607414 683 bp mRNA linear EST 25-FEB-2001
LOCUS
DEFINITION colonEST0306c10 colon carcinoma tissue cDNA library Homo sapiens
cDNA, mRNA sequence.
ACCESSION BE607414 GI:13123455
VERSION BE607414.1 GI:13123455
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 683)
AUTHORS Huang, Y.W., Wang, K., Zhang, J.Zh., Li, X.Y., Li, Y., Huang, D.O.,
Xie, Y., Mao, Y.M., Bao, L. and Sun, Zh.R.
TITLE Identification of genes differentially over-expressed in human
colon carcinoma using combination of SSH and cDNA microarray
analysis
JOURNAL Unpublished (2000)
COMMENT Contact: Huang Y.W.
Department of Experimental Medicine
Beijing 306 hospital, Beijing
No.9, Anxiang Beilei Road, Beijing, 100101, P.R.China
Tel: 8610-66356111
Fax: +86-10-66356111
Email: hywboy@sina.com.

FEATURES
source
1. .683
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="colon carcinoma tissue cDNA library"
/note="Organ: colon; Vector: pT Adv; Site_1: EcorI;
Site_2: EcorI"

ORIGIN
Query Match 54.2%; Score 681.4; DB 2; Length 683;
Best Local Similarity 99.9%; Pred. No. 1.4e-135;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
DB 1 ACATTACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 60
QY 576 CTAATATGCAAGATGATGCTGTCAGCGTTGATTTTCACATTCATGAGCTGAATGT 635
DB 61 CTAATATGCAAGATGATGCTGTCAGCGTTGATTTTCACATTCATGAGCTGAATGT 120
QY 636 TCAGAGCCTCTCCCATTTGAAGCTATATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695
DB 121 TCAGAGCCTCTCCCATTTGAAGCTATATTTATTTGGACCAAGAAAGCCCTGAATGAAT 180
QY 696 TCAACAATTAATATTCATGCGACTTCTCTGGAAGAGACTTGGAAAGGAATGTGTCT 755
DB 181 TCAACAATTAATATTCATGCGACTTCTCTGGAAGAGACTTGGAAAGGAATGTGTCT 240
QY 756 GGATTAGATGATGTTGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGATGCT 815
DB 241 GGATTAGATGATGTTGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGATGCT 300
QY 816 TCTACTGATGGAATTCAGTTTCTGCAATCATTTATTTGAAGAACTACCAAAATTAATGCTT 875
DB 301 TCTACTGATGGAATTCAGTTTCTGCAATCATTTATTTGAAGAACTACCAAAATTAATGCTT 360
QY 876 TAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAAGATGTTCACTTAATAGACAT 935
DB 361 TAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAAGATGTTCACTTAATAGACAT 420
QY 936 TTAATAATGATTATGATATCATCTGAATGAAGCAAGCTAAATATGTTTACAGACA 995
|||||

Db 421 TTTAAATAGTTATGTATACATCTGAATGAAAGCAAGCTAAATATGTTTACAGACCA 480
Qy 996 AAGTGTATTCACACTGTTTTTAAATCTAGCATTTATTCATTTTGGTTCATCAAGAGTG 1055
Db 481 AAGTGTATTCACACTGTTTTTAAATCTAGCATTTATTCATTTTGGTTCATCAAGAGTG 540
Qy 1056 GTTTCATATTTTTTTTACGTGGTGAATACCTTCTCATAGTCACATTCCTCAAGCT 1115
Db 541 GTTTCATATTTTTTTTACGTGGTGAATACCTTCTCATAGTCACATTCCTCAAGCT 600
Qy 1116 ATAAATTTGCAATATTTGTTGCTTTTGTCTTTTCTTCTTATATGCAATTTTAAAAA 1175
Db 601 ATAAATTTGCAATATTTGTTGCTTTTGTCTTTTCTTCTTATATGCAATTTTAAAAA 660
Qy 1176 ATATAAGCTACCAATCTTGT 1198
Db 661 ATATAAGCTACCAATCTTGT 683

RESULT 31
AL570753/c 836 bp mRNA linear EST 05-APR-2004
LOCUS AL570753 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1022YF04 3-PRIME, mRNA sequence.
ACCESSION AL570753
VERSION AL570753.3 GI:46236906
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 836)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31292170.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1022YF04&c=4941.f.
FEATURES
source
1. 836
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1022YF04"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f

Query Match 54.1%; Score 679.8; DB 1; Length 836;
Best Local Similarity 94.3%; Pred. No. 3.2e-135;
Matches 713; Conservative 4; Mismatches 37; Indels 2; Gaps 2;
ORIGIN

Qy 402 GAAAGGGGGAATGCTCTGAGGAGAGCTTGTGAGAGTCTTGACACCCCACTAACAAGCAG 461
Db 766 GAGAAAGGGGGAATGCTCTGAGGAGAGCTTGTGAGAGTCTTGACACCCCACTAACAAGCAG 707
Qy 462 TGTTCATGAGATTCATTAATTAATGCAATGATCTTGGGAAATTCGGAGGTGTACATTT 521
Db 706 TGTTCATGAGATTCATTAATTAATGCAATGATCTTGGGAAATTCGGAGGTGTACATTT 648

Qy 522 ACAAGATGCGTTCAATAGTGTCTAGAGAGTTTGTTCAGTGGCTCACTTGGGCTAAA 581
Db 647 ACAAGATGCGTTCAATAGTGTCTAGAGAGTTTGTTCAGTGGCTCACTTGGGCTAAA 588
Qy 582 TGCAGAAATGCAATGCTGTGAGGCTGTGATTTTACATTCATATGAGCTGAATGTTCAAGA 641
Db 587 TGCAGAAATGCAATGCTGTGAGGCTGTGATTTTACATTCATATGAGCTGAATGTTCAAGA 528
Qy 642 CCTCTTCCCATTTGAAGCTATATTTATTTTGAACCAAGAGGCCCTGAATGAATTCACA 701
Db 527 CCTCTTCCCATTTGAAGCTATATTTATTTTGAACCAAGAGGCCCTGAATGAATTCACA 468
Qy 702 ATTAATATTCATGCACTTCTGTGGAAGAGCTTTGGAAGAGTGTGCTGATTA 761
Db 467 ATTAATATTCATGCACTTCTGTGGAAGAGCTTTGGAAGAGTGTGCTGATTA 408
Qy 762 GTGAGATGTTGCTATCTGAGTGTGGAAGCTTTGCAATTAACCAAGAGAGATCTTCTACT 821
Db 407 GTGAGATGTTGCTATCTGAGTGTGGAAGCTTTGCAATTAACCAAGAGAGATCTTCTACT 348
Qy 822 GATGGAATTCAGTGTTCGTCATCTTATTTGAAGAACTACCAAAATTAATGCTTTAATTT 881
Db 347 GATGGAATTCAGTGTTCGTCATCTTATTTGAAGAACTACCAAAATTAATGCTTTAATTT 288
Qy 882 TCATTTGCTACTCTTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 941
Db 287 TCATTTGCTACTCTTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 228
Qy 942 TAAGTTATGTAATACATCTGAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGT 1001
Db 227 TAAGTTATGTAATACATCTGAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGT 168
Qy 1002 GATTTCACAGCTTTTAAATTTAGCATTAATTTGCTTCATCAAAAGTGTGTTTA 1061
Db 167 GATTTCACAGCTTTTAAATTTAGCATTAATTTGCTTCATCAAAAGTGTGTTTA 108
Qy 1062 AATATTTTTTTTA-GTGGTTAGAAATCTTCTTCATGACATCTCTCAACCTAATAT 1120
Db 107 AATATTTTTTTTA-GTGGTTAGAAATCTTCTTCATGACATCTCTCAACCTAATAT 48
Qy 1121 TTGGAATATGTTGTTGCTCTTTTGTGTTTCTCTTA 1156
Db 47 TTGGAATATGTTGTTGCTCTTTTGTGTTTCTCTTA 12

RESULT 32
AL553798 709 bp mRNA linear EST 30-MAR-2004
LOCUS AL553798 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1077YB01 5-PRIME, mRNA sequence.
ACCESSION AL553798
VERSION AL553798.3 GI:45858563
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31275612.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f

Query Match 54.1%; Score 679.8; DB 1; Length 836;
Best Local Similarity 94.3%; Pred. No. 3.2e-135;
Matches 713; Conservative 4; Mismatches 37; Indels 2; Gaps 2;
ORIGIN

D	b		655	GAGCTGAATGTTCAAGACCTCTTCCCATTAAGAATATA-TTANTTGACAAGAAAGCC	597
Oy			685	CTGAAATGAATTCAACAATTAATTCATCGACTCTTCTGTGGAMGAAGCTTTGTGAAG	744
D	b		596	CTGAAAATGAATTCACAATTAATTAATTCACCACTCTTCTGTGGAAAGGA-CTTTGTGAAG	537
Oy			745	GAATTGGGCGTGAATTAGTGATGATGCTATCTGGGTTGGGACCTTGTTCAATTAACCAA	804
D	b		536	GAATTGGGCGTGAATTAGTGATGATGCTATCTGGGTTGGGACCTTGTTCAATTAACCAA	477
Oy			805	AAGAGAGATGCCTTCTACTGATGATGAATTCAGTTTTCCGCATCATTATTAAGAACTACCAA	864
D	b		476	AAGAGAGATGCCTTCTACTGATGATGAATTCAGTTTTCCGCATCATTATTAAGAACTACCAA	417
Oy			865	AATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTATTAATGCTTGAATGGTTCAAC	924
D	b		416	AATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTATTAATGCTTGAATGGTTCAAC	357
Oy			925	TTAANTGACATTTTAAAAAAGCTTTATAGTATACATCTGAATGAAGAAAGCAACTAAATATG	984
D	b		356	TTAAATGACATTTTAAAAAAGCTTTATAGTATACATCTGAATGAAGAAAGCAACTAAATATG	297
Oy			985	TTTACAGACCAAGGTGATTTTCAACCTGTTTTTAAATCTAGCAATTATTCATTTTGGCTTC	1044
D	b		296	TTTACAGACCAAGGTGATTTTCAACCTGTTTTTAAATCTAGCAATTATTCATTTTGGCTTC	237
Oy			1045	AATCAAAAAGTGTTCCAATATTTTTTTTATGTTGGTGAATAATCTTCTTCATAGTCACAT	1104
D	b		236	AATCAAAAAGTGTTCCAATATTTTTTTTATGTTGGTGAATAATCTTCTTCATAGTCACAT	177
Oy			1105	TCTCTCAACCTATTAATTTGAAATATGTGTGGTCTTTTGTGTTTTTCTCTTAGATATAGA	1164
D	b		176	TCTCTCAACCTATTAATTTGAAATATGTGTGGTCTTTTGTGTTTTTCTCTTAGATATAGA	117
Oy			1165	TTTTTAAAAAAAATPTAAAGCTAACCACTTGTATCAATTTGTAAATGTPTAAGAAATTTT	1224
D	b		116	TTTTTAAAAAAAATPTAAAGCTAACCACTTGTATCAATTTGTAAATGTPTAAGAAATTTT	57
Oy			1225	TTTATATCTGTTAAATATMAAAATTAATTTTCCAACA	1257
D	b		56	TTTATATCTGTTAAATATMAAAATTAATTTTCCAACA	24
RESULT	34				
LOCUS	BM915288		1099 bp	mRNA	linear EST 12-MAR-2002
DEFINITION	AGENCOURT_6702310 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:5481457				
ACCESSION	BM915288				
VERSION	BM915288.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTP				
TITLE	CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
JOURNAL	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov				
COMMENT	Plate: LNCM2005 row: p column: 02 High quality sequence start: 26 High quality sequence stop: 565. Location/Qualifiers 1..1099				
FEATURES					
SOURCE					

Query Match	Best Local Match	Similarity	Score	DB	Length
Matches	738;	Conservative	0;	Mismatches	23;
				Indels	6;
				Gaps	4;
51	CGAGCCGCGCGAGCCAGACGCTGACCCAGCTTCTCTCTCGGTCCTCCGCTCCAG	110			
12	CGAGCCGCGCGAGCTAGACGCTGACCCAGCTTCTCTCTCGGTCCTCCGCTCCAG	71			
111	CTCGCGCTCGCGCGCGAGCCAGATGAGACCCAGAGGCGCGCGCGCTCCCGCGAG	170			
72	CTCGCGCTCGCGCGCGAGCCAGATGAGACCCAGAGGCGCGCGCTCCCGCGAG	131			
171	CGGCTCGCGCGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	230			
132	CGGCTCGCGCGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	191			
231	GAGATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	290			
192	GAGATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	251			
291	AATGGAATGCTTACAAAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	350			
252	AATGGAATGCTTACAAAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	311			
351	AATGGAATGCTTACAAAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	410			
312	AATGGAATGCTTACAAAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	371			
411	GAAATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	470			
372	GAAATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	431			
471	AGTTCATGATTTAATGAGATGATCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG	530			
432	AGTTCATGATTTAATGAGATGATCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG	491			
531	CGTTCATGATTTAATGAGATGATCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG	590			
492	CGTTCATGATTTAATGAGATGATCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG	551			
591	GCAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	650			
552	GCAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	611			
651	AATGGAATGCTTACAAAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	709			
612	AATGGAATGCTTACAAAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	671			
710	TCATGCG-ACCTTCT	767			
672	TCATGCG-ACCTTCT	731			
768	GTTCGATCT	811			
732	GTTCGATCT	778			

RESULT 35
BOG48112 986 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT 8507019 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297812
DEFINITION 5' mRNA sequence.
ACCESSION BOG48112.1 GI:21772284
VERSION BOG48112.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 986)
AUTHORS NIH-MGC http://mgi.mgi.mgc.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2507 row: n column: 21
High quality sequence stop: 520.
Location/Qualifiers
1..986
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6297812"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_100"
/note="Organ: liver; Vector: pOTB7, Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 53.5%; Score 672.6; DB 5; Length 986;
Best Local Similarity 96.8%; Pred. No. 1.2e-133;
Matches 698; Conservative 0; Mismatches 19; Indels 4; Gaps 1;

QY 37 GCGTCGCGCGCTCGAGCGCGCGCGAGCCAGACGCTGACCACTTCTCTCTCGGTC 96
DB 1 GCGTCGCGCGCTCGAGCGCGCGCGAGCCAGACGCTGACCACTTCTCTCTCGGTC 60
QY 97 TCTTCGCGCTCGAGCTCGCGCTCGCGCGAGCCAGACGCTGACCACTTCTCTCTCGGTC 156
DB 61 TCTTCGCGCTCGAGCTCGCGCTCGCGCGAGCCAGACGCTGACCACTTCTCTCTCGGTC 120
QY 157 CCGGCTCGCGCGAGCGCGCTCGCGCGCTCGGTCCTGCTGTCGAGCTGCGCGGCGC 216
DB 121 CCGGCTCGCGCGAGCGCGCTCGCGCGCTCGGTCCTGCTGTCGAGCTGCGCGGCGC 180
QY 217 CGTGAAGCGCTCTGAGATCCCAAGAGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGG 276
DB 181 CGTGAAGCGCTCTGAGATCCCAAGAGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGG 240
QY 277 TGGTGAAGCTGTATTAATGGAATGCTTAAAGAGGCGCAGAGAGTGCCTGCTGAGAGG 336
DB 241 TGGTGAAGCTGTATTAATGGAATGCTTAAAGAGGCGCAGAGAGTGCCTGCTGAGAGG 300
QY 337 GAGAGCTTGGGGCAATGTATTTCGGGTACACCTGGGATCCAGGTGGGATGATTC 396

DB 301 GAGAGCTTGGGGCAATGTATTTCGGGTACACCTGGGATCCAGGTGGGATGATTC 360
QY 397 AAGAGGAAAGAGGGAATGCTGAGGGAAGCTTTGAGAGTCTTGACACCCAACTACA 456
DB 361 AAGAGGAAAGAGGGAATGCTGAGGGAAGCTTTGAGAGTCTTGACACCCAACTACA 420
QY 457 AGCAGTGTTCATGAGAGTTCATTTAATGAGCTAGATCTTGGGAAATTTGGGAGTGA 516
DB 421 AGCAGTGTTCATGAGAGTTCATTTAATGAGCTAGATCTTGGGAAATTTGGGAGTGA 480
QY 517 CATTTACAAAGATGCTTCAATATGAGTCTTAAAGAGTTTGTTCAGTGCCTCAGC 576
DB 481 CATTTACAAAGATGCTTCAATATGAGTCTTAAAGAGTTTGTTCAGTGCCTCAGC 540
QY 577 TAAATGAGAAAGATGCTTCAATATGAGTCTTAAAGAGTTTGTTCAGTGCCTCAGC 636
DB 541 TAAATGAGAAAGATGCTTCAATATGAGTCTTAAAGAGTTTGTTCAGTGCCTCAGC 600
QY 637 CAGACCTCTTCCATTTAGAGCTTAAATTTATTTGACCAAGGAGCCCTGAATGAT 696
DB 601 CAGACCTCTTCCATTTAGAGCTTAAATTTATTTGACCAAGGAGCCCTGAATGAT 660
QY 697 CAACATTAATATTCATC---GCATCTTCTTGTGAGAGACTTTGTGAAGGAATGCT 752
DB 661 CAACATTAATATTCATC---GCATCTTCTTGTGAGAGACTTTGTGAAGGAATGCT 720
QY 753 G 753
DB 721 G 721

RESULT 36
BX386416 707 bp mRNA linear EST 27-APR-2004
LOCUS BX386416
DEFINITION BX386416 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1077YB01 5-PRIME, mRNA sequence.
ACCESSION BX386416.2 GI:46627527
VERSION BX386416
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 707)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30457424.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4941.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS1A1020B01Q1&c=4941.f.
Location/Qualifiers
1..707
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1077YB01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Db 323 GGATGATTCMAAGGGGAAAAAGGAGATGCTTAAAGGAAAGCTTTGAGGAGTCTTGAC 382
 QY 446 ACCCACTCAAGACAGTGTTCATGAGTTCATGATTAATGATGATCTTGAGAAAT 505
 Db 383 CCGAAACCTAATGACAGTGTTCGAGTTCGCTGAACTATGAGATGATCTTGAGAAAT 442
 QY 506 TCCGAGGTACATTTACAAAGATGCGTTCATTAATGCTTAAGATTTGTTGTCAGTG 565
 Db 443 TCCGAGGTACATTTACAAAGATGCGTTCATTAATGCTTAAGATTTGTTGTCAGTG 502
 QY 566 CTCACCTGCGCTAAATGAGAAATGATGCTGTCAGCGTGTGATTTACATTCATG 625
 Db 503 CTCGCTTCGCGCTAAATGAGAAATGATGCTGTCAGCGTGTGATTTACATTCATG 562
 QY 626 AGCTGAATGTCAGGACCTTCCCATTAAGATTAATTAATTTGAGACCAAGAGAGCC 685
 Db 563 AGCTGAATGTCAGGACCTTCCCATTAAGATTAATTAATTTGAGACCAAGAGAGCC 622
 QY 686 TGAATGAATTCACCAATTAATTAATGATGCTGTCAGCGTGTGATTTACATTCATG 745
 Db 623 TGAATGAATTCACCAATTAATTAATGATGCTGTCAGCGTGTGATTTACATTCATG 682
 QY 746 AATTGCTGCTGATTAAGATGATGCTGTCAGCGTGTGATTTACATTCATTCACCA 805
 Db 683 GATGCTGCTGATTAAGATGATGCTGTCAGCGTGTGATTTACATTCATTCACCA 742
 QY 806 AGAGATGCTGCTGATTAAGATGATGCTGTCAGCGTGTGATTTACATTCATTCACCA 865
 Db 743 AGAGATGCTGCTGATTAAGATGATGCTGTCAGCGTGTGATTTACATTCATTCACCA 802
 QY 866 AATAATGCTTAA--TTTTCAATTTGCTACCT-----CTTTTATTAATGCTTGAAT 917
 Db 803 AATAATGCTTAA--TTTTCAATTTGCTACCT-----CTTTTATTAATGCTTGAAT 862
 QY 918 GGTTCATTAATGATGATTT-----TAAATAATTAATGATGATGCTTGAATG--AAAG 970
 Db 863 GGTTCATTAATGATGATTT-----TAAATAATTAATGATGATGCTTGAATG--AAAG 922
 QY 971 CAAAGTAAATGATGATTTACAGACCAAGATGATTTACAGCTTTTAAATTAATGATG 1030
 Db 923 CAAAGTAAATGATGATTTACAGACCAAGATGATTTACAGCTTTTAAATTAATGATG 979
 QY 1031 ATTCAATTTGCTCAATCAAAAGTGTTCATTAATTTTATTTAGTGTGTTA 1081
 Db 980 AACCAATTTATTCACCAAGATGATGCTTCAATTTTATTTATTTATTTA 1030
 RESULT 39
 BQ005403/c 723 bp mRNA linear EST 26-MAR-2002
 LOCUS UI-H-E11-a2h-m-17-0-UI.s1 NCI_CGAP_E11 Homo sapiens cDNA clone
 DEFINITION IMAGE:5848888 3', mRNA sequence.
 ACCESSION BQ005403
 VERSION BQ005403.1 GI:19730303
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 723)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/BLN at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA

sequence: 30-62, >AT rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLA=Yes.
 FEATURES
 source
 Location/Qualifiers
 1..723
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="5848888"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP E11"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
 AACTTGCAC.
 TAG_TISSUE=chondrosarcoma
 TAG_LIB=UI-H-E11
 TAG_SEQ=AACTTGCAC"
 ORIGIN
 Query Match 52.1%; Score 655.4; DB 5; Length 723;
 Best Local Similarity 99.4%; Pred. No. 5,4e-130;
 Matches 689; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
 QY 565 GCTCACTTGGCTAAATGCAAAATGCAATGCTGTCAGCGTGTGATTTACATTCATG 624
 Db 713 GCTCACTTGGCTAAATGCAAAATGCAATGCTGTCAGCGTGTGATTTACATTCATG 654
 QY 625 GAGCTGAATGTCAGACCTCTCCCATTAATGATTAATTTATTTGACCAAGAGCC 684
 Db 653 GAGCTGAATGTCAGACCTCTCCCATTAATGATTAATTTATTTGACCAAGAGCC 594
 QY 685 CTGAATGAATCAACAATTAATTTACATTCAGACTTCTTCTGGAAGACCTTTGGAAG 744
 Db 593 CTGAATGAATCAACAATTAATTTACATTCAGACTTCTTCTGGAAGACCTTTGGAAG 534
 QY 745 GAATGCTGCTGATTAAGATGATGCTGTCAGCGTGTGATTTACATTCATTCACCA 804
 Db 533 GAATGCTGCTGATTAAGATGATGCTGTCAGCGTGTGATTTACATTCATTCACCA 474
 QY 805 AAGAGATGCTTCTACATGATGAATTCAGTTCCTGCAATCAATTAATGAAGACCA 864
 Db 473 AAGAGATGCTTCTACATGATGAATTCAGTTCCTGCAATCAATTAATGAAGACCA 414
 QY 865 AATAATGCTTAAATTTTATTTGCTACCTCTTTTATTAATGCTTGAATGCTTGC 924
 Db 413 AATAATGCTTAAATTTTATTTGCTACCTCTTTTATTAATGCTTGAATGCTTGC 354
 QY 925 TTAATGAATTTTAAATTAATGATTAATGATGATGATGATGATGATGATGATGATG 984
 Db 353 TTAATGAATTTTAAATTAATGATTAATGATGATGATGATGATGATGATGATGATG 294
 QY 985 TTAAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1044
 Db 293 TTAAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 234
 QY 1045 AATCAAAAGTGTTCATTAATTTTATTTAGTGTGATGAATCTTTCTTCAATGACAT 1104
 Db 233 AATCAAAAGTGTTCATTAATTTTATTTAGTGTGATGAATCTTTCTTCAATGACAT 174
 QY 1105 TCTTCAACCTAATTAATTTGATTAATTTGATGATGATGATGATGATGATGATGATG 1164

Db	173	TCTTCACACTTAATTT-GAATATTGTTGG-CTTTTGTITTTTCTTGATAGCA	116
Oy	1165	TTTTTAAATAATATAAGCTACCATCTTTGTACAATTTGTAAATTTT	122
Db	115	TTTTTAAAAAATATATAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGA-TTTT	57
Oy	1225	TTTATATCTGTTAAATATAAATATATTCCAAC	1257
Db	56	TTTATATCTGTTAAATATAAATATATTCCAAC	24
RESULT 40			
AKO76498	1166	hd MRNA linear HTC 03-APR-2000	
LOCUS			
DEFINITION	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:483429011 product:hypothetical Collagen triple helix repeat containing protein, full insert sequence.		
ACCESSION	AKO76498.1	GJ:26096845	
VERSION			
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
JOURNAL MEDLINE	High-efficiency full-length cDNA cloning		
PUBMED	99279253		
REFERENCE	Meeth. Enzymol. 303, 19-44 (1999)		
AUTHORS	10349636		
JOURNAL MEDLINE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
PUBMED	Normaliza-tion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	11042159		
JOURNAL MEDLINE	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashtou, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasliwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawat, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer			
Genome Res. 10 (11), 1757-1771 (2000)			
20530913			
11076861			
JOURNAL MEDLINE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
PUBMED	Functional annotation of a full-length mouse cDNA collection		
REFERENCE	Nature 409, 685-690 (2001)		
AUTHORS	5		
JOURNAL MEDLINE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II team.		
PUBMED	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
REFERENCE	Nature 420, 563-573 (2002)		
AUTHORS	6 (bases 1 to 1168)		
JOURNAL MEDLINE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizmoto, K., Hirooka, T., Hitozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawari, J., Kojima, Y., Komno, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohtsuo, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,		

TITLE	Toogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama kangawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/. Location/Qualifiers
FEATURES	source 1..1168 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:4833429011" /db_xref="taxon:10090" /clone="4833429011" /tissue_type="head" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" 76..814 /note="hypothetical Collagen triple helix repeat containing protein (InterPro IPR000087, evidence: InterPro) putative" 1148..1153 /note="putative" 1168 /note="putative"
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Query Match	51.8%; Score 651.6; DB 3; Length 1168;
Best Local Similarity	78.3%; Pred. No. 3.8e-129;
Matches 878; Conservative	0; Mismatches 219; Indels 25; Gaps 7;
Db	92 CGGTCTCCCGCCGCTTCAGACTCCGGCGGCCGCGACGCCGGAAGCATGCACCCCACAGG 151
Db	30 CCGACCCTTTAATCTTCTGCTCCGCGCTTCGACGCCACCATGCAACCCCCAAAG 89
Db	152 CCCGCGCCCTCCCGCCAGCGGCTCCGCGG-----CCTCTGCTGCTCTCTGCTTGCA 205
Db	90 CCGCGCGGCCCCCGCGAGCTGCTCTCGGCTCTTCTTGTGGTGGTGGTGGTGGTACA 149
Db	206 GTGCCCCCGCGCTGAGCGCTCTGAGATCCCAAAGGGAAGCAAAAGCGCAAGTCCG 265
Db	150 GTTGTCCGACCGATCAACGCGCTCTGAGAACCCCAAGGTGAAGCAAAAAGCGCTGATCCG 209
Db	266 GCAGAGGAGGTGTGGAAGCTGTATAATGAGATGCTTAACAAGGCGCAGAGAGTAGTC 325
Db	210 GCAAGGAGAGGTGTGAGACTGTATATAGATGTGTCTTCAAGAGCACAGAGAGATTCC 269
Db	326 TGCTGAGACGGAGACCCCTGGGCGCAATGTATTCTCCGGTACACCTGGGATCCAGGTG 385
Db	270 CGGTGTATGGGAGACCTTG6GGGCGAAGGCAATTCCTGGCACAACCTGGATCCAGGTG 329
Db	386 GGATGGATTCCAAGAGAAAAAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTCTTGAC 445
Db	330 GGATGGATTCCAAGGGGAAAAAGGGGGAATGTCTTAAGGGAAGGCTTTGAGAGTCTTGAC 389
Db	446 ACCCAATCAAGAGAGTGTATGAGAGTTCATTGAATATAGGCADATGCTTGGGAAAT 505
Db	390 CCCAATCAAGAGAGTGTGTGAGAGTTCCTGTAATCTATGACATATGATCTTGGGAAAT 449

[illegible]

FEATURES
source 1. 671
Location/Qualifiers
from Dr. M. Bento Soares, bento-soares@uol.com.br
The following repetitive elements were found in this CDNA
sequence: 1-28 >AT rich#low_complexity
Seq primer: M13 FORWARD
PolyA=Yes.

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/clone_1b="NCI CGAP FG1"
/note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: BclR I; Site 2: Not I;
NCI CGAP FG1 is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an BclR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG TISSUE=Enchondroma cell line (Mx of EN1 and EN2)
TAG_LIB=UI-H-FG1
TAG_SEQ=CGGTCACTC"

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ORIGIN

Query Match	51.7%	Score 649.8;	DB 5;	Length 671;
Best Local Similarity	99.5%	Pred. No. 8.6e-129;		
Matches 651; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	23	GAGATCCCAAGGGGAAGCAAAAGCCGAGCTCCGGCAGAGGAGTGTGTGACCTGTAT	299
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Qy	291	AATGAGATGTGCTTACAAAGGCGCAGCAGAGTGCTCCGTGTGAGACGGAGGCTTGGGACC	356
Db	611	AATGAGATGTGCTTACAAAGGCGCAGCAGAGTGCTCCGTGTGAGACGGAGGCTTGGGACC	552
Qy	351	AATGTTATTCCGGGTACACCTGTGGATCCCAAGTCGGGATGGAATTCAAAGAGAAAGGGG	410
Db	551	AATGGCATTTCCGGGTACACCTGGGATCCCAAGTCGGGATGGAATTCAAAGAGAAAGGGG	492
Qy	411	GAATGTCTAGGGGAAGCTTTAGAGAGTCTGGACACCACTACAAAGCAGTGTTCATGG	476
Db	491	GAATGTCTAGGGGAAGCTTTAGAGAGTCTGGAGACCCAACTACAAAGCAGTGTTCATGG	433
Qy	471	AGTTCAATTGAATTATGCGATAGACTTGGGAAATTTGGGAGTGCATTTACAAAGATG	530
Db	431	AGTTCAATTGAATTATGCGATAGACTTGGGAAATTTGGGAGTGCATTTACAAAGATG	372
Qy	531	CGTTCAATATAGTGTCTAAAGATTTTGTTCAGTGGCTCATTTGGGCTPAAAATGCAAAAT	596
Db	371	CGTTCAAAATAGTGTCTTAAGATTTTGTTCAGTGGCTCATTTGGGCTPAAAATGCAAAAT	312
Qy	591	GCATGCTGTCAAGGTGTGGTATTCACATTCATGATGAGCTGAATGTGAGACCTCTCCG	656
Db	311	GCATGCTGTCAAGGTGTGGTATTCACATTCATGATGAGCTGAATGTGAGACCTCTCTCC	252
Qy	651	ATTGAAGCTATATTAATTATTTGACCAAGGAAGCCCTGAAATGAATTCACAATTAATATT	710
Db	251	ATTGAAGCTATATTAATTATTTGACCAAGGAAGCCCTGAAATGAATTCACAATTAATATT	192
Qy	711	CATCGCACTTCTTGTGTGAGAGACTTTGTGAAGAAATTGGTGTGCAATTATGTGAATGTT	770

Db 191 CATCGCACTTCTTCTGTGGAGAGACTTTGTGAAGAAATGTCGATTAATGATGATTT 132
Qy 771 GCTATCTGGGTTGGAGCTTGTTCAGATTAACCAAAAGAGATGCTTCTAATGATGAT 830
Db 131 GCTATCTGGGTTGGAGCTTGTTCAGATTAACCAAAAGAGATGCTTCTAATGATGAT 72
Qy 831 TCAGTTTCTCGCATCATTAATTAAGAACTACCAAAATAATGCTTAAATTTTCA 884
Db 71 TCAGTTTCTCGCATCATTAATTAAGAACTACCAAAATAATGCTTAAATTTTCA 18
RESULT 42
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LOCUS 601276538F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617432 5',
DEFINITION mRNA sequence.
ACCESSION BE87335
VERSION BE87335.1 GI:9332700
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 688)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L16M264 row: 1 column: 09
High quality sequence start: 10
High quality sequence stop: 686.
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/note="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 51.1%; Score 641.8; DB 2; Length 688;
Best Local Similarity 99.5%; Pred. No. 4.5e-127;
Matches 654; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 GGAAGAGAGCGCGCGGTGAAGAGCGCATTAATGAGCTGCGCGCTCGAGCGCGG 60
Db 33 GGAAGAGAGCGCGCGGTGAAGAGCGCATTAATGAGCTGCGCGCTCGAGCGCGG 92
Qy 61 CGAGAGCGAGCGCTGACACGCTTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 93 CGAGAGCGAGCGCTGACACGCTTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 152
Qy 121 CCGGAGCGCGGAGCGCATTAATGAGCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 153 CCGGAGCGCGGAGCGCATTAATGAGCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 212

Qy 181 GCTCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 213 GCTCTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272
Qy 241 AGGGAGCAAAAGGCGAGCTTCCGCGAGAGAGAGTGTGAGCTGTATTAATGAAATGT 300
Db 273 AGGGAGCAAAAGGCGAGCTTCCGCGAGAGAGAGTGTGAGCTGTATTAATGAAATGT 332
Qy 301 GCTTCAAGGGCGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 333 GCTTCAAGGGCGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
Qy 361 CGGATGACCTTGGATCCAGAGTGGAGTGTGATTAAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 393 CGGATGACCTTGGATCCAGAGTGGAGTGTGATTAAGAGAGAGAGAGAGAGAGAGAGAG 452
Qy 421 GGGAAAGCTTTGAGAGAGTCTGGAACCCAACTTCAAGAGAGAGAGAGAGAGAGAGAG 480
Db 453 GGGAAAGCTTTGAGAGAGTCTGGAACCCAACTTCAAGAGAGAGAGAGAGAGAGAGAG 512
Qy 481 ATTATGATGATCTTGGGAAATTTGGAGAGTGTATTAATTAAGAGAGAGAGAGAGAGAG 540
Db 513 ATTATGATGATCTTGGGAAATTTGGAGAGTGTATTAATTAAGAGAGAGAGAGAGAGAG 572
Qy 541 GTGCTTAAAGATTGTTGTCAGTGTGCTCATTGCTTAAATGAGAGAGAGAGAGAGAG 600
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DEFINITION mRNA sequence.
ACCESSION BE896915
VERSION BE896915.1 GI:10361827
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 688)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L16M9762 row: 1 column: 09
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 51.0%; Score 641; DB 2; Length 688;

Best Local Similarity 98.8%; Pred. No. 6,7e-127; Matches 677; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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Oy 23 GCGCATTTGATGACAGCTTGGCGGCTCGGAGCGGCGGAGCCAGACGCTGACCACT 82
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Oy 83 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142
Db 62 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
Oy 143 ACCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
Db 122 ACCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
Oy 203 GCGAGTGGCGCGCGCGCGCGCGCGCGCGCTCTGAGATCCCGAGGAGGAGGAGGAGG 262
Db 182 GCGAGTGGCGCGCGCGCGCGCGCGCGCGCTCTGAGATCCCGAGGAGGAGGAGGAGG 241
Oy 263 CCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 322
Db 242 CCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301
Oy 323 GCGTGTGAGAGCGGAGGCGCTGGGCGCAATGTTATTCGGGGTACACCTGGGATCCCA 382
Db 302 GCGTGTGAGAGCGGAGGCGCTGGGCGCAATGTTATTCGGGGTACACCTGGGATCCCA 361
Oy 383 TCGGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 442
Db 362 TCGGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
Oy 443 GACACCCAACTACAGACAGTGTTCATGAGATTCATGAGATTCATGAGATTCATG 502
Db 422 GACACCCAACTACAGACAGTGTTCATGAGATTCATGAGATTCATGAGATTCATG 481
Oy 503 AATTGGGAGGATGATTCATGAGATTCATGAGATTCATGAGATTCATGAGATTCAT 562
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Oy 623 TGGAGCTGATGATTCAGAGCTTCTTCATGAGCTATGATGATGATGATGATGATGAT 681
Db 600 TGGAGCTGATGATTCAGAGCTTCTTCATGAGCTATGATGATGATGATGATGATGAT 659
Oy 682 GCCCTGAATGATTCATGATTCATGATTCATGATTCATGATTCATGATTCATGAT 706
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RESULT 44

LOCUS BX386415 670 bp mRNA linear EST 27-APR-2004

DEFINITION BX386415 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

ACCESSION BX386415

VERSION BX386415.2 GI:46622720

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 670) Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.

TITLES Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 8, 2003 this sequence version replaced gi:30455436.

Genoscope - Centre National de Sequencage

BP 191 9106 Evry cedex - France

Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

4941.f

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdnaf/b=CS1A1020B01NP1&c=4941.f>.

Location/Qualifiers

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/note="1st strand cDNA was primed with a NotI-oligo (dt)

primer. Five prime end enriched, double-strand cDNA was

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sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 50.6%; Score 636.4; DB 5; Length 670;

Best Local Similarity 98.0%; Pred. No. 6.5e-126; Matches 643; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Oy 179 CGGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 238
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Oy 229 CAAGGGAGACAAAGGGCGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 298
Db 609 CAAGGGAGACAAAGGGCGAGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 550
Oy 229 GTGCTTACAAAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 358
Db 549 GTGCTTACAAAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 490
Oy 359 TCCGGGTACACTGGAGATCCAGAGTCCGAGATGATTCAGAGAGAGAGAGAGAGAG 418
Db 489 CCGGGGTACACTGGAGATCCAGAGTCCGAGATGATTCAGAGAGAGAGAGAGAGAG 430
Oy 419 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478
Db 429 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 370
Oy 479 GAAATTATGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
Db 369 GAAATTATGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310
Oy 539 TAGTCTCTAAGAGATTTGTTCAAGTGTCACTTCCGCTAAAGATGAGAGATGAGT 598
Db 309 TAGTCTCTAAGAGATTTGTTCAAGTGTCACTTCCGCTAAAGATGAGAGATGAGT 250
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Db 249 TCAGCGTTGATTTTCAATTCATGAGAGTGTTCAGAGAGTGTTCAGAGAGTGTTCAG 190
Oy 659 TATAATTATTTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
Db 189 TATAATTATTTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
Oy 719 TTCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778
Db 129 TTCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
Oy 779 GGTGGCACTTGTTCAGATTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834
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RESULT 45
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 DEFINITION UI-H-FG1-bj1-j-13-0-UI 3', mRNA sequence.
 ACCESSION BU624261
 VERSION BU624261.1 GI:23290476
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 654)
 NCICGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-28, >AT-rich#Low_complexity
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

1..654
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 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FGI"
 /note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FGI is a normalized cDNA library obtained from a
 pool of mRNA from 2 cell lines from Enchondroma tissues.
 The library was constructed according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is CGGTCACTC. The cell lines were provided by Dr.
 James Martin from the University of Iowa.
 TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
 TAG_LIB=UI-H-FGI
 TAG_SEQ=CGGTCACTC"

ORIGIN

Query Match 50.4%; Score 633.8; DB 5; Length 654;
 Best Local Similarity 99.7%; Pred. No. 2,3e-125;
 Matches 635; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 248 GCAAAAGGCGGCGACTCCGAGAGGAGGCTGTGACCTGTATATAGTAATGTCTTACA 307
 DB 654 GCAAAAGGCGGCGACTCCGAGAGGAGGCTGTGACCTGTATATAGTAATGTCTTACA 595
 QY 308 AGGCGCAGCAGAGTGCTGTGTGAGAGCGGAGCCCTGAGGCAATGTATATCCGGGTAC 367
 DB 594 AGGCGCAGCAGAGTGCTGTGTGAGAGCGGAGCCCTGAGGCAATGTATATCCGGGTAC 535
 QY 368 ACCTGGAGTCCAGGTCGGAGTGATTCAGAGAAAGGGGGAATGTCTGAGGGGAAG 427

DB 534 ACCTGGAGTCCAGGTCGGAGTGATTCAGAGAAAGGGGGAATGTCTGAGGGGAAG 475
 QY 428 CTTTGAGAGTCTGTGACACCCCACTACAGAGAGTTCATGAGTGAATTAATG 487
 DB 474 CTTTGAGAGTCTGTGACACCCCACTACAGAGAGTTCATGAGTGAATTAATG 415
 QY 488 CATGATCTTGGGAAATTCGCGAGTGTACATTTA CAAAGATGCGTTCAATAGTCTCT 547
 DB 414 CATGATCTTGGGAAATTCGCGAGTGTACATTTA CAAAGATGCGTTCAATAGTCTCT 355
 QY 548 AAGAGTTTGTTCAGTGTCTCACTTGGCTTAATATGCAAAATGATGTCGACCGT 607
 DB 354 AAGAGTTTGTTCAGTGTCTCACTTGGCTTAATATGCAAAATGATGTCGACCGT 295
 QY 608 GTATTTCACTTAATAGAGGCTGAATGTCAGACCTCTCCCATTTGAAGCTATATTTA 667
 DB 294 GTATTTCACTTAATAGAGGCTGAATGTCAGACCTCTCCCATTTGAAGCTATATTTA 235
 QY 668 TTTGACCAAGAGGCTGTGAAATGAAATTCACAAATTAATTCATTCGACTTCTTCTGT 727
 DB 234 TTTGACCAAGAGGCTGTGAAATGAAATTCACAAATTAATTCATTCGACTTCTTCTGT 175
 QY 728 GGAAGACTTTTGGAAGAAATTTGCTGATTAAGATGTTGCTATCGGTTGGGAC 787
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 QY 788 TTTGTCAGATTACCAAAAGAGATGCTTCACTGAGTGAATTCAGTTTCTCGCATAT 847
 DB 114 TTTGTCAGATTACCAAAAGAGATGCTTCACTGAGTGAATTCAGTTTCTCGCATAT 55
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 DB 54 TATGAGAACTACCAAAATTAATGCTTTAATTTCA 18

RESULT 46
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 LOCUS AL553771 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1077YB01 3-PRIME, mRNA sequence.
 AL553771
 ACCESSION AL553771.3 GI:45858536
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 676)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31275585.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4941.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/s=CS0D1077CA01NP1&c=4941.f>.

FEATURES

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 DEFINITION mRNA sequence.
 ACCESSION BG421228
 VERSION BG421228.1 GI:13327734
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1023)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNC1324 row: f column: 05
 High quality sequence stop: 679.
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 /clone_1ib="NIH MGC 14"
 /note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN
 Query Match 48.2%; Score 606.2; DB 4; Length 1023;
 Best Local Similarity 91.3%; Pred. No. 2.1e-119;
 Matches 722; Conservative 0; Mismatches 58; Indels 11; Gaps 7;

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 QY 300 TGGTTACAAGGGCCACAGAGAGTGCCTGTGTGAGACGGGAGCCCTGGGGCCAAATTAT 359
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 QY 360 CCGGGTACACCTGGGATCCAGGTGGGATGGAATTCAAGAGAAAGGGGAAATGCTG 419
 DB 377 CCGGGTACACCTGGGATCCAGGTGGGATGGAATTCAAGAGAAAGGGGAAATGCTG 436
 QY 420 AGGAAAGCTTTGAGAGTCTTGACACCCAACTACAGAGTGTTCATGAGTTTCATTG 479
 DB 437 AGGAAAGCTTTGAGAGTCTTGACACCCAACTACAGAGTGTTCATGAGTTTCATTG 496
 QY 480 A-ATTATGCAATGATCTTGGGAAA--TTGGGAGGTACATTACAAAGATGCTG 535
 DB 497 ACATTATGGCATGATCTTGGGAAAATTGCCGAGGTGTACATTACAAAGATGCTG 556
 QY 536 --AAATAGTCTTAAGAGTGTTCAGTGTCTCATCTTGGCTTAAATGCAAGAAATGCA 593
 DB 557 CAATATAGTCTTAAAGATTTTGTCCAGTGTCTTGGCTTAAATGCAAGAAATGCA 616
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 DB 617 TTGCTGCACGCTGGGATTTTCAATTCAATGAGCTGAATGTGAGAACCTTCCCAT 676
 QY 653 TGA--GCTTATATTTATTTGGACCAAGAGAGCCCTGAATATTTCAATTAATAT 710
 DB 677 TGAAGGCTATATTTACTTGGGACCAAGAGAGCCCTGAATATTTCAATTAATAT 736
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 DEFINITION AGENCOURT 11289616 NIH_MGC_135 Mus musculus cDNA clone
 IMAGE:30140382 5', mRNA sequence.
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 VERSION CB201936.1 GI:28236469
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 849)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. David Rowe
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDAM0046 row: f column: 07
 High quality sequence stop: 710.
 Location/Qualifiers
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 /clone="IMAGE:30140382"

FEATURES

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Qy		963	ATGAAAAGCAAGCTAAATATGTTTACGACCAAGTGATTCACAGCTGTTTAA	1022
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Qy		1083	AATACCTTCTTCATAGTACATTTCTCACTTAATTTGGAATATGTTGCTTT	1142
Db		187	AATACCTTCTTCATAGTACATTTCTCACTTAATTTGGAATATGTTGCTTT	128
Qy		1143	TGTTTTTCTCTTATAGATTTTAAATTAATTAATTAATTAATTAATTAAT	1202
Db		127	TGTTTTTCTCTTATAGATTTTAAATTAATTAATTAATTAATTAATTAAT	68
Qy		1203	TTTGTAAATGTTAAGATTTTATTAATCTGTTAAATTAATTAATTTCCACA	1257
Db		67	TTTGTAAATGTTAAGATTTTATTAATCTGTTAAATTAATTAATTTCCACA	14

Search completed: December 25, 2004, 00:26:01
 Job time : 4416 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p1us_p2n model

Run on: December 25, 2004, 05:33:27 ; Search time 4298 Seconds
(without alignments)
2673.661 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301
Sequence: 1 MRPQPAASPORTLRGLLL.....GDASTGMSVSRITIEELPK 243

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO.spool/US10063734/runat.22122004.101734.8925/app_query.fasta.1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=xge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human4.cdi -LIST=100
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063734@CGN_1.1.3731@runat.22122004.101734.8925 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEOUDERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -IONGLIG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: *
1: gb_da: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_by: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	729	6	AR454023 Sequence
2	1301	100.0	732	6	AR454022 Sequence
3	1301	100.0	837	6	AR454024 Sequence
4	1301	100.0	837	6	AR454025 Sequence

5	1301	100.0	1257	6	AX092390 Sequence
6	1301	100.0	1257	6	AX376298 Sequence
7	1301	100.0	1257	6	AX454660 Sequence
8	1301	100.0	1257	6	AX459648 Sequence
9	1301	100.0	1257	6	AX491138 Sequence
10	1301	100.0	1257	6	AX697562 Sequence
11	1301	100.0	1257	6	AXY38914 Homo sapi
12	1294	99.5	732	6	CO714369 Sequence
13	1294	99.5	720	6	BD006704 Novel pol
14	1294	99.5	1220	6	AR405953 Sequence
15	1294	99.5	1221	9	AY136825 Homo sapi
16	1294	99.5	1236	6	BC014245 Homo sapi
17	1294	99.5	1257	6	BD269636 Human sec
18	1294	99.5	1284	6	AX829144 Sequence
19	1291	99.2	1342	6	BD223153 98 human
20	1281	99.2	1342	6	AR243851 Sequence
21	1266	97.3	1286	6	BD223185 98 human
22	1266	97.3	1286	6	AR243886 Sequence
23	1258.5	96.7	1288	6	BD193030 207 human
24	1258.5	96.7	1288	6	CO822026 Sequence
25	1216	93.5	1192	6	AR405952 Sequence
26	1216	93.5	1217	10	AY136824 Rattus no
27	1211	93.1	734	6	AR405955 Sequence
28	1132.5	87.0	1190	9	AK130063 Homo sapi
29	1053.5	81.0	1215	9	AF395488 Homo sapi
30	1052	80.9	1009	5	BX35556 Gallus ga
31	919	70.6	1290	5	BC079494 Danio rer
32	734	56.4	403	6	AR405954 Sequence
33	720	55.3	860	6	AX285214 Sequence
34	650	50.0	539	6	CO412972 Sequence
35	628	48.3	516	6	CO407408 Sequence
36	626	48.1	471	6	AX340025 Sequence
37	626	48.1	683	6	AR280558 Sequence
38	626	48.1	683	6	AR283054 Sequence
39	626	48.1	683	6	AR341827 Sequence
40	626	48.1	683	6	AR343822 Sequence
41	626	48.1	683	6	AR351023 Sequence
42	626	48.1	683	6	AR352789 Sequence
43	626	48.1	683	6	AR453603 Sequence
44	626	48.1	683	6	AX302743 Sequence
45	620	47.7	683	6	AX375790 Sequence
46	526	41.2	687	6	AX067343 Sequence
47	476	36.6	555	6	CO514013 Sequence
48	467	35.9	271	6	AX284686 Sequence
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52	428.5	32.9	160197	9	AP004221 Homo sapi
53	427	32.8	453	6	CO394673 Sequence
54	427	32.8	453	6	CO401024 Sequence
55	417.5	32.1	323534	2	AC121173 Rattus no
56	415	31.9	208553	2	AC145088 Mus muscu
57	407	31.3	1544	6	CO498468 Sequence
58	398.5	30.6	235421	2	AC131363 Rattus no
59	388	29.8	74798	2	AC069352 Homo sapi
60	374.5	28.8	158212	5	BX649637 Zebrafish
61	374	28.7	398	6	CO664298 Sequence
62	373	28.7	395	6	CO664147 Sequence
63	369	28.4	474	6	CO484187 Sequence
64	368	28.3	560	6	AX339938 Sequence
65	356	27.4	213269	5	AL844521 Zebrafish
66	310	23.8	466	6	CO712169 Sequence
67	276	21.2	475	6	AX284559 Sequence
68	258	19.8	166810	9	AL590222 Human DNA
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71	139	10.7	198411	10	AL731670 Rattus no
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 DB 601 TGTGAAGGAATTCGTCTGATTAAGTATGATGTTGCTATCTGGGTGGCACTTGTCAAGT 660
 QY 221 TyrProlysglyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240
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 DEFINITION AR454024
 ACCESSION AR454024.1 GI:42686814
 VERSION AR454024.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES 1 (bases 1 to 837)
 AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.,
 Hepler,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of breast
 cancer
 JOURNAL Patent: US 6680197-A 512 20-JAN-2004;
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 /mol_type="genomic DNA"
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 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProlysglylysglnysAla 40
 DB 166 CTGCTGCACTGCCCGCCGCTGAGCGCTCTGAGATCCCCAGGGGAGAGCAAAAGGGG 225
 QY 41 GlnLeuArgGlnArgGlnValValAlaLeuLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
 DB 226 CAGCTCCGGCAGAGGAGGTGGTGAACCTGTATATGATGTGCTTACAGAGGCCAGCA 285
 QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80
 DB 286 GGAGTGCCTGGTTCGAGACGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 345
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 DB 346 CCAAGTCGGAGTGAATTCAGAGAGAGAAAGGGGAAATGCTCAGAGAAAGCTTTGAGAG 405
 QY 101 SerTPThrProAsnTyrIysGlnCysSerTPSerSerLeuAsnTyrGlyIleAspLeu 120
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 QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
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 QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
 DB 586 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTATATTTATTTGAGCA 645
 QY 181 GlySerProGlyMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyIleu 200
 DB 646 GGAAAGCCCTGAATGATTCACAAATTAATTCATCGACACTTCTGCGAGAGACTT 705
 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTPValGlyThrCysSerAsp 220
 DB 706 TGTGAAGGAATTCGTCTGATTAAGTATGATGTTGCTATCTGGGTGGCACTTGTCAAGT 765
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 QY 241 LeuProlyse 243
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 DEFINITION AR454025
 ACCESSION AR454025
 VERSION AR454025.1 GI:42686815
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES 1 (bases 1 to 837)
 AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.,
 Hepler,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6680197-A 513 20-JAN-2004;
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ORIGIN

Alignment Scores:
Pred. No.: 5 46e-96 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR454025 (1-837)

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Db 106 ATGGACACCCCAAGGCGCCGCGCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlyGlyGly 40
Db 166 CTGCTGCAAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 225
QY 41 GlnLeuArgGlnArgGlyValValAlaPheLeuTyraSerGlyMetCysLeuGlnGlyProAla 60
Db 226 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTATTAAGAAATGGCTTACAGAGGCGCAGA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 286 GGAGTGCTGTGGTGAAGCGGAGCGCTGGGCGCAATGTTATCCGCGTACCTGGGATC 345
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 346 CCAAGTGGGAGATGATTCAGAGAGAGAGAGAGAGAGAGATGTCTAGAGAGAGCTTTGAGAG 405
QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120
Db 406 TCCGTGACACCCCACTACAGAGAGTGTTCATGAGATTCATTAATTAATGAGATTCCT 465
QY 121 GlyIleIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 466 GGGAAATTTGGGAGTGTACATTTACAAAGATCGCTTCAATAGCTCTTAAGATTTTG 525
QY 141 PheSerGlySerLeuArgLeuIleGlyCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db 526 TTCAATGAGAGTGTTCAGAGCTCTTCCCACTTGAAGCTATTAATTTATTTGAGACCA 585
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QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
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QY 201 CysGlnGlyIleGlyAlaGlyLeuValAlaPheValAlaIleIleIleIleIleIleIleIle 220
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QY 221 TyrProIleGlyAspAlaSerThrIleTyrlsAsnSerValSerArgIleIleIleGlnGly 240
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QY 241 LeuProIleGly 243
Db 826 CTACCAAAA 834

RESULT 5
AX092390

LOCUS AX092390 1257 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 121 from Patent WO0116318.
ACCESSION AX092390
VERSION AX092390.1 GI:13444509
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Eaton,D.L., Filvaroff,E., Gerlstein,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding the same
Patent: WO 0116318-A 121 08-MAR-2001;
JOURNAL Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1..1257
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Alignment Scores:
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Score: 1301.00 Matches: 243
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Query Match: 100.00% Indels: 0
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US-10-063-734-122 (1-243) x AX092390 (1-1257)

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Db 198 CTGCTGCAAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257
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Db 258 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTATTAAGAAATGGCTTACAGAGGCGCAGA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GGAGTGCTGTGGTGAAGCGGAGCGCTGGGCGCAATGTTATTCGCGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
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QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120
Db 438 TCCGTGACACCCCACTACAGAGAGTGTTCATGAGATTCATTAATTAATTTATTTGAGACCA 497
QY 121 GlyIleIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTTGGGAGTGTACATTTACAAAGATCGCTTCAATAGCTCTTAAGAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuIleGlyCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160
Db 558 TTCAATGAGAGTGTTCAGAGCTCTTCCCACTTGAAGCTATTAATTTATTTGAGACCA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleIleIleIleIleIle 180
Db 618 TTCAATGAGAGTGTTCAGAGCTCTTCCCACTTGAAGCTATTAATTTATTTGAGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
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QY 201 CygIuGlYIleGlyValaGlyLeuValaAlaIleTPValGlyThrCysSerAp 220
Db 728 TGTGAAGGAATTGGCTGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLySGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAAGGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLyS 243
Db 858 CTACCAAAA 866
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LOCUS Sequence 365 from Patent WO0168848.
DEFINITION AX376298
ACCESSION AX376298
VERSION AX376298.1 GI:19170540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Baker, K.P., Chen, J., Deenoyers, L., Goddard, A., Godowski, P., J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 365 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Alignment Scores:
Pred. No.: 8.65e-96 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProLySGlyValGluVala 40
Db 198 CTGCTGAGGTGCGCCGCGCTGAGGCGCTGAGGTGCTCCCAAGGAGGAGGAGG 257
QY 41 GlnLeuArgGlnArgGluValaValaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 317
QY 61 GlyValProGlyArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle 80
Db 318 GGAGTGCCTGTGAGAGCGGAGCCCTGGGGCAATGTATTCCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLySGlyValGluGlyLeuArgGlyLeuArgGlyLeu 100
Db 378 CCAAGTCTGGGATGATTCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 101 SerTrpThrProAsnTyrLySGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCTCGACACCCACTACAGACGTGTTCATGAGATTCAATTGCAATATGATGATCTT 497

QY 121 GlyValIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
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QY 141 PheSerGlySerLeuArgLeuLySGlyArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
Db 558 TTCAGTGTCTCATTCTGGCTAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluValaIleIleTyrLeuAspGln 180
Db 618 TTCAATGAGCTGAATGTTCAGGACCTCTCCCATTTAGATTAATTAATTTGAGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGAAATTCACAAATTAATATATTCACACTTCTTGTGTGAAGACTT 737
QY 201 CygIuGlYIleGlyValaGlyLeuValaAlaIleTPValGlyThrCysSerAp 220
Db 728 TGTGAAGGAATTGGCTGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLySGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAAGGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLyS 243
Db 858 CTACCAAAA 866
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AX454660 1257 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 245 from Patent WO0208284.
DEFINITION AX454660
ACCESSION AX454660
VERSION AX454660.1 GI:21713954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.B., Goddard, A.,
Godowski, P., J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 245 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary B. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 8.65e-96 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-063-734-122 (1-243) x AX454660 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20


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Db      138 ATGCCAGCCGAGGCGCCGCGCTCCCGCAGCGCTCCGCGCTCTGCTCTG 197
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlysglylysglnlyVala 40
Db      198 CTGCTGCGAGCTCCCGCGCTCGAGCGCTCTGAGATCCCGAGGGAGGAGGAGG 257
Qy      41 GlnLeuArgGlnArgGlnValaValaAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60
Db      258 CAGCTCCGCGAGGAGGAGGTGCTGACCTGTATTAAGATGATGCTTACAGAGGCGACGCA 317
Qy      61 GlyValProGlyArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle 80
Db      318 GGAGGCTCTGCTCGAGAGCGGAGCCCTGGGCGCAAGTTATTCGGGTACACCTGGAGATC 377
Qy      81 ProGlyArgAspGlyPheIysGlyGlnCysLeuArgGlnGlySerPheGlnGlu 100
Db      378 CCAAGTCCGGAGTGCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
Qy      101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120
Db      438 TCCTGAGACACCACTACAGACAGAGTGTTCATGAGATTCATGATTAATGAGATGATCTT 497
Qy      121 GlyIysIleAlaGlnCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValIleu 140
Db      498 GGGAAATTTGCGGAGTGTACATTCAGAAAGATGCGTTCAAAATAGTCTTAAGAGATTGG 557
Qy      141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpIyrPheThr 160
Db      558 TTCAGTGCCTCACTTCGGCTAAATGCAAGAAATGCAATGCTGTCAGGCTTGGATTTTACA 617
Qy      161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180
Db      618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTATATATTATTGGACCAA 677
Qy      181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db      678 GGAAGCCCTGAATGATTAATCAACATTAATTCATGCACTCTCTGTGAAGGACTT 737
Qy      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      738 TGTGAAGAAATTGGTGTGATTAATGATGATGATGATGATGATGATGATGATGATGAT 797
Qy      221 TyrProlysglyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlu 240
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Qy      241 LeuProlys 243
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LOCUS
DEFINITION
ACCESSION
AX459648.1   GI:21725519
VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE
AUTHORS
Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Polakis,P.,
Williams,P.M., Wood,W.I., Wu,T.D. and Zhang,Z.
TITLE
Compositions and methods for the diagnosis and treatment of tumor
JOURNAL
PATENT: WO 0216602-A 2 28-FEB-2002;
GENENTECH, INC. (US)

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FEATURES

SOURCE

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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:    100.00%
DB:              6
Gaps:            0

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US-10-063-734-122 (1-243) x AX459648 (1-1257)

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Db      318 GGAGTGCCTGCTCGAGACGAGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGAGATC 377
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Db      438 TCCTGAGACACCACTACAGACAGAGTGTTCATGAGATTCATGATTAATGAGATGATCTT 497
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Qy      141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpIyrPheThr 160
Db      558 TTCAGTGCCTCACTTCGGCTAAATGCAAGAAATGCAATGCTGTCAGGCTTGGATTTTACA 617
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Qy      181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
Db      678 GGAAGCCCTGAATGATTAATCAACATTAATTCATGCACTCTTCTGTGAAGGACTT 737
Qy      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      738 TGTGAAGAAATTGGTGTGATTAATGATGATGATGATGATGATGATGATGATGATGAT 797
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Qy      241 LeuProlys 243
Db      858 CTACCAAAA 866

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RESULT 9
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LOCUS
DEFINITION
ACCESSION
AX491138
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.,
 and Ye, W.
 TITLE Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
 JOURNAL Patent: WO 0200690-A 245 03-JAN-2002;
 Genentech, Inc. (US)
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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 ORIGIN
 Alignment Scores:
 Pred. No.: 8,65e-96 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-063-734-122 (1-243) x AX491138 (1-1257)
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 Db 738 TGTGAAGGAATGTGTGTGATTAAGTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 797
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 Db 858 CTACCAAAA 866
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 DEFINITION
 VERSION AX697362
 KEYWORDS GI:29498494
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
 Baton, D.L., Gao, W.Q., Pan, J., Borstein, D., Fong, S., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,
 Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A., and Watanabe, C.K.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0078961-A 430 28-DEC-2000;
 Genentech Inc. (US)
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 /organism="Homo sapiens"
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 Alignment Scores:
 Pred. No.: 8,65e-96 Length: 1257
 Score: 1301.00 Matches: 243
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
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 QY 61 GlyValProGlyValArgAspGlySerProGlyValAlaAsnValLeuProGlyTyrrProGlyTyr 80
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 QY 81 ProGlyValArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 378 CCAAGTCGGGATGATTCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
 QY 101 SerTrpThrProAsnTyrrLysGlnCysSerTrpSerSerLeuAsnTyrrGlyIleAspLeu 120
 Db 438 TCTTGACACCCCACTACAGAGGTTCATGAGTTTCATTGAAATTAATGAGCATAGATCTT 497
 QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
 Db 498 GGGAAATTCGGAGGTGTACATTACAAAGATGCTTCAAAATGTGCTTAAAGATTTTG 557
 QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160

Db 558 TTCAGTGCCTCCTCGCTAAATGCAAAATGCAATGCTGTCAGCGTTGGTATTTCACA 617
Qy 161 PheannglyalagluCySerSerglyProleupProilegualalelletYrleuAaspGln 180
Db 618 TTCATGAGAGCTGGAATGTTCAAGACCTCTTCCATTGAACTATATTATTGGAACCA 677
Qy 181 GlySerProglumecAasSerThrIleasnIleHisArgThrserserValgluglu 200
Db 678 GGAACCCCTGGAATGATTCACAAATTAATTCATGCACCTCTCTGTGGAAGGACTT 737
Qy 201 CysgluglylleglyalaglyleuValaspValAlaIletrpValgluYhrCysSerAap 220
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Qy 221 TyrProlysglyaspAlaserThrIleTyrPasnSerValserArgIlelleleglu 240
Db 798 TACCAAAAGAGATGCTCTTCTAGTGAATGCAATTCAGTTTCTCGCATCTATTGAAGA 857
Qy 241 LeuProlyS 243
Db 858 CTACCAAAA 866

RESULT 11
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LOCUS AY358914
DEFINITION Homo sapiens clone DNA76393 CTRC1 (UNQ762) mRNA, complete cds.
ACCESSION AY358914.1 GI:37182945
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1257)
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robble, E., Sanchez, C.,
Stenonfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Schoen, J., Vagte, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K.,
Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, M.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 1257)
Clark, H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
LOCATION/Qualifiers
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/clone="DNA76393"
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ORIGIN
Alignment Scores:
Pred. No.: 8,65e-96 Length: 1257
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Query Match: 100.00% Indels: 0
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Qy 21 LeuLeuGlnLeuProAlaIleProSerSerAlaSerGluIleProlysglylyVal 40
Db 198 CTGCTGAGCTGCGCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAGGCG 257
Qy 41 GlnLeuArgGlnArgGluValValaspLeuTyrAsnGlyMetCysleuGlnGlyProAla 60
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Qy 61 GlyValProGlyArgaspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGAGTCCCTGGATCGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 377
Qy 81 ProGlyArgaspGlyPheIleGlyGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAAGTCCGAGTGAATTCAAAGAGAAAGGGGGAATGTGAGGGAACCTTTGAGAG 437
Qy 101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerleuAsnTyrGlyIleAspLeu 120
Db 438 TCTCGAACCACCACTACAGACAGTGTTCATGAGTTCATTAATTAATGCAATGATCTT 497
Qy 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGAAGAAATTCGGAGGTGATCAATTAAGAAAGTGGTTCAAAATGTGCTTAAGATTTC 557
Qy 141 PheSerGlySerleuArgleuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
Db 558 TTCAGTGCCTCCTCGCTAAATGCAAAATGCAATGCAATGCAATGCAATGCAATGCA 617
Qy 161 PheannglyalagluCySerSerglyProleupProilegualalelletYrleuAaspGln 180
Db 618 TTCATGAGAGCTGGAATGTTCAAGACCTCTTCCATTGAACTATATTATTGGAACCA 677
Qy 181 GlySerProglumecAasSerThrIleasnIleHisArgThrserserValgluglu 200
Db 678 GGAAGCCCTGGAATGATTCACAAATTAATTCATGCACCTCTCTGTGGAAGGACTT 737
Qy 201 CysgluglylleglyalaglyleuValaspValAlaIletrpValgluYhrCysSerAap 220
Db 738 TGTGAAGAGATGGTGTGATGATGAGATGTTGATCTGAGTGGCACTTGTTCAGAT 797
Qy 221 TyrProlysglyaspAlaserThrIleTyrPasnSerValserArgIlelleleglu 240
Db 798 TACCAAAAGAGATGCTCTTCTAGTGAATGCAATTCAGTTTCTCGCATCTATTGAAGA 857
Qy 241 LeuProlyS 243
Db 858 CTACCAAAA 866

RESULT 12
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LOCUS CQ714369 732 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 303 from Patent WO02068579.
ACCESSION CQ714369
VERSION CQ714369.1 GI:42275226
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 Ventner, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
 Kites, such as nucleic acid arrays, comprising a majority of
 humenexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 303 06-SEP-2002;
 PE Corporation (NY) (US)
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 Alignment Scores:
 Pred. No.: 1,72e-95 Length: 732
 Score: 1294.00 Matches: 242
 Percent Similarity: 99.59% Conservative: 0
 Best Local Similarity: 99.59% Mismatches: 1
 Query Match: 99.46% Indels: 0
 DB: 6 Gaps: 0
 US-10-063-734-122 (1-243) x CQ714369 (1-732)
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 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyLeuGlnLeu 40
 DB 61 CTGCTCGACGCTCCCGCCCGCCGCTCGAGCGCTTCGAGATCCCGAGGAGGAGGCG 120
 QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyraGlyMetCysLeuGlnGlyProAla 60
 DB 121 CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGAAATGTGTACAGGCGCAGCA 180
 QY 61 GlyValProGlyValArgAspGlySerProGlyValAlaSerValIleProGlyThrProGlyIle 80
 DB 181 GGAGTGCCTGTGTGACACGGGAGCCCTGGGGCCAAATGGCAATCCGGGTACACCTGGGATC 240
 QY 81 ProGlyArgAspGlyPheLeuGlyGlnLeuGlyGlnCysLeuArgGlnSerPheGlnGln 100
 DB 241 CCGAGTCCGAGATGATTCAGAGAGAAAGGAGAAATGTGTGAGGAGAACTTTGAGGAG 300
 QY 101 SerTrpThrProAlaTrpLeuGlnCysSerTrpSerSerLeuAlaSerValIleAspLeu 120
 DB 301 TCCTGAGACACCAACTACAAAGAGTGTTCATGAGTTCAATTATGATGATGATCTT 360
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 DB 361 GGGAAATATGCGAGATGATTCATTAACAAGATCGTTCAAAATGATCTTAAAGATTTTG 420
 QY 141 PheSerGlySerLeuArgLeuLeuGlnCysArgAsnAlaCysGlnGlnArgTrpPheThr 160
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QY 241 LeuProGly 243
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 RESULT 13
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 DEFINITION Novel polypeptide.
 ACCESSION BD006704
 VERSION BD006704.1 GI:18635075
 KEYWORDS JP 2001029090-A/7.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 732)
 Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.
 Novel polypeptide
 Patent: JP 2001029090-A 7 06-FEB-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Homo sapiens (human)
 PN JP 2001029090-A/7
 PD 06-FEB-2001
 PF 19-MAY-2000 JP 2000147530
 PR
 PI YASUAKI ITO, SHINICHI MOGI, HIDEYUKI TANAKA, SHOICHI OKUBO, PI
 KAZUHIRO OGI
 PC C12N15/00, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
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 PC A61P5/00, A61P9/00, A61P11/00, A61P25/00, A61P25/18, A61P31/00, PC
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 ORIGIN
 Alignment Scores:
 Pred. No.: 1,72e-95 Length: 732
 Score: 1294.00 Matches: 242
 Percent Similarity: 99.59% Conservative: 0
 Best Local Similarity: 99.59% Mismatches: 1
 Query Match: 99.46% Indels: 0
 DB: 6 Gaps: 0
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 DB 1 ATGCGACCCCGAGGCCCCCGCCCTCCCGACGCGCTCCGCGCCCTCCGCTCCG 60
 QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyLeuGlnLeu 40
 DB 61 CTGCTCGACGCTCCCGCCCGCCGCTCGAGCGCTTCGAGATCCCGAGGAGGAGGCG 120
 QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyraGlyMetCysLeuGlnGlyProAla 60
 DB 121 CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGAAATGTGTACAGGCGCAGCA 180
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Qy 101 SerTPThProAsnTYrIySGlyCysSerTPSerSerLeuAsnTYrGlyIleAspLeu 120
Db 301 TCCTGGACGCCAACACACAGCATGCTTCATGAGATTCATTAATTAATGAGATGATCTT 360
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Qy 221 TyrProIySGlyAspAlaSerThrGlyTPAsnSerValSerAArgIleIleIleGluGlu 240
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Qy 241 LeuProIyS 243
Db 721 CTACCAAAA 729

RESULT 14
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DEFINITION Sequence 3 from patent US 6630325.
ACCESSION AR405953
VERSION AR405953.1 GI:40155009
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1220)
AUTHORS Lindner,V. and Friesel,R.E.
TITL Composition, methods and kits relating to remodel
JOURNAL Patent: US 6630325-A 3 07-OCT-2003;
FEATURES
SOURCE location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 3,07e-95 Length: 1220
Score: 1294.00 Matches: 242
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Qy 121 GlyIySIIeAlGlyCysThrPheThrIyMetAArgSerAsnSerAlaLeuAArgValLeu 140
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DEFINITION Homo sapiens collagen triple helix repeat-containing protein 1
ACCESSION AY136825
VERSION AY136825.1 GI:25989620
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
1 (bases 1 to 1221)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITL Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Lehner,W., Moore,D.P., Harmon,K.J., Mancini,M.L. and Lindner,V.
Expression of the novel collagen triple helix repeat-containing
gene (Cthrc1) suggests functions in multiple organ systems
Unpublished
REFERENCE
2 (bases 1 to 1221)
AUTHORS Lindner,V.
TITL Direct Submission
JOURNAL Submitted (29-JUL-2002) Center for Molecular Medicine, Maine
Medical Center Research Institute, 81 Research Drive, Scarborough,
ME 04074, USA
FEATURES
SOURCE location/Qualifiers
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Alignment Scores:
Pred. No.: 3.07e-95 Length: 1221
Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Beet Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: Gaps: 0
US-10-063-734-122 (1-243) x AY136825 (1-1221)

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Db 824 CTACCAAAA 832

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REFERENCE

1 (bases 1 to 1236)
Strasberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F., Diatchenko, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Stappleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ueda, T.B., Toshiyuki, S., Carinci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skaleja, V., Smallus, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE

human and mouse cDNA sequences

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED

12477932

REFERENCE

2 (bases 1 to 1236)

AUTHORS

Strasberg, R.

JOURNAL

Direct Submission

Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:15559789.

REMARK

CONTACT: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ruben Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisec.nih.gov/>
Contact: nisc.mgc@nih.gov
Ahter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrilian, P.D., McKloskey, J.C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN.ac: <http://image.lnl.gov>
Series: IRBL plate: 30 Row: 1 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction.

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Location/Qualifiers
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CDS

gene

ORIGIN

Alignment Scores:

Pred. No.: 3.12e-95 Length: 1236
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Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 9 Gaps: 0

US-10-063-734-122 (1-243) x BC014245 (1-1236)

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QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLLeProLyGlyGInLySAla 40
Db 160 CTGCTGCAAGCTGCCCGCGCTGCGAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 219
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Db 220 CAGCTCCGGCAGAGGAGGTGCTGACCTGTATATGATGTGCTTACAAAGGCGCAGCA 279
QY 61 GlyValProGlyATGAspGlySerProGlyAlaAsnValLLeProGlyThrProGlyLLe 80
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QY 81 ProGlyATGAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 340 CCAAGTCGGAGATGATCAAG 399
QY 101 SerTPThrProAsnTYRLeuGInCysSerTPSerserLeuAsnTYRGLYLLAspLeu 120
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QY 121 GlyTysLLeaGInCysThrPheThrLysMetATGAspSerAsnSerAlaLeuArgValLeu 140
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QY 241 LeuProLyS 243
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RESULT 17

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LOCUS BD269636 Human secretory proteins.
DEFINITION BD269636
ACCESSION BD269636.1 GI:33079404
KEYWORDS JP 2002537805-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS 1 (bases 1 to 1257)
Tang,T.Y., Lal,P., Baughn,M.R., Yue,H., Young,J.A., Lu,D.A.M. and
Azimzal,Y. Human secretory proteins
Patent: JP 2002537805-A 5 12-NOV-2002;
JOURNAL INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002537805-A/5
PF 12-NOV-2002
PI 03-MAR-2000 JP 2000602763
PR 05-MAR-1999 US 60/123117
PI TOM Y TANG, PREETI LAL, MARIAH R BAUGHN, HENRY YUE, JANICE AU PI
YOUNG.

PI DYUNG AINA M LU, YALDA AZIMZAI
PC C12N15/09,A01K67/027,A61K38/00,A61K45/00,A61P1/00,
PC A61P9/00,
PC A61P25/00,A61P29/00,A61P31/00,A61P35/00,C07K14/47,C07K16/18,
PC C12N1/15,
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source

Location/Qualifiers
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Score: 1294.00 Matches: 242
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 99.46% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x BD269636 (1-1257)

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyAla 40
DB 192 CTGCTGACGCTGCGCCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAAAGGCG 251

QY 41 GlnLeuArgGlnArgGluValValAspLeuTyraGlyMetCysLeuGlnGlyProAla 60
DB 252 CAGCTCCGGCAGAGGAGGAGGCTGAGACTGTATTAATGGAATGCTTACAGGCGCAGCA 311

QY 61 GlyValProGlyValArgAspGlySerProGlyValAsnValLeuProGlyThrProGlyIle 80
DB 312 GGAAGTCCCTGCTGCAACCGGAGCCCTGGGGCCAAATGCAATCCGGGTACACCTGGGATC 371

QY 81 ProGlyValArgAspGlyPheLeuGlyGlyValGlyCysLeuArgGlyLeuSerPheGlnGlu 100
DB 372 CCAAGTCGGAGATGATTCAGAGAGAAAGGGGAAATGCTGAGGAGAAAGCTTGAAGAG 431

QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120
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QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
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QY 141 PheSerGlySerLeuArgLeuLeuValCysArgAsnAlaCysGlyGlnArgTrpPheThr 160
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QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
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QY 201 CysGluGlyIleGlyValGlyValAspValAlaIleTrpValGlyThrCysSerAsp 220
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QY 221 TyrProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
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RESULT 18
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LOCUS AX829144
DEFINITION Sequence 37 from Patent WO02059377.
ACCESSION AX829144
VERSION AX829144.1 GI:39838921
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Mack, D.H., Gish, K.C. and Afar, D.
METHODS OF DIAGNOSIS OF BREAST CANCER, COMPOSITIONS AND METHODS OF
SCREENING FOR MODULATORS OF BREAST CANCER
PATENT: WO 02059377-A 37 01-AUG-2002;
JOURNAL EOS Biotechnology, Inc. (US)
FEATURES
Location/Qualifiers

source

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ORIGIN

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Best Local Similarity:	99.59%	Mismatches:	1
Query Match:	99.46%	Indels:	0
DB:	6	Gaps:	0

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QY 41 GlnLeuArgGlnArgGluValValAspLeuTyraGlyMetCysLeuGlnGlyProAla 60
DB 263 CAGCTCCGGCAGAGGAGGAGGCTGAGACTGTATTAATGGAATGCTTACAGGCGCAGCA 322

QY 61 GlyValProGlyValArgAspGlySerProGlyValAsnValLeuProGlyThrProGlyIle 80
DB 323 GGAAGTCCCTGCTGCAACCGGAGCCCTGGGGCCAAATGCAATCCGGGTACACCTGGGATC 382

QY 81 ProGlyValArgAspGlyPheLeuGlyGlyValGlyCysLeuArgGlyLeuSerPheGlnGlu 100
DB 383 CCAAGTCGGAGATGATTCAGAGAGAAAGGGGAAATGCTGAGGAGAAAGCTTGAAGAG 442

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QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
DB 503 GGGAAATATGCGGAGGTGATCATTTACAAAGATGCGTTCAAAATGATGCTCTAAAGATTGTT 562

QY 141 PheSerGlySerLeuArgLeuLeuValCysArgAsnAlaCysGlyGlnArgTrpPheThr 160
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LOCUS BD223153
DEFINITION 98 human secretory proteins.
ACCESSION BD223153

VERSION BD223153.1 GI:33032923
 KEYWORDS JP 2002521055-A/88.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 1342)
 AUTHORS Komatsoulis,G.A., Rosen,C.A., Ruben,S.M., Duan,R., Moore,P.A., Shi,Y., Lafleur,D., Wei,Y.F., Ni,Y., Florence,K.A., Young,P.E., Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H.S. and Mucenski,M.
 TITLE 98 human secretory proteins
 JOURNAL Patent: JP 2002521055-A 88 16-JUL-2002;
 COMMENT HUMAN GENOME SCIENCES INC
 OS Homo sapiens (human)
 PN JP 2002521055-A/88
 PD 16-JUL-2002
 PF 29-JUL-1999 JP 2000562480
 PR 30-JUL-1998 US 60/094657,05-AUG-1998 US 60/095486 PR
 06-AUG-1998 US 60/095455,06-AUG-1998 US 60/095454 PR
 12-AUG-1998 US 60/096319
 PI GEORGE A KOMATSOULIS, CRAIG A ROSEN, STEVEN M RUBEN, ROXANNE DUAN
 .PI PAUL A MOORE, YANGU SHI, DAVID LAFLEUR, YING FEI WEI, JIAN NI, PI KIMBERLY A FLORENCE, PAUL E YOUNG, LAURIE A BREWER, DANIEL R PI SOPEY,
 PI GREGORY A ENDRESS, REINHARD EBNER, HENRIK S OLSEN, MICHAEL PI MUCENSKI
 PC C12N15/09,A61K31/713,A61K38/00,A61K48/00,C07K14/47,C07K16/18, PC C12N1/15,
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 Best Local Similarity: 99.18% Mismatches: 1
 Query Match: 99.23% Indels: 0
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 DEFINITION Sequence 89 from patent US 6476195.
 ACCESSION AR243851
 VERSION AR243851.1 GI:27291344
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 1342)
 AUTHORS Komatsoulis G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A., Shi, Y., Lafleur, D.W., Wei, Y.F., Ni, Y., Florence, K.A., Young, P.E., Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and Mucenski, M.
 TITLE Secreted protein HNFGF20
 JOURNAL Patent: US 6476195-A 89 05-NOV-2002;
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 Best Local Similarity: 99.18% Mismatches: 1
 Query Match: 99.23% Indels: 0
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DB 501 GGGAAATATGGCGAGGTGACATTTACAAAGATGCGTTCAAAATAGTCTTAAAGATTTTG 560
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DB 621 TTCATGAGAGTGAATGTTCAGAGACCTCTCCCATTAAGCATTAATTAATTTGAGCA 680
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RESULT 21
BD223185 1286 bp DNA linear PAT 17-JUL-2003
LOCUS BD223185 98 human secretory proteins.
DEFINITION BD223185
ACCESSION BD223185.1 GI:33032955
VERSION JP 2002521055-A/120.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1286)
AUTHORS Komatsoulis,G.A., Rosen,C.A., Ruben,S.M., Duan,R., Moore,P.A.,
Shi,Y., Lafleur,D., Wei,Y.F., Ni,J., Florence,K.A., Young,P.E.,
Breuer,L.A., Soppet,D.R., Endress,G.A., Edner,R., Olsen,H.S. and
Mucenski,M.
TITLE 98 human secretory proteins
JOURNAL Patent: JP 2002521055-A 120 16-JUL-2002;
HUMAN GENOME SCIENCES INC
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PN JP 2002521055-A/120
PD 16-JUL-2002
PF 29-JUL-1999 JP 2000562480
PR 30-JUL-1998 US 60/094577, 05-AUG-1998 US 60/095486 PR
06-AUG-1998 US 60/095455, 06-AUG-1998 US 60/095454 PR
12-AUG-1998 US 60/096319
PI GEORGE A KOMATSOULIS, CRAIG A ROSEN, STEVEN
M RUBEN, ROXANNE DUAN,
PI PAUL A MOORE, YANGGU SHI, DAVID LAFLEUR, YING FEI, WEI JIAN NI, PI
KIMBERLY A FLORENCE, PAUL E YOUNG, LAURIE A BREWER, DANIEL R PI
SOPPET,
PI GREGORY A ENDRESS, REINHARD EBNER, HENRIK S OLSEN, MICHAEL PI
MUCENSKI
PC C12N15/09, A61K31/713, A61K38/00, A61K48/00, C07K14/47, C07K16/18,
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Query Match: 97.31% Indels: 1
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 ACCESSION AR243886
 VERSION AR243886.1 GI:27291379
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1286)
 AUTHORS Komatsu, S., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A., Shi, Y., Lafleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P., Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and Mucenki, M.
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 JOURNAL Patent: US 6476195-A 124 05-NOV-2002;
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 Score: 1266.00 Matches: 241
 Percent Similarity: 99.18% Conservatve: 0
 Best Local Similarity: 99.18% Mismatches: 2
 Query Match: 97.31% Indels: 1
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 Qy 61 GlnValProGlnArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80

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 Qy 101 SerTyrThrProAsnTyrLysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
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 LOCUS 207 human secreted proteins.
 DEFINITION BD193030
 ACCESSION BD193030.1 GI:33002769
 VERSION JP 2002516573-A/124.
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 1288)
 AUTHORS Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A., Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y., Florence, C., Florence, K., Lafleur, D.W., Ni, J., Fan, P., Wei, Y.F., Fischer, C.L., Soppet, D.R., Li, Y., Ze, Z., Kyaw, H., Yu, G.L., Feng, P., Dillon, P.J., Endress, G.A. and Carter, K.C.
 TITLE 207 human secreted proteins
 JOURNAL Patent: JP 2002516573-A 124 04-JUN-2002;
 HUMAN GENOME SCIENCES INC
 COMMENT
 PD 04-JUN-2002
 PF 04-JUN-1998 JP 1995502815
 PR 06-JUN-1997 US 60/048915, 06-JUN-1997 US 60/048882 PR
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05-SEP-1997 US 60/057661,05-SEP-1997 US 60/057647 PR
18-DEC-1997 US 60/070923
PI PAUL, YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A ROSEN,
PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER, PI PAUL A MOORE,
PI YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVID W LAFFEUR, PI JUAN NI,
PI PING PAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SOPPET, YI LI, PI ZHIZHEN ZENG,
PI HIA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, GREGORY A PI ENDRESS,
PI KENNETH C CARTER
PC A01N37/18, A01N43/04, C12Q1/00, C12Q1/02, C12Q1/68, C12N5/00 PC, C12N5/06, C12N15/00,
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DEFINITION Sequence 125 from Patent EP1428833.
ACCESSION C0822026
VERSION C0822026.1 GI:49020742
KEYWORDS
SOURCE
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REFERENCE
AUTHORS Hu J.S., Olsen, H.S., Ebner, R., Laffeur, D.N., Ni, J., Fan, P., Wei, Y.F., Florence, C., Florence, K., Soppet, D.R., Li, Y., Zeng, Z., Kyaw, H., Yu, G.L., Fischer, C.L., Soppet, D.R., Li, Y., Zeng, Z., Kyaw, H., Yu, G.L., Feng, P., Dillon, P.J., Endress, G.A. and Carter, K.C.
TITLE 207 human secreted proteins
JOURNAL Patent: EP 1428833-A 125 16-JUN-2004;
Human Genome Sciences, Inc. (US)
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ORIGIN
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Pred. No.: 2,39e-92 Length: 1288
Score: 1258.50 Matches: 240
Percent Similarity: 99.18% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 2
Query Match: 96.73% Indels: 1
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ACCESSION AR405952
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AUTHORS Lindner,V. and Friesel,R.E.
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Db 757 TCAATTAATCCCAAGAGAGAGCGCTTCTACTGAGTGGATTTGTGTGTCGCGCATCATCAT 816
QY 239 GluGlnLeuProLys 243
Db 817 GAAGAACTACCAAAA 831

RESULT 26
AY136824 1217 bp mRNA linear ROD 01-DEC-2002
LOCUS AY136824
DEFINITION Rattus norvegicus collagen triple helix repeat-containing protein 1
ACCESSION AY136824
VERSION AY136824.1 GI:25989618
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
```

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1217)
AUTHORS Lehnert, W., Moore, D. P., Harmon, K. J., Mancini, M. L. and Lindner, V.
TITLE Expression of the novel collagen triple helix repeat-containing
gene (chrcl) suggests functions in multiple organ systems
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1217)
Lindner, V.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2002) Center for Molecular Medicine, Maine
Medical Center Research Institute, 81 Research Drive, Scarborough,
ME 04074, USA

FEATURES
source location/Qualifiers
1..1217 /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/feature_type="8 day balloon-injured carotid artery"
1..1217
/gene="Chrcl"
117..854 /gene="Chrcl"
/note="matrix protein"
/codon_start=1
/product="collagen triple helix repeat-containing protein
1"
/protein_id="AA15748.1"
/db_xref="GI:2598619"
/translation="MHQRRASPOLLLGLPIVLLLLDLSAPSSASEPKKORALI
KOREVVDLNGMLQDPAGVPRDPSPGANGIPGTGIRGRGFKESKESPEE
SWTPYKQCSWSLNYGIDLGRIACETFKMSNSALRYLFSGSLRLKCRNACQRY
PTFNAGSCSGPLIEAIYLDGSPELNNTINIHRTSSVEGLCEGIGLVVAIIVWG
TSDYPKGDASTGMNSVSRITIEELPK"

ORIGIN
Alignment Scores:
Pred. No.: 6,03e-89 Length: 1217
Score: 1216.00 Matches: 231
Percent Similarity: 95.51% Conservative: 3
Best Local Similarity: 94.29% Mismatches: 9
Query Match: 93.47% Indels: 2
DB: 10 Gaps: 1

US-10-063-734-122 (1-243) x AY136824 (1-1217)

QY 1 MetAArgProGlnGlyProAlaAlaSerProGlnAArgLeuAArgGly-----LeuLeuLeu 18
DB 117 ATGCACCCCAAGGCGCGCGCTCCACAGCTGCTCGGCTCTTCTTGCTA 176
QY 19 LeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProlyGlyLeuGln 38
DB 177 CTGCTGCTTCTGAGCTGTCGCGCGCTCCAGGCTCTGAGAAATCCCAAGGGAAGCAA 236
QY 39 LysAlaGlnLeuAArgGlnAArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGly 58
DB 237 AAAGCGCTGATCCGCGAGAGGAAAGTGTAAGACTGTATATATGAGATGCGCTACAAAGA 296
QY 59 ProAlaGlyValProGlyAArgAArgGlySerProGlyAlaAsnValIleProGlyThrPro 78
DB 297 CCAGCAGGAGTTCCTGCTGCGATGGAGACCCCTGGGGCCAAATGGCAATTCCTGGCACACCG 356
QY 79 GlyIleProGlyAArgAArgGlyPheLeuGlyGluLeuGlyGluCysLeuAArgGlySerPhe 98
DB 357 GGAATCCCGAGCTCGGATGATTCAAAGAGAGAAAGGAGTCTTAAGGAAACTTT 416
QY 99 GluGluSerTyrThrProAlaTyrIleGlnCysSerTyrSerSerLeuAlaTyrGlyIle 118
DB 417 GAGGATCTCGAGCCCAAACTACAGCAGTGTTCATGAGATTCACTAATATATGCAAT 476

QY 119 AspLeuGlyIleValIleAlaGluCysThrPheThrIleMetAArgSerAsnSerAlaLeuArg 138
DB 477 GATCTGGGAAATATGCCGAATGTACATTCACAAAGATGCCATCCACAGCGCTCTTCA 536
QY 139 ValLeuPheSerGlySerLeuAArgLeuLysCysAArgAlaAcysCysGlnAArgTyr 158
DB 537 GTTCTGTTACAGTGGCTCCCTTCGCTCAATGCAGAAATGCTGTGCTGCACAGCTGGAT 596
QY 159 PheThrPheAsnGlyValIleGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeu 178
DB 597 TTTACCTTAATAGAGAGCTGAATGTACAGACCTCTTCCATTGAAGCTATCATCTATCTG 656
QY 179 AspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlu 198
DB 657 GACCAAGAGAGCCCTGAGTAAATTCACATTAATATTCATCGTACTTCCCTCCGGGAA 716
QY 199 GlyLeuCysGluGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCys 218
DB 717 GGACTCTGTAAGGAGATTTGCTGCTGAGCTGTAAGACGTGGCCATCTGGGCTCGCACCTGT 776
QY 219 SerAspTyrTyrProLysGlyAspAlaSerThrGlyTyrPheAsnSerValSerArgIleIle 238
DB 777 TCAGATTACCCCAAGAGAGACGCTTCTACTGGGTGAAATTCGTGTCCGCAATCATATT 836
QY 239 GluGluLeuProLys 243
DB 837 GAGAACTACCAAAA 851

RESULT 27
AR405955
LOCUS AR405955 734 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6630325.
ACCESSION AR405955
KEYWORDS AR405955.1 GI:40155011
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 734)
AUTHORS Lindner, V. and Friesel, R.E.
TITLE Compositions, methods and kits relating to remodel
JOURNAL Patent: US 6630325-A 9 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..734
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 8,62e-89 Length: 734
Score: 1211.00 Matches: 230
Percent Similarity: 95.88% Conservative: 3
Best Local Similarity: 94.65% Mismatches: 8
Query Match: 93.08% Indels: 2
DB: 6 Gaps: 1

US-10-063-734-122 (1-243) x AR405955 (1-734)

QY 3 ProGlnGlyProAlaAlaSerProGlnAArgLeuAArgGly-----LeuLeuLeuLeu 20
DB 6 CCCCAAGGCGCGCGCTCCACAGCTGCTCGGCTCTTCTTGCTA 65
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProlyGlyLeuGlnValAla 40
DB 66 CTTTCTGAGCTGTCGCGCGCTCCAGCGCTCTGAGAAATCCCAAGGTGAAGCAAAAAGCG 125
QY 41 GlnLeuAArgGlnAArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 126 CTGATCCGACAGAGGAAATGTAGCTGTATATATGAGATGCTCTACAGACCAAGCA 185
QY 61 GlyValProGlyAArgAArgGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 186 GGAATTCCTGCTGCGATGGAGCCCTGGGCAATGCAATTCCTGCGACACCGGGAATC 245

Pred. No.: 8,376-76 Length: 1009
 Score: 1052.00 Matches: 200
 Percent Similarity: 89.25% Conservative: 16
 Best Local Similarity: 82.64% Mismatches: 18
 Query Match: 80.86% Indels: 8
 Gaps: 4
 DB: 5
 US-10-063-734-122 (1-243) x BX935556 (1-1009)

QY	2	ArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeuLeu	21
Db	11	CGCCCGC---GGCCCCGCC-----ATGCCCGCGCGCCCGCTGCTCTCTGGCGCTG	58
QY	22	LeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyLeuGlnLeuAlaGln	41
Db	59	CTG-----CTGGGCTCGCGCGCTCGCGCGACAGCCCGGGGGAACAGGAGCG---	106
QY	42	LeuArgGlnArgGlyValValAlaSerLeuTyraGlnGlyMetCysLeuGlnGlyProAlaGly	61
Db	107	GCGGCGCGCGCGGAGGTCTGAGGCGCTGACACAGCGCGCTGCTGCTGACGCGCGCCAGCGCG	166
QY	62	ValProGlyArgAspGlySerProGlyAlaAlaValIleProGlyThrProGlyIlePro	81
Db	167	GTCCCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGG	226
QY	82	GlyArgAspGlyPheLeuGlyGlyLeuGlyGlyLeuArgGlyLeuSerGlyLeuSer	101
Db	227	GCGCGGACCGGCGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGG	286
QY	102	ThrProAlaProAlaProAlaProAlaProAlaProAlaProAlaProAlaProAlaPro	121
Db	287	TGGAGCGCGCACTTCAACAGAGTCTGAGAGCGGACGAGTCTGAGAGTCTGAGAGTCTG	346
QY	122	LysIleAlaGlyCysThrPheThrIleMetArgSerSerSerAlaLeuArgValLeuPhe	141
Db	347	AAATAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	406
QY	142	SerGlySerLeuArgGlyLeuGlyCysArgGlnAlaCysCysGlnArgTyrPheThrPhe	161
Db	407	AGTGAATGCTGCTCGCGCTGAGAGCGGACCGGACCGGACCGGACCGGACCGGACCGG	466
QY	162	AsnGlyIleGlyCysSerGlyProLeuProIleGlyAlaIleIleIleLeuAspGlnGly	181
Db	467	AATGAGAGAGATGAG	526
QY	182	SerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeuGlyCys	201
Db	527	AGTCGGAGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG	586
QY	202	GlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAspTyr	221
Db	587	GAAGGAGATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	646
QY	222	ProGlyLeuAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGlnGlnLeu	241
Db	647	CCCGAGGAGATGCTTCTACTGAGAGATTCAGTCTCCGATCATCATGAGAGAGAGAGAG	706
QY	242	ProGlyLeu 243	
Db	707	CCAAA 712	

RESULT 31
 LOCUS BC079494 1290 bp mRNA linear VRT 03-AUG-2004
 DEFINITION Danio rerio cDNA clone MGC:101075 IMAGE:7153214, complete cds.
 ACCESSION BC079494
 VERSION BC079494.1 GI:50927421
 KEYWORDS MGC.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE
 AUTHORS
 1 (bases 1 to 1290)
 Straube, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Schaefer, T.E., Brownstein, M.J., Udell, T.B., Toshbuck, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mulvaney, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, X., Gibbs, R.A.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Sanchez, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Buetow, K.H., Krzywicki, M.I., Skalska, U., Smalins, D.E.,
 Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)
 12477932
 2 (bases 1 to 1290)
 Director MGC Project.
 Direct Submission
 Submitted (02-AUG-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Genome Institute of Singapore
 cDNA Library Preparation: S. Mathavan, Chia-Lin Wei, and Yijun
 Ruan, Genome Institute of Singapore
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINU)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland.
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nigti.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Leric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mestrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stancir, P., Thomas, P.J., Touchman, J.W.,
 Teurigon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINU at: <http://image.llnl.gov>
 Series: IRAL Plate: 60 Row: m Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, Similarity but not identity to protein.
 Location/Qualifiers
 1..1290
 /organism="Danio rerio"
 /mol_type="mRNA"
 /strain="Singapore local strain"
 /db_xref="taxon:7955"
 /clone="MGC:101075 IMAGE:7153214"
 /tissue_type="Embryo, 72 different stages (from just
 fertilized embryos to 72 hours just hatched baby fish)"
 /clone_lib="GIS2F001_1a"
 /lab_host="DH10B"
 /note="Vector: pDNR-LIB"
 77..772
 /codon_start=1
 /product="Unknown (protein for MGC:101075)"
 /protein_id="AAH79494.1"

CDS

ORIGIN

Alignment Scores:

Pred. No.: 4.32e-49 Length: 860

Score: 720.00 Matches: 134

Percent Similarity: 98.54% Conservative: 1

Best Local Similarity: 97.81% Mismatches: 2

Query Match: 55.34% Indels: 0

DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX285214 (1-860)

QY 107 LysGlnCysSerTrpSerSerLeuAsnTrpGlyTlleAspLeuGlyLysTlleAlaGluCys 126

DB 837 AGAAACATGTCATGAGGTCATGATTAATGGCATGATCTGGGAAATGGGAGTGT 778

QY 127 ThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146

DB 777 ACATTTCACAAACATGCTTCACAAATGCTCTAAGAGTTTGTTCAGTGCTCATTGCT 718

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTrpTrpPheThrPheAsnGlyAlaGluCys 166

DB 717 CTAAATGCAAGAAATGATGCTGTCAGCGTTGGTATTTCACATTCATGAGCTGATGT 658

QY 167 SerGlyProLeuProTlleGlnAlaTlleIleTrpLeuAspGlnGlySerProGluMetAsn 186

DB 657 TCAGAACCTCTCCCATTAAGCTTAATTAATTTGACCAAGAAAGCCCTGAAATGAAT 598

QY 187 SerThrIleAsnTlleHisArgThrSerSerValGluGlyLeuGlnGlyTlleGlyAla 206

DB 597 TCACAAATTAATATTCATGATGCACTTCTCTGAGAAAGACTTTGTAAAGAAATGGTGT 538

QY 207 GlyLeuValAspValAlaTlleTrpValGlyTrpCysSerAspTrpProLysGlyAspAla 226

DB 537 GGATTAAGGAGATGTGCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAAAGATGTCT 478

QY 227 SerThrGlyTrpAsnSerValSerArgTlleTlleGlnGluLeuProLys 243

DB 477 TCTACTGATGAAATTCAGTTCTTCGCATCATTAATTAAGAACTACCAAAA 427

RESULT 34

LOCUS CQ412972 539 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 20043 from Patent WO0170979.

ACCESSION CQ412972

VERSION CQ412972.1 GI:41320753

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Lee, J. and Lillie, J.

AUTHORS

TITLE

Genes, compositions, kits, and method for identification, assessment, prevention and therapy of ovarian cancer

JOURNAL

Patent: WO 0170979-A 20043 27-SEP-2001;

Millennium Pharmaceuticals, Inc. (US)

FEATURES

source

1. 539

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1.14e-43 Length: 539

Score: 650.00 Matches: 116

Percent Similarity: 98.31% Conservative: 0

Best Local Similarity: 98.31% Mismatches: 2

Query Match: 49.96% Indels: 0

DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x CQ412972 (1-539)

QY 51 TyraenGlyMetCysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGly 70

DB 165 TATATGGAATGTGTTTCAAGGCGCAGAGATGCTGTGACAGCGGAGCCCTGGG 244

QY 71 AlaAsnValTlleProGlyThrProGlyTlleProGlyArgAspGlyPheLysGlyLys 90

DB 245 GCCAATGCAATTCGCGGTACACCTGGGATCCAGATGGGATGATTAAGGAGAAAG 304

QY 91 GlyGluCysLeuArgGlnSerPheGlnGlnSerTrpThrProAsnTrpLysGlnCysSer 110

DB 305 GGGGATGCTGAGGAGAAAGCTTTGAGAGTCTTGACACCACTACAGCAGTGTCA 364

QY 111 TrpSerSerLeuAsnTrpGlyTlleAspLeuGlyLysTlleAlaGluCysThrPheThrLys 130

DB 365 TGAGATTCATTGAATTAATGACATGATCTTGAGAAATTTGGAGTGTACATTACAAAG 424

QY 131 MetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuLysCysArg 150

DB 425 ATGCGTCAAAATAGTGTCTAAGAGTTTGTTCAGTGCTCATTGCGGCTAAATGACAG 484

QY 151 AsnAlaCysCysGlnArgTrpTrpPheThrPheAsnGlyAlaGluCysSerGly 168

DB 485 AATGCAATCTGTCCGCGTTGGATTTCAATTCATGAGCTGAAATGTCAGGA 538

RESULT 35

LOCUS CQ407408 516 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 14479 from Patent WO0170979.

ACCESSION CQ407408

VERSION CQ407408.1 GI:4135189

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Lee, J. and Lillie, J.

AUTHORS

TITLE

Genes, compositions, kits, and method for identification, assessment, prevention and therapy of ovarian cancer

JOURNAL

Patent: WO 0170979-A 14479 27-SEP-2001;

Millennium Pharmaceuticals, Inc. (US)

FEATURES

source

1. 516

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 6.45e-42 Length: 516

Score: 628.00 Matches: 111

Percent Similarity: 96.55% Conservative: 1

Best Local Similarity: 95.69% Mismatches: 4

Query Match: 48.27% Indels: 0

DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x CQ407408 (1-516)

QY 51 TyraenGlyMetCysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGly 70

DB 167 TATATGGAATGTGTTTCAAGGCGCAGAGATGCTGTGAGACGGGAGCCCTGGG 226

QY 71 AlaAsnValTlleProGlyThrProGlyTlleProGlyArgAspGlyPheLysGlyLys 90

DB 227 GCCAATGCAATTCGCGGTACACCTGGGATCCAGATGGGATTCAAAGGAGAAAG 286

QY 91 GlyGluCysLeuArgGlnSerPheGlnGlnSerTrpThrProAsnTrpLysGlnCysSer 110

DB 287 GGGGATGCTGAGGAGAAAGCTTTGAGAGTCTTGAGACCACTACAGCAGTGTCA 346

QY 111 TrpSerSerLeuAsnTrpGlyTlleAspLeuGlyLysTlleAlaGluCysThrPheThrLys 130

Db 347 TGGAGTTCATTGATTAATGCGATAGATCTTGGGAAATTTGGAGCTGATCATTACAAAG 406
Qy 131 MetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuGlySerArg 150
Db 407 ATGCGTTCAAAATAGTCTCTAAAGATGTTTGTTCAGAGGCTCACTTGGCTAAATGCAAA 466
Qy 151 AanaIaCyGcGlnArgTPrTyRPhethrPheAsnGlyAlaGluCys 166
Db 467 AATGATGCTGTCGCCGCTTGATTTCACTTCATTCAGAGCTGAAATGT 514

RESULT 36
AX340025 471 bp DNA linear PAT 10-JAN-2002
LOCUS Sequence 272 from Patent WO0196388.
DEFINITION AX340025
ACCESSION AX340025 GI:18136006
VERSION AX340025.1 GI:18136006
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 Jiang, Y., Harlocker, S.L. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0196388-A 272 20-DEC-2001;
FEATURES
source CORIXA CORPORATION (US)
1. .471
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 8.43e-42 Length: 471
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX340025 (1-471)

Qy 127 ThrPheThrIyMeArGSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
Db 1 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAAGATTTTGTTCAGTGCCTCATTCCG 60
Qy 147 LeuIyCyArgAsnIaCyGcGlnArgTPrTyRPhethrPheAsnGlyAlaGluCys 166
Db 61 CTAAATGCAAGAAATGCGATGCTGTCAGCGTTGATTTTCATTCATTCAGAGCTGAATGT 120
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAsn 186
Db 121 TCGAGACCTCTTCCATTGAGAGCTATATATTATTGAGACCAAGAGCCCTGAAATGAAT 180
Qy 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCyGcGlnGlyIleGlyAla 206
Db 181 TCACACATTAATTAATTCATGCACTTCTTGTGGAAGGACCTTGTGAAGGAATTTGGTGCT 240
Qy 207 GlyLeuValAspValAlaIleTPrValGlyThrCySerAspTrpProGlySerGlyAspAla 226
Db 241 GGATTGATGATGATGCTATCTGAGTGGCACTTGTCAGATTAACCAAAAGAGATGCT 300
Qy 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlys 243
Db 301 TCACACTGATGGAATTCAGTTTCTCGCATCATTAATGGAAGAACTACCAAAA 351

RESULT 37
AR280558 683 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 63 from patent US 6518237.
DEFINITION AR280558
ACCESSION AR280558

VERSION AR280558.1 GI:29716028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Yuguo, J., Dillon, D.C., Mitcham, J.L. and Xu, J.
TITLE Compositions for treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6518237-A 63 11-FEB-2003;
FEATURES
source Location/Qualifiers
1. .683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.28e-41 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR280558 (1-683)

Qy 127 ThrPheThrIyMeArGSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
Db 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAAGATTTTGTTCAGTGCCTCATTCCG 624
Qy 147 LeuIyCyArgAsnIaCyGcGlnArgTPrTyRPhethrPheAsnGlyAlaGluCys 166
Db 623 CTAAATGCAAGAAATGCGATGCTGTCAGCGTTGATTTTCATTCATTCAGAGCTGAATGT 564
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAsn 186
Db 563 TCGAGACCTCTTCCATTGAGAGCTATATATTATTGAGACCAAGAGCCCTGAAATGAAT 504
Qy 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCyGcGlnGlyIleGlyAla 206
Db 503 TCACACATTAATTAATTCATGCACTTCTTGTGGAAGGACCTTGTGAAGGAATTTGGTGCT 444
Qy 207 GlyLeuValAspValAlaIleTPrValGlyThrCySerAspTrpProGlySerGlyAspAla 226
Db 443 GGATTGATGATGATGCTATCTGAGTGGCACTTGTCAGATTAACCAAAAGAGATGCT 384
Qy 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlys 243
Db 383 TCACACTGATGGAATTCAGTTTCTCGCATCATTAATGGAAGAACTACCAAAA 333

RESULT 38
AR283054/c 683 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 63 from patent US 6528054.
DEFINITION AR283054
ACCESSION AR283054
VERSION AR283054.1 GI:29719881
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6528054-A 63 04-MAR-2003;
FEATURES
source Location/Qualifiers
1. .683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:

Pred. No.: 1,286-41 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR283054 (1-683)

QY 127 ThrPheThrIlyMeArSerSerAenSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
DB 683 ACATTACAAAGATGGCTTCAATATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 147 LeuIlySvArGAsnAlaCySvSgInArGTrpTyRPhetThrPheAsnGlyAlaGluCyS 166
DB 623 CTAAGATGCAAGAAATCATGCTGCTGAGCCGTGGTATTCACATTCATGAGCTGAATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAen 186
DB 563 TCAGAGACCTCTCCCATTTAGCTATTAATTTATTTGACCAAGAACCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArGTrhSerSerValGluGlyLeuCySgInGlyIleGlyAla 206
DB 503 TCACCAATTAAATTCATCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATGGTGT 444
QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySerAspTyRProLySgIyAspAla 226
DB 443 GGATTAGTGAGATGTTGCTATCTGGGTGGVACTTGTTCAGATTACCAAGAGATGTCT 384
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProLyS 243
DB 383 TCTACTGGATGGAATTCAGTTCTCGATCATTAATTAAGAACTACCAAAA 333

RESULT 39
AR341827/c
LOCUS AR341827 683 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6573368.
ACCESSION AR341827
VERSION AR341827.1 GI:33736404
KEYWORDS
SOURCE
ORGANISM
Unclasseified.

REFERENCE
AUTHORS YuguJ., Dillon,D.C., Mitcham,J.L. and Xu,J.
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6573368-A 63 03-JUN-2003;
FEATURES
LOCATION/Qualifiers
SOURCE 1. 683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1,286-41 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR341827 (1-683)

QY 127 ThrPheThrIlyMeArSerSerAenSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
DB 683 ACATTACAAAGATGGCTTCAATATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 147 LeuIlySvArGAsnAlaCySvSgInArGTrpTyRPhetThrPheAsnGlyAlaGluCyS 166
DB 623 CTAAGATGCAAGAAATCATGCTGCTGAGCCGTGGTATTCACATTCATGAGCTGAATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAen 186

DB 563 TCAGAGACCTCTCCCATTTAGCTATTAATTTATTTGACCAAGAAAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArGTrhSerSerValGluGlyLeuCySgInGlyIleGlyAla 206
DB 503 TCACCAATTAAATTCATCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATGGTGT 444
QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySerAspTyRProLySgIyAspAla 226
DB 443 GGATTAGTGAGATGTTGCTATCTGGGTGGVACTTGTTCAGATTACCAAGAGATGTCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProLyS 243
DB 383 TCTACTGGATGGAATTCAGTTCTCGATCATTAATTAAGAACTACCAAAA 333

RESULT 40
AR343822/c
LOCUS AR343822 683 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6579973.
ACCESSION AR343822
VERSION AR343822.1 GI:33739722
KEYWORDS
SOURCE
ORGANISM
Unclasseified.

REFERENCE
AUTHORS YuguJ., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6579973-A 63 17-JUN-2003;
FEATURES
LOCATION/Qualifiers
SOURCE 1. 683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1,286-41 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR343822 (1-683)

QY 127 ThrPheThrIlyMeArSerSerAenSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
DB 683 ACATTACAAAGATGGCTTCAATATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 147 LeuIlySvArGAsnAlaCySvSgInArGTrpTyRPhetThrPheAsnGlyAlaGluCyS 166
DB 623 CTAAGATGCAAGAAATCATGCTGCTGAGCCGTGGTATTCACATTCATGAGCTGAATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAen 186
DB 563 TCAGAGACCTCTCCCATTTAGCTATTAATTTATTTGACCAAGAAAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArGTrhSerSerValGluGlyLeuCySgInGlyIleGlyAla 206
DB 503 TCACCAATTAAATTCATCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATGGTGT 444
QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySerAspTyRProLySgIyAspAla 226
DB 443 GGATTAGTGAGATGTTGCTATCTGGGTGGVACTTGTTCAGATTACCAAGAGATGTCT 384
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProLyS 243
DB 383 TCTACTGGATGGAATTCAGTTCTCGATCATTAATTAAGAACTACCAAAA 333

RESULT 41
AR351023/c
LOCUS AR351023 683 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 63 from patent US 6586572.
ACCESSION AR351023
VERSION AR351023.1 GI:33752702
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6586572-A 63 01-JUL-2003;
FEATURES Location/Qualifiers
source 1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-41	Length:	683
Score:	626.00	Matches:	117
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.12%	Indels:	0
DB:	6	Gaps:	0

US-10-063-734-122 (1-243) x AR351023 (1-683)

QY 127 ThrPheThrLyMetArgSerAsnSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
DB 683 ACATTACAAAGATCGCTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTCGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTPYrPheThrPheAsnGlyValaGluCys 166
DB 623 CTAAATGCAAGAAATGATGCTGTCAGCGGTGGATTCACATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCAATGAGCTATTAATTTTGGACCAAGAGCCCTGAATGAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGluGlyIleGlyAla 206
DB 503 TCAACATTAATATTCATGCACTTCTGTGGAAGCACTTGTGAAGAAATGGTGTCT 444

QY 207 GlyLeuValAspValAlaIleTPValGlyThrCysSerAspTYrProLysGlyAspAla 226
DB 443 GGATTAGTGATGTCTATCTGCGTGGYACTGTTCAAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProLys 243
DB 383 TCTACTGATGGAATTCAGTTCTCGATCATTAATGAAGAACTACCAAA 333

RESULT 42
AR352789/c
LOCUS AR352789 683 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6590076.
ACCESSION AR352789
VERSION AR352789.1 GI:33758194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Yugu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use
JOURNAL Patent: US 6590076-A 63 08-JUL-2003;
FEATURES Location/Qualifiers
source 1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-41	Length:	683
Score:	626.00	Matches:	117
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.12%	Indels:	0
DB:	6	Gaps:	0

US-10-063-734-122 (1-243) x AR352789 (1-683)

QY 127 ThrPheThrLyMetArgSerAsnSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
DB 683 ACATTACAAAGATCGCTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTCGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTPYrPheThrPheAsnGlyValaGluCys 166
DB 623 CTAAATGCAAGAAATGATGCTGTCAGCGGTGGATTCACATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCAATGAGCTATTAATTTTGGACCAAGAGCCCTGAATGAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGluGlyIleGlyAla 206
DB 503 TCAACATTAATATTCATGCACTTCTGTGGAAGCACTTGTGAAGAAATGGTGTCT 444

QY 207 GlyLeuValAspValAlaIleTPValGlyThrCysSerAspTYrProLysGlyAspAla 226
DB 443 GGATTAGTGATGTCTATCTGCGTGGYACTTTCAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProLys 243
DB 383 TCTACTGATGGAATTCAGTTCTCGATCATTAATGAAGAACTACCAAA 333

RESULT 43
AR453603/c
LOCUS AR453603 683 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 63 from patent US 6680197.
ACCESSION AR453603
VERSION AR453603.1 GI:42686393
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 683)
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: US 6680197-A 63 20-JAN-2004;
FEATURES Location/Qualifiers
source 1..683
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	1,28e-41	Length:	683
Score:	626.00	Matches:	117
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.12%	Indels:	0
DB:	6	Gaps:	0

US-10-063-734-122 (1-243) x AR453603 (1-683)

QY 127 ThrPheThrLyMetArgSerAsnSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
DB 683 ACATTACAAAGATCGCTCAATATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTCGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTPYrPheThrPheAsnGlyValaGluCys 166
DB 623 CTAAATGCAAGAAATGATGCTGTCAGCGGTGGATTCACATTCATGAGCTGATGT 564

Db 623 CTAAGATGAGAAAGCATGCTGTCAGCGTGGATTTCACATTCATGAGCTGATG 564
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
Db 563 TCAGAGACCTCTCCCATTTGAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAAT 504
Qy 167 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGlnGlyIleGlyAla 206
Db 503 TCACACATTAATATTCATGACACTTCTCTGTGGAAGACACTTTGTGAAGAAATGGTGCT 444
Qy 207 GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyProIlysgIyaAspAla 226
Db 443 GGATTAGTGAGATGTGCTATCTGGGTGGAGTGTTCGATTCAGATTAACCAAGAGATGCT 384
Qy 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProIlys 243
Db 383 TCTACTGGATGGAATTCAGTTTCTCGATCATCTATTATGAAAGACTACCAAA 333
RESULT 44
AX302743/c 683 bp DNA linear PAT 30-NOV-2001
LOCUS AX302743 Sequence 63 from Patent WO0179286.
DEFINITION AX302743
ACCESSION AX302743
VERSION AX302743.1 GI:17383244
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and
Hepler,W.T.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: WO 0179286-A 63 25-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..683
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.28e-41 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: Gaps: 0
US-10-063-734-122 (1-243) x AX302743 (1-683)
Qy 127 TherPhetrIlyMeArSerSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
Db 683 ACATTTCACAAAGATCGCTCAATATGCTCTCAAGAGTTTGTTCAGAGCTCAGCTCGG 624
Qy 147 LeuIysCysArgAsnAlaCysCysGlnArgTrpTyRheThrPheAsnGlyAlaGluCys 166
Db 623 CTAAGATGAGAAAGCATGCTGTCAGCGTGGATTTCACATTCATGAGCTGATGCT 564
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
Db 563 TCAGAGACCTCTCCCATTTGAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAAT 504
Qy 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGlnGlyIleGlyAla 206
Db 503 TCACACATTAATATTCATGACACTTCTCTGTGGAAGACACTTTGTGAAGAAATGGTGCT 444
Qy 207 GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyProIlysgIyaAspAla 226
Db 443 GGATTAGTGAGATGTGCTATCTGGGTGGAGTGTTCGATTCAGATTAACCAAGAGATGCT 384

Qy 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProIlys 243
Db 383 TCTACTGGATGGAATTCAGTTTCTCGATCATCTATTATGAAAGACTACCAAA 333
RESULT 45
AX375790/c 683 bp DNA linear PAT 01-MAR-2002
LOCUS AX375790 Sequence 3 from Patent WO0173031.
DEFINITION AX375790
ACCESSION AX375790
VERSION AX375790.1 GI:19170293
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J. and Stolk,J.A.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer
JOURNAL Patent: WO 0173031-A 3 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..683
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 3.91e-41 Length: 683
Score: 620.00 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 1
Query Match: 47.66% Indels: 0
DB: Gaps: 0
US-10-063-734-122 (1-243) x AX375790 (1-683)
Qy 127 TherPhetrIlyMeArSerSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
Db 683 ACATTTCACAAAGATCGCTCAATATGCTCTCAAGAGTTTGTTCAGAGCTCAGCTCGG 624
Qy 147 LeuIysCysArgAsnAlaCysCysGlnArgTrpTyRheThrPheAsnGlyAlaGluCys 166
Db 623 CTAAGATGAGAAAGCATGCTGTCAGCGTGGATTTCACATTCATGAGCTGATGCT 564
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186
Db 563 TCAGAGACCTCTCCCATTTGAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAAT 504
Qy 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGlnGlyIleGlyAla 206
Db 503 TCACACATTAATATTCATGACACTTCTCTGTGGAAGACACTTTGTGAAGAAATGGTGCT 444
Qy 207 GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyProIlysgIyaAspAla 226
Db 443 GGATTAGTGAGATGTGCTATCTGGGTGGAGTGTTCGATTCAGATTAACCAAGAGATGCT 384
Qy 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProIlys 243
Db 383 TCTACTGGATGGAATTCAGTTTCTCGATCATCTATTATGAAAGACTACCAAA 333
RESULT 46
AX067343 687 bp DNA linear PAT 24-JAN-2001
LOCUS AX067343 Sequence 47 from Patent WO0078960.
DEFINITION AX067343
ACCESSION AX067343
VERSION AX067343.1 GI:12544967
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Yuglu, J. and Mitcham, J.L.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer

JOURNAL Cancer
Patent: WO 0078960-A 47 28-DEC-2000;
CORIXA CORPORATION (US)
Location/Qualifiers

FEATURES
source 1. 687
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. 687
/note="n = A,T,C or G"

ORIGIN
Alignment Scores:
Pred. No.: 2,376-34 Length: 687
Score: 536.00 Matches: 98
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 1
Query Match: 41.20% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX067343 (1-687)

QY 145 LeuArgLeuLysGlyAspAsnAlaCysGlyAsnArgTrpPheThrPheAsnGlyAla 164
DB 1 CTTGGCTAAAGATGCAAGATGATGCTGTCAGCGTTGATTTACATTCAATGAGAGCT 60

QY 165 GluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGlu 184
DB 61 GATGTGTSAGACCTCTTCCCATGAAAGCTAATATTATTTGACCAAGAAAGCCCTGAA 120

QY 185 MetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyGlyIle 204
DB 121 ATGAATTTCAACATTAATATTCAATCCACATTTCTTGTGGAGAGACCTTGTGAAGAAAT 180

QY 205 GlyAlaGlyLeuValAspValAlaIleTyrValGlyTyrCysSerAspTyrProGlyGly 224
DB 181 GGTCGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 225 AspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeuProGly 243
DB 241 GATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 297

RESULT 47
COS14013 COS14013 555 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 45880 from Patent WO0160860.
DEFINITION COS14013
ACCESSION COS14013
VERSION COS14013.1 GI:41480277
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 45880 23-APR-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
source 1. 555
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1,296-29 Length: 555
Score: 476.00 Matches: 88
Percent Similarity: 100.00% Mismatches: 1
Conservative: 1

Best Local Similarity: 98.88% Mismatches: 0
Query Match: 36.59% Indels: 0
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x COS14013 (1-555)

QY 126 CysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeu 145
DB 288 TGTACATTTCACAAAGATGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGCTCAGCT 347

QY 146 ArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAsnGlyAlaGlu 165
DB 348 CCGTTAAATGACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407

QY 166 CysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMet 185
DB 408 TGTTCAGGACCTTCTCCCATTAAGCTAATATTATTTGACCAAGAAAGCCCTGAAATG 467

QY 186 AsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyGlyIleGly 205
DB 468 AATTCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 527

QY 206 AlaGlyLeuValAspValAlaIleTyr 214
DB 528 GCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 554

RESULT 48
AX284686 AX284686 271 bp DNA linear PAT 20-NOV-2001
LOCUS Sequence 491 from Patent WO0179556.
DEFINITION AX284686
ACCESSION AX284686
VERSION AX284686.1 GI:17045374
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Little, J., Brown, J.L., Bolt, A. and van Hufel, C.
TITLE Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers
JOURNAL Patent: WO 0179556-A 491 25-OCT-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
source 1. 271
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3,066-29 Length: 271
Score: 467.00 Matches: 90
Percent Similarity: 98.90% Conservative: 0
Best Local Similarity: 98.90% Mismatches: 0
Query Match: 35.90% Indels: 1
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX284686 (1-271)

QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 1 ACATTTACAAAGATGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGCTCAGCT 60

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAsnGlyAlaGluGly 166
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 Direct Submission
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 Research, 320 Charles Street, Cambridge, MA 02141, USA
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 Direct Submission
 Submitted (17-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
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; Patent No. 6476195
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; FILE REFERENCE: P2031P1
; CURRENT FILING DATE: 2000-01-24
; EARLIER FILING DATE: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
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QY 188 GCTGCTCTGCTGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTG 247
DB 191 GCTGCTCTGCTGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCT 250
QY 248 GCAAAAAGCGCGAGCTCCGCGCAGAGGAGAGGTGTGACCTGTATTAATGGAATGTCTT 307
DB 251 GCAAAAAGCGCGAGCTCCGCGCAGAGGAGAGGTGTGACCTGTATTAATGGAATGTCTT 310
QY 308 AGGCGCAGCAGAGAGTCTGCTGCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 367
DB 311 AGGCGCAGCAGAGAGTCTGCTGCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 370
QY 368 ACTGCGGATCCAGGTGCGAGTGTATTCAAAAGAAAAGGGGAGATGTCTGAGGGAAG 427
DB 371 ACTGCGGATCCAGGTGCGAGTGTATTCAAAAGAAAAGGGGAGATGTCTGAGGGAAG 430
QY 428 CTTTGAAGAGTCTGCGACACCACTAACAAGAGTGTTCATGAGTTCAATTAATGAG 487
DB 431 CTTTGAAGAGTCTGCGACACCACTAACAAGAGTGTTCATGAGTTCAATTAATGAG 490
QY 488 CATGATCTTGGGAAATTTGGGAGGTACATTTTCAAAAGATGGTTCAATTAATGAGCTCT 547
DB 488 CATGATCTTGGGAAATTTGGGAGGTACATTTTCAAAAGATGGTTCAATTAATGAGCTCT 547
```

```
DB 491 CATGATCTTGGGAAATTTGGGAGGTACATTTACAAAAGATGGCTTCAATTAATGCTCT 550
QY 548 AAGAGTTTGTTCAGTGTGCTCACTTCGCTTAAATGCAAGAAATGCAATGCTGTAGCTTG 607
DB 551 AAGAGTTTGTTCAGTGTGCTCACTTCGCTTAAATGCAAGAAATGCAATGCTGTAGCTTG 610
QY 608 GTATTTCACTTCAATGAGCTGAATGTTCAGAGACTCTTCCATTAAGCTAATTAATTA 667
DB 611 GTATTTCACTTCAATGAGCTGAATGTTCAGAGACTCTTCCATTAAGCTAATTAATTA 670
QY 668 TTTGACCAAGAGAGCCCTGAATGAATTCACCAATTAATTAATTCATGCACTTCTCTGT 727
DB 671 TTTGACCAAGAGAGCCCTGAATGAATTCACCAATTAATTAATTCATGCACTTCTCTGT 730
QY 728 GGAAGACTTTGTGAAGAAATTTGTGCTGATTTGTGATGATGCTATCGGTTGGAC 787
DB 731 GGAAGACTTTGTGAAGAAATTTGTGCTGATTTGTGATGATGCTATCGGTTGGAC 790
QY 788 TTTGACATTAACCAAAAGAGATGCTTCACTGATGAGAAATTCAGTTCTCGCATCAT 847
DB 791 TTTGACATTAACCAAAAGAGATGCTTCACTGATGAGAAATTCAGTTCTCGCATCAT 850
QY 848 TATTGAGACTTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTTATATAT 907
DB 851 TATTGAGACTTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTTATATAT 910
QY 908 GCCTTGAATGCTTCACTTAAATGACATTTTAAATTAATGATTAATGATTAATGATTA 967
DB 911 GCCTTGAATGCTTCACTTAAATGACATTTTAAATTAATGATTAATGATTAATGATTA 970
QY 968 AAGCAAGCTAATATGTTTACAGACCAAGTGTATTTCACTGTTTAAATCTAGC 1027
DB 971 AAGCAAGCTAATATGTTTACAGACCAAGTGTATTTCACTGTTTAAATCTAGC 1030
QY 1028 ATTATCACTTTGCTTCAATTAAGTGTTCATATTTTGTAGTTGTTAGAAATAC 1087
DB 1031 ATTATCACTTTGCTTCAATTAAGTGTTCATATTTTGTAGTTGTTAGAAATAC 1090
QY 1088 TTTCTTCACTGATTCATCTCTCAACCTTAATTTGGAATGTTGTGCTTTTGT 1147
DB 1091 TTTCTTCACTGATTCATCTCTCAACCTTAATTTGGAATGTTGTGCTTTTGT 1150
QY 1148 TTTCTTCACTGATTCATCTCTCAACCTTAATTTGGAATGTTGTGCTTTTGT 1207
DB 1151 TTTCTTCACTGATTCATCTCTCAACCTTAATTTGGAATGTTGTGCTTTTGT 1210
QY 1208 AAATGTTAAGATTTTATTAATATCTGTTAAATTAATTAATTTTCCACA 1257
DB 1211 AAATGTTAAGATTTTATTAATATCTGTTAAATTAATTAATTTTCCAAA 1260

RESULT 2
US-09-489-847-124
; Sequence 124, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT FILING DATE: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
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NUMBER OF SEQ ID NOS: 376
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 124
LENGTH: 1286
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1284)
OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-124

Query Match 97.3%; Score 1222.8; DB 4; Length 1286;
Best Local Similarity 99.7%; Pred. No. 5.3e-282;
Matches 1246; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 8 GCGCGCGGGGTAAAGGCGCATTTGATGACGCTGCGGCGGCTCGAGAGCGCGGAGCC 67
DB 2 GCGCGCGGGGTAAAGGCGCATTTGATGACGCTGCGGCGGCTCGAGAGCGCGGAG-C 60
QY 68 AAGCGTGAACAAGTCT 127
DB 61 AAGCGTGAACAAGTCT 120
QY 128 GCGCGAGCGCATGCGACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 187
DB 121 GCGCGAGCGCATGCGACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 188 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
DB 181 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 248 GGAAGAGGCGGCGCT 307
DB 241 GGAAGAGGCGGCGCT 299
QY 308 AGGCGCAGCAGAGAGTCT 367
DB 300 AGGCGCAGCAGAGAGTCT 359
QY 368 ACCTGGAGTCCAGGTCGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 360 ACCTGGAGTCCAGGTCGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
QY 428 CTTTGAAGAGTCT 487
DB 420 CTTTGAAGAGTCT 479
QY 488 CATAGATCTTGGGAAATTTGCGGAGTATCATTTACAAAGATGCGTTCAATATGATGCT 547
DB 480 CATAGATCTTGGGAAATTTGCGGAGTATCATTTACAAAGATGCGTTCAATATGATGCT 539
QY 548 AAGAGTTTTTGTCTAGTGTCT 607
DB 540 AAGAGTTTTTGTCTAGTGTCT 599
QY 608 GATTTTCAATTCATGAGTCTGATGATTTTCAAGAGCTCTCTCTCTCTCTCTCTCTCTCT 667
DB 600 GATTTTCAATTCATGAGTCTGATGATTTTCAAGAGCTCTCTCTCTCTCTCTCTCTCTCT 659
QY 668 TTTGAGCAAGAGAGCGCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 727
DB 660 TTTGAGCAAGAGAGCGCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 719
QY 728 GGAAGAGCTTTTGAAGAGATTTGCTGATTTAGTGAATTTGCTATCTGAGTTGGAC 787
DB 720 GGAAGAGCTTTTGAAGAGATTTGCTGATTTAGTGAATTTGCTATCTGAGTTGGAC 779
QY 788 TTTGTTCAATTCATGAGTCTGATGATTTTCAAGAGCTCTCTCTCTCTCTCTCTCTCTCT 847
DB 780 TTTGTTCAATTCATGAGTCTGATGATTTTCAAGAGCTCTCTCTCTCTCTCTCTCTCTCT 839
QY 848 TATTAAGAGATTAAG 907

DB 840 TATTAAGAGATTAAG 899
QY 908 GCGTTGGAATGGTTACCTTAAATGACATTTTAAATAGTTATGATACATGATGAATGA 967
DB 900 GCGTTGGAATGGTTACCTTAAATGACATTTTAAATAGTTATGATACATGATGAATGA 959
QY 968 AAGCAAGCTAAATATGTTTACAGACCAAGAGTATGATTTTCACTGTTTTTAAATCTAGC 1027
DB 960 AAGCAAGCTAAATATGTTTACAGACCAAGAGTATGATTTTCACTGTTTTTAAATCTAGC 1019
QY 1028 ATTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTTTTTGTGTTAGAAATAC 1087
DB 1020 ATTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTTTTTGTGTTAGAAATAC 1079
QY 1088 TTTCTTCAATGATCAATTTCTGACACCTATTAATTTGGAATATGTTGTTGTTTGT 1147
DB 1080 TTTCTTCAATGATCAATTTCTGACACCTATTAATTTGGAATATGTTGTTGTTTGT 1139
QY 1148 TTTCTTCAATGATCAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1207
DB 1140 TTTCTTCAATGATCAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1199
QY 1208 AAATGTTAAGATTTTTTTTATATCTGTTAAATTAATTAATTAATTAATTAATTAAT 1257
DB 1200 AAATGTTAAGATTTTTTTTATATCTGTTAAATTAATTAATTAATTAATTAATTAAT 1249

RESULT 3
US-09-692-081-3
Sequence 3, Application US/09692081
Patent No. 6630325

GENERAL INFORMATION:
APPLICANT: LINDNER, Volkhard
APPLICANT: FRISSEL, Robert F.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
CURRENT APPLICATION NUMBER: US/09/692,081
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
LENGTH: 1220
TYPE: DNA
ORGANISM: Homo sapiens
US-09-692-081-3

Query Match 95.4%; Score 1199.8; DB 4; Length 1220;
Best Local Similarity 99.8%; Pred. No. 1.6e-276;
Matches 1212; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 43 GCGGCTCTCGAGCGGCGGAGCGGAGCGTACGACGCTCTCTCTCTCTCTCTCTCTCTCT 102
DB 6 GCGGCTCTCGAGCGGCGGAGCGGAGCGTACGACGCTCTCTCTCTCTCTCTCTCTCTCT 65
QY 103 GCGTCAAGTCTCGGCTGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 162
DB 66 GCGTCAAGTCTCGGCTGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 125
QY 163 CCCGCAAGGAGTCTCGGCGGCT 222
DB 126 CCCGCAAGGAGTCTCGGCGGCT 185
QY 223 GCGCTCTGAGATCTCCCAAGGAGGAGCAAAAGGCGCAGCTCTCGGAGAGGAGTGTGG 282
DB 186 GCGCTCTGAGATCTCCCAAGGAGGAGCAAAAGGCGCAGCTCTCGGAGAGGAGTGTGG 245
QY 283 ACCTGTTATATGAGATGTGCTTACAAAGGCGGAGCGGAGTGTGCTGTTGAGAGCGGAGCC 342
DB 246 ACCTGTTATATGAGATGTGCTTACAAAGGCGGAGCGGAGTGTGCTGTTGAGAGCGGAGCC 305
QY 343 CTGGGCGCAATGTTATCTCGGAGTACCTGGAGTCCAGAGTGTGGATGATTAAGAGAG 402

Db 306 CTGGGGCCAATGCGATCCGGGTACACCTGGAGTCCAGGTGGATGATTCAAAGGAG 365
Qy 403 AAAAGGGGGAATGTCTGAGAGGAAGCTTTGAGAGTCTTGACACCCACTCAAGACAGT 462
Db 366 AAAAGGGGGAATGTCTGAGAGGAAGCTTTGAGAGTCTTGACACCCACTCAAGACAGT 425
Qy 463 GTTCATGAGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 522
Db 426 GTTCATGAGATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 485
Qy 523 CAAAGATGCGCTCAATAGTGTCTTAAGATTTTGTTCAGTGGCTCACTTGGCTTAAT 582
Db 486 CAAAGATGCGCTCAATAGTGTCTTAAGATTTTGTTCAGTGGCTCACTTGGCTTAAT 545
Qy 583 GCAGAAATGCAATGCTGAGCGTGTGATTTTCACTCAATCAATGAGCTGAATTTCAAGAC 642
Db 546 GCAGAAATGCAATGCTGAGCGTGTGATTTTCACTCAATCAATGAGCTGAATTTCAAGAC 605
Qy 643 CTCTTCCCATGGAAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 702
Db 606 CTCTTCCCATGGAAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 665
Qy 703 TTAATATCATGCGACTCTCTGTGGAAGGACTTGTGGAAGGAAATGGTGTGATTAAG 762
Db 666 TTAATATCATGCGACTCTCTGTGGAAGGACTTGTGGAAGGAAATGGTGTGATTAAG 725
Qy 763 TGAATGTGCTATCTGAGTGGCACTTGTTCAGATTAATCAAGAGAGAGTGTCTTACTG 822
Db 726 TGAATGTGCTATCTGAGTGGCACTTGTTCAGATTAATCAAGAGAGAGTGTCTTACTG 785
Qy 823 GATGGAATTCAGTTTCTGCGATCATTAATTAATTAATTAATTAATTAATTAATTAATTT 882
Db 786 GATGGAATTCAGTTTCTGCGATCATTAATTAATTAATTAATTAATTAATTAATTT 845
Qy 883 CATTTGCTACCTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 942
Db 846 CATTTGCTACCTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTT 905
Qy 943 AAGTTTATGATACATCTGAATGAAGCAAGTAAATGTTTACAGACCAAGTGTG 1002
Db 906 AAGTTTATGATACATCTGAATGAAGCAAGTAAATGTTTACAGACCAAGTGTG 965
Qy 1003 ATTTCACGCTGTTTAAATCTAGCATTAATTAATTAATTAATTAATTAATTAATTT 1062
Db 966 ATTTCACGCTGTTTAAATCTAGCATTAATTAATTAATTAATTAATTAATTT 1025
Qy 1063 TATTTTATGATGTTAGTGAATTAATTAATTAATTAATTAATTAATTAATTT 1122
Db 1026 TATTTTATGATGTTAGTGAATTAATTAATTAATTAATTAATTAATTT 1084
Qy 1123 GGAATATGTTGTGCTTTTGTCTTTCTTATAGATTAATTAATTAATTAATTAATTA 1182
Db 1085 GGAATATGTTGTGCTTTTGTCTTTCTTATAGATTAATTAATTAATTAATTAATTA 1144
Qy 1183 AGCTACCAATTTTGTGATTAATTAATTAATTAATTAATTAATTAATTT 1242
Db 1145 AGCTACCAATTTTGTGATTAATTAATTAATTAATTAATTAATTT 1204
Qy 1243 AAATTAATTTCCACA 1257
Db 1205 AAATTAATTTCCACA 1219

RESULT 4

US-09-205-258-125
; Sequence 125, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 125
LENGTH: 1288
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1286)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-125

Query Match 95.2%; Score 1197; DB 4; Length 1288;

Best Local Similarity 99.3%; Pred. No. 7.5e-276; Mismatches 2; Indels 5; Gaps 4;

Matches 1242; Conservative 2; Mismatches 2; Indels 5; Gaps 4;

QY 8 GGGGCGGGGTGAAGAGCGCATTTGATGCAAGCTGCGGCGGCTCGAGAGCGGCGGAGCC 67
DB 1 GGGGCGGGGTGAAGAGCGCATTTGATGCAAGCTGCGGCGGCTCGAGAGCGGCGGAGCC 59
QY 68 AGAGCGTGACACAGCTTCTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCT 127
DB 60 AGAGCGTGACACAGCTTCTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCT 119
QY 128 GCGGAGAGCGATGCGAGCCCGAGGCGGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCT 187
DB 120 GCGGAGAGCGATGCGAGCCCGAGGCGGCGGCTCTCGGCTCTCGGCTCTCGGCTCTCGGCTCT 179
QY 188 GGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
DB 180 GGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
QY 248 GCAAAAGGCGGAGCTCTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
DB 240 GCAAAAGGCGGAGCTCTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 297
QY 308 AGGAGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 367
DB 298 AGGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
QY 368 ACCTGGGATCCAGGCTCGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 358 ACCTGGGATCCAGGCTCGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
QY 428 CTTTGAAGAGTCTGAGACACCACTACAGAGCTTCAATGAGTTCATTTGATTTATGAG 487
DB 418 CTTTGAAGAGTCTGAGACACCACTACAGAGCTTCAATGAGTTCATTTGATTTATGAG 477
QY 488 CATAGATCTTGGAGAAATTCGAGAGTGAATTCATTTAAGAGTTCATTTAAGAGTTCATTTA 547
DB 478 CATAGATCTTGGAGAAATTCGAGAGTGAATTCATTTAAGAGTTCATTTAAGAGTTCATTTA 537
QY 548 AAGAGTTTGTTCAGTGTCTCACTCGGCTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
DB 538 AAGAGTTTGTTCAGTGTCTCACTCGGCTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
QY 608 GATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 667
DB 598 GATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 657
QY 668 TTTGAGCAAGAGAGCGCTGAATTCAGAGTTCATTCATTCATTCATTCATTCATTCATTCAT 727
DB 658 TTTGAGCAAGAGAGCGCTGAATTCAGAGTTCATTCATTCATTCATTCATTCATTCATTCAT 717
QY 728 GGAAGAGCTTTGAGAGAGATTCGCTGAGTTCATTCATTCATTCATTCATTCATTCATTCAT 787

DB 718 GGAAGAGCTTTGAGAGAGATTCGCTGAGTTCATTCATTCATTCATTCATTCATTCATTCAT 777
QY 768 TTTGAGCAAGAGAGCGCTGAATTCAGAGTTCATTCATTCATTCATTCATTCATTCATTCAT 847
DB 778 TTTGAGCAAGAGAGCGCTGAATTCAGAGTTCATTCATTCATTCATTCATTCATTCATTCAT 837
QY 848 TATTCAG 907
DB 838 TATTCAG 897
QY 908 GCGTGGAGTGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 967
DB 898 GCGTGGAGTGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 957
QY 968 AGCAAGAGTAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1027
DB 958 AGCAAGAGTAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1016
QY 1028 ATTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1087
DB 1017 ATTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1076
QY 1088 TTTCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1146
DB 1077 TTTCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1136
QY 1147 TTTCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1206
DB 1137 TTTCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1196
QY 1207 TAAATGTGAAGATTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1257
DB 1197 TAAATGTGAAGATTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1247

RESULT 5

US-09-834-759-512

; Sequence 512, Application US/09834759

; Patent No. 6680197

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yugu

; APPLICANT: Dillon, David C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Hairlock, Susan L.

; APPLICANT: Henderson, Robert A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.470C9

; CURRENT APPLICATION NUMBER: US/09/834,759

; CURRENT FILING DATE: 2001-04-13

; NUMBER OF SEQ ID NOS: 547

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 512

; LENGTH: 837

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-834-759-512

Query Match 65.7%; Score 826; DB 4; Length 837;

Best Local Similarity 99.9%; Pred. No. 1.8e-187;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 32 ATGAGCGCTGCGGCGGCTCGAGAGCGGCGGAGCGAGAGCGAGAGAGAGAGAGAGAGAGAGAG 91
DB 1 ATGAGCGCTGCGGCGGCTCGAGAGCGGCGGAGCGAGAGCGAGAGCGAGAGAGAGAGAGAGAG 59
QY 92 CGGTCTCTCGGCTCTCGAGCTCCGCGCTGCGGCGAGCGGAGAGAGAGAGAGAGAGAGAGAG 151
DB 60 CGGTCTCTCGGCTCTCGAGCTCCGCGCTGCGGCGAGCGGAGAGAGAGAGAGAGAGAGAGAG 119
QY 152 CCGCGCGGCTCGGCGAGGAGCTCGGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 211

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Db      120 CCCCCCCCCCTCCCGCAGCGGCTCGCGGCTCCGCTGCTCTGCTCTGCAAGTGGC 179
Qy      212 CGCGCGCTGCGAGCGGCTCTGAGATCCCAAGGGGAAAGCAAAAGGGGAGCTCCGGCAGAG 271
Db      180 CGCGCGCTGCGAGCGGCTCTGAGATCCCAAGGGGAAAGCAAAAGGGGAGCTCCGGCAGAG 239
Qy      272 GGAAGTGTGAGCACTGTATTAATGATGTGCTTACAGAGGCCAGAGAGTCTGTGTG 331
Db      240 GGAAGTGTGAGCACTGTATTAATGATGTGCTTACAGAGGCCAGAGAGTCTGTGTG 299
Qy      332 AGAGGGAGCGCTCGGGGCAATGTATTCCGGGTACACCTGGGATCCAGTCCGGATGG 391
Db      300 AGAGGGAGCGCTCGGGGCAATGTATTCCGGGTACACCTGGGATCCAGTCCGGATGG 359
Qy      392 ATTCAAGAGGAAAGGGGGAATGTCTGAGGAAAGCTTGGAGAGTCTTGACACCCAA 451
Db      360 ATTCAAGAGGAAAGGGGGAATGTCTGAGGAAAGCTTGGAGAGTCTTGACACCCAA 419
Qy      452 CTACAGAGAGTGTTCATGAGATTCAATTATGAGATAGATCTTGGGAAATTTGCCGA 511
Db      420 CTACAGAGAGTGTTCATGAGATTCAATTATGAGATAGATCTTGGGAAATTTGCCGA 479
Qy      512 GTGTACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACT 571
Db      480 GTGTACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACT 539
Qy      572 TCGGCTAAATTCAGAAATGCAATGCTGTACAGCGTTGATTTACATTCATTCAGAGCTGA 631
Db      540 TCGGCTAAATTCAGAAATGCAATGCTGTACAGCGTTGATTTACATTCATTCAGAGCTGA 599
Qy      632 ATGTTCAGAGCTCTTCCCATTTAGACTAATATTTATTTGACCAAGAAAGCCCTGAAT 691
Db      600 ATGTTCAGAGCTCTTCCCATTTAGACTAATATTTATTTGACCAAGAAAGCCCTGAAT 659
Qy      692 GAATTCACCAATTAATATTCATTCGCACTTCTGTGGAAGAGCTTTGTGGAAGAAATGG 751
Db      660 GAATTCACCAATTAATATTCATTCGCACTTCTGTGGAAGAGCTTTGTGGAAGAAATGG 719
Qy      752 TGCATGATTAGTGTGATGCTATCTGGGTGGGCACTTGTGCAATTAACCAAAAGAGA 811
Db      720 TGCATGATTAGTGTGATGCTATCTGGGTGGGCACTTGTGCAATTAACCAAAAGAGA 779
Qy      812 TGCTTCTACTGATGAAATTCAGATTCTGCAATCAATTAATGAAGACTACCAAAATTA 869
Db      780 TGCTTCTACTGATGAAATTCAGATTCTGCAATCAATTAATGAAGACTACCAAAATTA 837

```

RESULT 6
US-09-834-759-513
Sequence 513, Application US/09834759
Patent No. 6680197

GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 513
LENGTH: 837
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-513

Query Match 65.7%; Score 826; DB 4; Length 837;
Best Local Similarity 99.9%; Pred. No. 1.8e-187;
Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

Qy      32 ATGCAGCTTGGCGGCGGCTCGAGCGGCGGAGCCAGACGCTGACCAAGCTTCTCTCT 91
Db      1 ATGCAGCTTGGCGGCGGCTCGAGCGGCGGAG-CAGAGCTGACCAAGCTTCTCTCT 59
Qy      92 CGGTCTCTCGGCTCCAGCTCCGCGCTCGCGGCAACCGGGAGCCATGAGACCCAGAG 151
Db      60 CGGTCTCTCGGCTCCAGCTCCGCGCTCGCGGCAACCGGGAGCCATGAGACCCAGAG 119
Qy      152 CCCGCGCGCTCCCGGAGCGGCTCCGCGGCTCTGCTCTGCTGCTGAGCTGGC 211
Db      120 CCCGCGCGCTCCCGGAGCGGCTCCGCGGCTCTGCTCTGCTGCTGAGCTGGC 179
Qy      212 CGCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGGCGCAGCTCCGGCAGAG 271
Db      180 CGCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAAGGCGCAGCTCCGGCAGAG 239
Qy      272 GGAAGTGTGAGCACTGTATTAATGATGTGCTTACAGAGGCCAGAGAGTGTGCTGTG 331
Db      240 GGAAGTGTGAGCACTGTATTAATGATGTGCTTACAGAGGCCAGAGAGTGTGCTGTG 299
Qy      332 AGAGGGAGCGCTCGGGGCAATGTATTCCGGGTACACCTGGGATCCAGTCCGGATGG 391
Db      300 AGAGGGAGCGCTCGGGGCAATGTATTCCGGGTACACCTGGGATCCAGTCCGGATGG 359
Qy      392 ATTCAAGAGGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGAGTCTTGACACCCAA 451
Db      360 ATTCAAGAGGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGAGTCTTGACACCCAA 419
Qy      452 CTACAGAGAGTGTTCATGAGATTCAATTATGAGATAGATCTTGGGAAATTTGCCGA 511
Db      420 CTACAGAGAGTGTTCATGAGATTCAATTATGAGATAGATCTTGGGAAATTTGCCGA 479
Qy      512 GTGTACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACT 571
Db      480 GTGTACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACT 539
Qy      572 TCGGCTAAATTCAGAAATGCAATGCTGTACAGCGTTGATTTACATTCATTCAGAGCTGA 631
Db      540 TCGGCTAAATTCAGAAATGCAATGCTGTACAGCGTTGATTTACATTCATTCAGAGCTGA 599
Qy      632 ATGTTCAGAGCTCTTCCCATTTAGACTAATATTTATTTGACCAAGAAAGCCCTGAAT 691
Db      600 ATGTTCAGAGCTCTTCCCATTTAGACTAATATTTATTTGACCAAGAAAGCCCTGAAT 659
Qy      692 GAATTCACCAATTAATATTCATTCGCACTTCTGTGGAAGAGCTTTGTGGAAGAAATGG 751
Db      660 GAATTCACCAATTAATATTCATTCGCACTTCTGTGGAAGAGCTTTGTGGAAGAAATGG 719
Qy      752 TGCATGATTAGTGTGATGCTATCTGGGTGGGCACTTGTGCAATTAACCAAAAGAGA 811
Db      720 TGCATGATTAGTGTGATGCTATCTGGGTGGGCACTTGTGCAATTAACCAAAAGAGA 779
Qy      812 TGCTTCTACTGATGAAATTCAGATTCTGCAATCAATTAATGAAGACTACCAAAATTA 869
Db      780 TGCTTCTACTGATGAAATTCAGATTCTGCAATCAATTAATGAAGACTACCAAAATTA 837

```

RESULT 7
US-09-834-759-510
Sequence 510, Application US/09834759
Patent No. 6680197

GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiaqun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-510

Query Match 58.2%; Score 732; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 4,3e-165;

Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 ATGCGACCCAGAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197
DB 1 ATGCCAGCCCGAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
QY 198 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 257
DB 61 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 120
QY 258 GAGCTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 317
DB 121 CAGCTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 180
QY 318 GAGTGCCTGCTGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 377
DB 181 GAGTGCCTGCTGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 240
QY 378 CAGGTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 437
DB 241 CAGGTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 300
QY 438 TCCTGGACACCCAGCTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 497
DB 301 TCCTGGACACCCAGCTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 360
QY 498 GGGAAATTTGCGAGTGTACATTTACAAAGATCGTTCAATAGTCTTAAGATTTTG 557
DB 361 GGGAAATTTGCGAGTGTACATTTACAAAGATCGTTCAATAGTCTTAAGATTTTG 420
QY 558 TTCAGTGCCTCACTTGGCTAAATGAGCAATGAGTGTGACGCTTGAATTTTACA 617
DB 421 TTCAGTGCCTCACTTGGCTAAATGAGCAATGAGTGTGACGCTTGAATTTTACA 480
QY 618 TTCATGAGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTTAAATTTTGAACCA 677
DB 481 TTCATGAGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTTAAATTTTGAACCA 540
QY 678 GGAAGCCCTGAATGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 737
DB 541 GGAAGCCCTGAATGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 600
QY 738 TGTGAAGGAAATGCTGATTAATGAGATGTTGCTATCTGAGTTGGCACTTGTCAGAT 797
DB 601 TGTGAAGGAAATGCTGATTAATGAGATGTTGCTATCTGAGTTGGCACTTGTCAGAT 660
QY 798 TACCCAAAAGAGAGCTTCTACTGATGAGATGCTTCTGAGTCAATTAATTAATTA 857
DB 661 TACCCAAAAGAGAGCTTCTACTGATGAGATGCTTCTGAGTCAATTAATTAATTA 720
QY 858 CTACCAAAATTA 869
DB 721 CTACCAAAATTA 732

RESULT 8
US-09-834-759-511
; Sequence 511, Application US/09834759

; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 511
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-511

Query Match 58.0%; Score 729; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 2,3e-164;

Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 ATGCGACCCAGAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197
DB 1 ATGCCAGCCCGAGGCGCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60
QY 198 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 257
DB 61 CTGCTGCACTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCG 120
QY 258 GAGCTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 317
DB 121 CAGCTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 180
QY 318 GAGTGCCTGCTGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 377
DB 181 GAGTGCCTGCTGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 240
QY 378 CAGGTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 437
DB 241 CAGGTCCGCGCAGAGGAGGTGAGCTGTAAATGAAATGCTTACAAAGGCCAGCA 300
QY 438 TCCTGGACACCCAGCTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 497
DB 301 TCCTGGACACCCAGCTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 360
QY 498 GGGAAATTTGCGAGTGTACATTTACAAAGATCGTTCAATAGTCTTAAGATTTTG 557
DB 361 GGGAAATTTGCGAGTGTACATTTACAAAGATCGTTCAATAGTCTTAAGATTTTG 420
QY 558 TTCAGTGCCTCACTTGGCTAAATGAGCAATGAGTGTGACGCTTGAATTTTACA 617
DB 421 TTCAGTGCCTCACTTGGCTAAATGAGCAATGAGTGTGACGCTTGAATTTTACA 480
QY 618 TTCATGAGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTTAAATTTTGAACCA 677
DB 481 TTCATGAGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTTAAATTTTGAACCA 540
QY 678 GGAAGCCCTGAATGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 737
DB 541 GGAAGCCCTGAATGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 600
QY 738 TGTGAAGGAAATGCTGATTAATGAGATGTTGCTATCTGAGTTGGCACTTGTCAGAT 797
DB 601 TGTGAAGGAAATGCTGATTAATGAGATGTTGCTATCTGAGTTGGCACTTGTCAGAT 660
QY 798 TACCCAAAAGAGAGCTTCTACTGATGAGATGCTTCTGAGTCAATTAATTAATTA 857
DB 661 TACCCAAAAGAGAGCTTCTACTGATGAGATGCTTCTGAGTCAATTAATTAATTA 720

QY 858 CTACCAAA 866
Db 721 CTACCAAAA 729

RESULT 9

US-09-222-575-63/c
; Sequence 63, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yuguil, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222.575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-63

Query Match 54.2%; Score 681.8; DB 3; Length 683;

Best Local Similarity 99.6%; Pred. No. 3.9e-153;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
Db 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 576 CTAAATATGCAAGATGATGCTGCTGACGCTGCTGATTTTTCACATTCAATGAGCTGAATGT 635
Db 623 CTAAATATGCAAGATGATGCTGCTGACGCTGCTGATTTTTCACATTCAATGAGCTGAATGT 564
QY 636 TCAGAGCTCTTCCCATTTGAAGCTATTAATTTATTTGGAACCAAGAGCCCTGAATGAAT 695
Db 563 TCAGAGCTCTTCCCATTTGAAGCTATTAATTTATTTGGAACCAAGAGCCCTGAATGAAT 504
QY 696 TCACAAATTAATATTCATGCACTTCTCTGGAAGACCTTTGGAAGATTTGCT 755
Db 503 TCACAAATTAATATTCATGCACTTCTCTGGAAGACCTTTGGAAGATTTGCT 444
QY 756 GGATTAAGATGATGCTGATCTGAGTGGGCTGGCACTTGTTCAGATTACCCAAAGAGATGCT 815
Db 443 GGATTAAGATGATGCTGATCTGAGTGGGCTGGCACTTGTTCAGATTACCCAAAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTTCTGCACTATTAATTTGGAACCTCAAAATTAATGCTT 875
Db 383 TCTACTGATGGAATTCAGTTTCTGCACTATTAATTTGGAACCTCAAAATTAATGCTT 324
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGACCTTGAATGCTTCACTTAATGACAT 935
Db 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGACCTTGAATGCTTCACTTAATGACAT 264
QY 936 TTTTAAATTAAGTTTATGATATCATCTGAATGAAAGCAAGCTAAATATGTTTACAGCCA 995
Db 263 TTTTAAATTAAGTTTATGATATCATCTGAATGAAAGCAAGCTAAATATGTTTACAGCCA 204
QY 996 AAGTGATTTTCACTGTTTATTAATCTAGCATTAATCTTGTCTCAATCAAAAGTG 1055
Db 203 AAGTGATTTTCACTGTTTATTAATCTAGCATTAATCTTGTCTCAATCAAAAGTG 144
QY 1056 GTTTCATATTTTATTTAGTTGTTAGATATCTTCTCAATGACATTTCTCAACT 1115
Db 143 GTTTCATATTTTATTTAGTTGTTAGATATCTTCTCAATGACATTTCTCAACT 84
QY 1116 ATAATTTGGAATATGTTGTGCTCTTTGTTTCTTCTTATGATGACATTTTAAAAA 1175

Db 83 ATAATTTGGAATATGTTGTGCTCTTTGTTTCTTCTTATGATGACATTTTAAAAA 24
QY 1176 ATAATTAAGCTACCAATCTTGT 1198
Db 23 ATAATTAAGCTACCAATCTTGT 1

RESULT 10

US-09-389-681-63/c
; Sequence 63, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuguil, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389.681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;

Best Local Similarity 99.6%; Pred. No. 3.9e-153;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
Db 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
QY 576 CTAAATATGCAAGATGATGCTGCTGACGCTGCTGATTTTTCACATTCAATGAGCTGAATGT 635
Db 623 CTAAATATGCAAGATGATGCTGCTGACGCTGCTGATTTTTCACATTCAATGAGCTGAATGT 564
QY 636 TCAGAGCTCTTCCCATTTGAAGCTATTAATTTATTTGGAACCAAGAGCCCTGAATGAAT 695
Db 563 TCAGAGCTCTTCCCATTTGAAGCTATTAATTTATTTGGAACCAAGAGCCCTGAATGAAT 504
QY 696 TCACAAATTAATATTCATGCACTTCTCTGGAAGACCTTTGGAAGATTTGCT 755
Db 503 TCACAAATTAATATTCATGCACTTCTCTGGAAGACCTTTGGAAGATTTGCT 444
QY 756 GGATTAAGATGATGCTGATCTGAGTGGGCTGGCACTTGTTCAGATTACCCAAAGAGATGCT 815
Db 443 GGATTAAGATGATGCTGATCTGAGTGGGCTGGCACTTGTTCAGATTACCCAAAGAGATGCT 384
QY 816 TCTACTGATGGAATTCAGTTTCTGCACTATTAATTTGGAACCTCAAAATTAATGCTT 875
Db 383 TCTACTGATGGAATTCAGTTTCTGCACTATTAATTTGGAACCTCAAAATTAATGCTT 324
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGACCTTGAATGCTTCACTTAATGACAT 935
Db 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGACCTTGAATGCTTCACTTAATGACAT 264
QY 936 TTTTAAATTAAGTTTATGATATCATCTGAATGAAAGCAAGCTAAATATGTTTACAGCCA 995
Db 263 TTTTAAATTAAGTTTATGATATCATCTGAATGAAAGCAAGCTAAATATGTTTACAGCCA 204
QY 996 AAGTGATTTTCACTGTTTATTAATCTAGCATTAATCTTGTCTCAATCAAAAGTG 1055
Db 203 AAGTGATTTTCACTGTTTATTAATCTAGCATTAATCTTGTCTCAATCAAAAGTG 144
QY 1056 GTTTCATATTTTATTTAGTTGTTAGATATCTTCTCAATGACATTTCTCAACT 1115
Db 143 GTTTCATATTTTATTTAGTTGTTAGATATCTTCTCAATGACATTTCTCAACT 84

Db 203 AAGGTGATTTACACGCTTTTAAATCTAGCATTAATCATTTTCTTCATCAAGAGG 144
Qy 1056 GTTTCATATTTTATTTTATTTAGTTGGTTAGAAATCTTCTCATAGTCAATCTTCAACCT 1115
Db 143 GTTTCATATTTTATTTTATTTAGTTGGTTAGAAATCTTCTTCATAGTCAATCTTCAACCT 84
Qy 1116 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 1175
Db 83 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 24
Qy 1176 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 1175
Db 23 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 24

RESULT 13
US-09-433-826B-63/C
; Sequence 63, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.9e-153;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 516 ACATTTCAGAAAGATGCGTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
Db 683 ACATTTCAGAAAGATGCGTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
Qy 576 CTAAATGCGAAGATGCGTCTGTCAGCGTTGGTATTTCACTTCATGAGCTGAATGT 635
Db 623 CTAAATGCGAAGATGCGTCTGTCAGCGTTGGTATTTCACTTCATGAGCTGAATGT 564
Qy 636 TCAGAGACCTCTCCCATTTGAGAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 695
Db 563 TCAGAGACCTCTCCCATTTGAGAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 504
Qy 696 TCACAAATTAATTAATTCATGCACTTCTCTGGAAGAGACTTGTGAGAAATGGTGTCT 755
Db 503 TCACAAATTAATTAATTCATGCACTTCTCTGGAAGAGACTTGTGAGAAATGGTGTCT 444
Qy 756 GGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTTGTCAGATTAACCAAGAAAGATGCT 815
Db 443 GGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTTGTCAGATTAACCAAGAAAGATGCT 384
Qy 816 TCTACTGAGTGAATTCAGTTTCTGTCGATCATTAATGAAGAACTACCAAAATTAATGCTT 875
Db 324 TCTACTGAGTGAATTCAGTTTCTGTCGATCATTAATGAAGAACTACCAAAATTAATGCTT 324
Qy 876 TAAATTTTCACTTCTCTCTTTTATTTATATGCTTGAATGGTCACTTAATGACAT 935
Db 323 TAAATTTTCACTTCTCTCTTTTATTTATATGCTTGAATGGTCACTTAATGACAT 264
Qy 936 TTAATTTTCACTTCTCTCTTTTATTTATATGCTTGAATGGTCACTTAATGACAT 995

Db 263 TTAATAAGTTATATGATATACATCTGAATGAAAAAGCAAGCTAAATATGTTTACAGACCA 204
Qy 996 AAGGTGATTTACACGCTTTTAAATCTAGCATTAATCATTTTGTTCATCAAGAGG 1055
Db 203 AAGGTGATTTACACGCTTTTAAATCTAGCATTAATCATTTTGTTCATCAAGAGG 144
Qy 1056 GTTTCATATTTTATTTTATTTAGTTGGTTAGAAATCTTCTCATAGTCAATCTTCAACCT 1115
Db 143 GTTTCATATTTTATTTTATTTAGTTGGTTAGAAATCTTCTTCATAGTCAATCTTCAACCT 84
Qy 1116 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 1175
Db 83 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 24
Qy 1176 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 1175
Db 23 ATATTTGGAAATATTTGTTGCTTTTCTTTCTCTAGTATAGCATTTTAAAAA 24

RESULT 14
US-09-604-287A-63/C
; Sequence 63, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.9e-153;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 516 ACATTTCAGAAAGATGCGTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 575
Db 683 ACATTTCAGAAAGATGCGTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTCGG 624
Qy 576 CTAAATGCGAAGATGCGTCTGTCAGCGTTGGTATTTCACTTCATGAGCTGAATGT 635
Db 623 CTAAATGCGAAGATGCGTCTGTCAGCGTTGGTATTTCACTTCATGAGCTGAATGT 564
Qy 636 TCAGAGACCTCTCCCATTTGAGAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 695
Db 563 TCAGAGACCTCTCCCATTTGAGAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 504
Qy 696 TCACAAATTAATTAATTCATGCACTTCTCTGGAAGAGACTTGTGAGAAATGGTGTCT 755
Db 503 TCACAAATTAATTAATTCATGCACTTCTCTGGAAGAGACTTGTGAGAAATGGTGTCT 444
Qy 756 GGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTTGTCAGATTAACCAAGAAAGATGCT 815
Db 443 GGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTTGTCAGATTAACCAAGAAAGATGCT 384
Qy 816 TCTACTGAGTGAATTCAGTTTCTGTCGATCATTAATGAAGAACTACCAAAATTAATGCTT 875
Db 324 TCTACTGAGTGAATTCAGTTTCTGTCGATCATTAATGAAGAACTACCAAAATTAATGCTT 324
Qy 876 TAAATTTTCACTTCTCTCTTTTATTTATATGCTTGAATGGTCACTTAATGACAT 935


```
Db 253 TATAATGGATGTCCTACAGAGCAGAGAGGTTCTGTGTGCGATGGAGCCCTGGG 312
Qy 348 GCCATGTTATTCCTGGGTACACCTGGGATCCAGGTGCGGATGGATTCAAGAGAAAG 407
Db 313 GCCAATGGCATTCCTGGCACACCGGGAATCCCGAGTGGGATGGATTCAAGAGAGAA 372
Qy 408 GGGGAATGTCTGAGGAAAGCTTTGAGGAGTCTTGAGACCCCACTACAAAGCAGTTCA 467
Db 373 GGGGAGTCTTAAAGGAAAGCTTTGAGGAGTCTTGAGACCCCACTACAAAGCAGTTCA 432
Qy 468 TGGAGTTCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 527
Db 433 TGGAGTTCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 492
Qy 528 ATGCGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 587
Db 493 ATGCGATCCAAACGCGCTCTTCAAGTTCTGTTCAAGTGGCTCGCTCGCTCAATGCA 552
Qy 588 AATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 647
Db 553 AATGCTTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 612
Qy 648 CCCATGGAAGCTATATATATATATATATATATATATATATATATATATATATATAT 707
Db 613 CCCATGGAAGCTATATATATATATATATATATATATATATATATATATATATATAT 672
Qy 708 ATTCATGCACTTCTTCTGATGAGAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 767
Db 673 ATTCATGCACTTCTTCTGATGAGAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
Qy 768 GTTGCTATCGAGGATGAGAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 827
Db 733 GTTGCTATCGAGGATGAGAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 792
Qy 828 AATTCAGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 879
Db 793 AATTCAGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 852
Qy 880 TTTCATTTGCTACCTCTTTTATATATATATATATATATATATATATATATATATAT 939
Db 853 TCCCTGCTCATTTATTTATATATATATATATATATATATATATATATATATATAT 912
Qy 940 -AATAGTTATGATATATATATATATATATATATATATATATATATATATATATAT 997
Db 913 GAAGTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972
Qy 998 GTGTGATTTCACTGTTTATATATATATATATATATATATATATATATATATATAT 1057
Db 973 GTGTGATTTCACTGTTTATATATATATATATATATATATATATATATATATATAT 1029
Qy 1058 TTTCATATATATATATATATATATATATATATATATATATATATATATATATAT 1072
Db 1030 TTCAGATATATATATATATATATATATATATATATATATATATATATATATAT 1044

RESULT 19
US-09-692-081-9
; Sequence 9, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 9
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Artificial Sequence
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:myc-tagged
; OTHER INFORMATION: REMODEL construct
US-09-692-081-9
Query Match 45.1%; Score 566.6; DB 4; Length 734;
Best Local Similarity 87.0%; Pred. No. 1.2e-125;
Matches 636; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

Qy 142 GACCCCAAGGCCCCCGCCCTTCCCGCAGGCGCTCCGGGCTCC-----TGTCTTC 195
Db 4 GCCCCCAAGGCCCCCGCCCTTCCCGCAGGCGCTCCGGGCTTCTTCTGCTCACTCC 63
Qy 196 TGTCTGTGAGTGTGCGCGCGCGCTGAGAGCGCTCTGAGATGCCCAAGGGAGAGAAAAG 255
Db 4 GCCCCCAAGGCCCCCGCCCTTCCCGCAGGCGCTCCGGGCTTCTTCTGCTCACTCC 63
Qy 256 CCAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315
Db 124 CGCTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183
Qy 316 CAGAGAGTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375
Db 184 CAGAGAGTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Qy 376 TCCGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
Db 244 TCCGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
Qy 436 AGTCTGAGACCCCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
Db 304 AATCTGAGACCCCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
Qy 496 TTGGGAAAATTGCGAGAGTGTATTTACAAAGATGCTTCAATATGCTCTTAAGATT 555
Db 364 TTGGGAAAATTGCGAGAGTGTATTTACAAAGATGCTTCAATATGCTCTTCAAGATT 423
Qy 556 TGTTCAGTGGGCTCACTTGGGCTTAAATGAGAAATGAGATGCTGAGGTTGATTTCA 615
Db 424 TGTTCAGTGGGCTCACTTGGGCTTAAATGAGAAATGAGATGCTGAGGTTGATTTCA 483
Qy 616 CATTCATGAGAGTGAATGTTGAGAGCTCTTCCATGAGAGCTATTAATTTATTTGAGAG 675
Db 484 CCTTATATGAGAGTGAATGTTGAGAGCTCTTCCATGAGAGCTATTAATTTATTTGAGAG 543
Qy 676 AAGGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 735
Db 544 AAGGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 603
Qy 736 TTTTGAAGAGATTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 795
Db 604 TCTGTGAAGAGATTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
Qy 796 ATTACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 855
Db 664 ATTACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 723
Qy 856 AACTACCAAAA 866
Db 724 AACTACCAAAA 734

RESULT 20
US-09-692-081-6/c
; Sequence 6, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 403
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: REMODEL
; OTHER INFORMATION: antisense ribonucleoprobe
; US-09-692-081-6

Query Match      26.2%; Score 329.4; DB 4; Length 403;
Best Local Similarity 88.6%; Pred. No. 3.3e-69;
Matches 357; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 425 AAGCTTGGAGAGTCTTGACACCCCACTACAGAGTGTTCATGAGTTCATTGAAATTA 484
Db 403 AAGCTTGGAGAGTCTTGACACCCCACTACAGAGTGTTCATGAGTTCATTGAAATTA 344
QY 485 TGGCATATGATCTTGGGAAATTTGCGAGTGTACATTTCACAAAGATGCGTTCAATATAGTC 544
Db 343 TGGCATATGATCTTGGGAAATTTGCGAGTGTACATTTCACAAAGATGCGATCCAAAGCGGC 284
QY 545 TCTAAGGTTTGTTCAGTGGCTCACTCGGCTTAATAGCAGAAATGCAATGCTGTCAAGG 604
Db 283 TCTTGAAGTTCGTTCAGTGGCTCGCTCGCTCAAGAGAAATGCTGTGTCAAGG 224
QY 605 TTGGTATTTCAATTCATGAGTGAATGTTTCAAGACCTCTTCCATTGAAGTATAT 664
Db 223 CTGGATATTTTACCTTTAATGAGTGAATGTTTCAAGACCTCTTCCATTGAAGTATAT 164
QY 665 TTATTTGGACCAAGAAACCCCTGAAATGATTCACAAATTAATTCATGCACTTCTTC 724
Db 163 CTATCTGGACCAAGAAACCCCTGAGTAAATTCACATTAATTCATGCACTTCTTC 104
QY 725 TGTGAAGACCTTGTGAAGAAATGCTGTGATTAAGATGTTGCTATCTGGGTGG 784
Db 103 CGTGAAGACCTCTGTGAAGGATTTGTGCTGAGCTGTGAGCGTGGCATCTGGGTGG 44
QY 785 CACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGAGATG 827
Db 43 CACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGAGATG 1

RESULT 21
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAB1 promoters
; US-09-806-708B-22

Query Match      5.5%; Score 68.8; DB 4; Length 1141;
Best Local Similarity 12.5%; Pred. No. 7.4e-07;
Matches 121; Conservative 353; Mismatches 483; Indels 8; Gaps 3;

QY 291 AATGGAATGTGCTTACAAAGGCCACGACGAGTGTCTGTGACAGCGGAGCCCTGGGACC 350
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Db 77 RWMKGWYKKKWBCCANNTSBRYHARWMDMTAYBMTMTNWKMGKTRHRHWRMBABDT 136
QY 351 AATGTTATTCGGGGTACACCTGGGATCCACAGTGGGATGATTCAAGAGAGAAAGGG 410
Db 137 VDHHTVYTAANNATTTTCMDDDKTRTWMKKNNAATGMDDTKTYHWNKNGBTJYVWV 196
QY 411 GAATGCTGAGGAAAGCTTGTAGAGAGTCTGACACCCCACTACAGAGTGTTCATG 470
Db 197 RYKTDSDMSBKRMVYGBWMMKWSYDYTYWVWVMDCKRKYRWRVTRBMMNVV--- 253
QY 471 AGTTCAATTAATTTATGCGATGATCTTGGGAAATTCGCGAGTGTACATTACAAAGATG 530
Db 254 --AMDTAHRRRYNNQWBTBAMAYRRYTMNNNNNAKAKCKAKYGMWRABVNSTCTTWS 311
QY 531 CGTTCAATTAATGCTTACAGCTTGTGATGAGTGTCTGACCTGCGCTCAAAATGAGAAAT 590
Db 312 KTTKRTSCMANNCBAGDANKDHKMKMSAPMGYNNNNNNNNWYTKAABRMBWVH 371
QY 591 GCATGCTGTGACGCTGTGATTTTCAATTCATGAGAGTGAATGTTTCAGACCTCTTCCC 650
Db 372 SAMKWHANNAHYBRKMTBYKRTYVNNNNNGTTMREMAWYKMDMBGTYYNNNG 431
QY 651 ATGGAAGTATATTTATTTGACACCAAGAAAGCCCTGAAATGAATTCACATTAATATT 710
Db 432 GRITYGWTKNKMWYTKYKMANCKMRAMDHKCTHNNNTTWKMYKTYMNNCYKMSMTNGK 491
QY 711 CATGCACTCTCTCGTGGAAGACCTTGTGAAGAAATGTGTGCTGATTAAGATGATTT 770
Db 492 SHRBAALVYTYMMWRHYAHANNNDWYMKACTTKYIVCSKMMNNNAATMTKSSWNT 551
QY 771 GCTATCTGGGTTGACCTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGAAT 830
Db 552 TSRYYRWKNNNSWFRSDTBSMRANNYARABHYGYMTRMBWBSHTMBHBA--GAHY 610
QY 831 TCAGTTCTCGCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCAATTGCT 890
Db 611 WMBWYBAKCHCMKAWYKAKYKAGAGSNNNNNNNNNNNNNNNNNNATCARPDYAAARWYA 670
QY 891 ACTCTTTTTTATATGACCTTGTGATGCTTCACTTAATGACATTTTAATAAGTTTAT 950
Db 671 MANNAKYHYGAANNA--YTHANNWGCWNNNATDTRKTYKNNNNNNNAGTWMKNNNNNA 728
QY 951 GTATPACATCTGATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACA 1010
Db 729 KNASAAKNVYAAAVKAAKHWRMANKWAMGWHADAAABTTDRKNNGAYKYTTNNNT 788
QY 1011 CTGTTTAAATCTAGCATATTTCATTTTCTTCATCAATCAAAAGTGTTCATATTTT 1070
Db 789 YRGVVTYTAADGANNNNNNNNNNNNNNNNNNNGMSDWYTWYAYVYGTNNNNNNNNNAYAW 848
QY 1071 TTAGTGTAGATATCTTCTTCATGATGACATCTCTCAACCTAATTTGAATATT 1130
Db 849 WTNKMYTTTDRMBATTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 908
QY 1131 GTTGTGATCTTTGTTTCTCTTACTATAGATTTTAAAAAATATAAAGCTACGA 1190
Db 909 YNRGTARNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 968
QY 1191 ATCTTGTACAAATTTGTAATGTTAAGATTTTATATCTGTTAAATATAAATATT 1250
Db 969 TTCRYKNNCTWYMTTTRTYAAATRWKTNATGSMTRCATGAKNNNNWYWGKTRWT 1028
QY 1251 TCCAA 1255
Db 1029 AYRWA 1033

RESULT 22
US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
```

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; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bouguetelret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Amick
; TITLE OF INVENTION: BIOMETRIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1123..3123
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 3124..3297
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 3871..4072
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 5552..5633
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 5758..5880
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: 5996..6099
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: 6349..6509
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: 7379..7522
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: 8645..8854
; OTHER INFORMATION: exon 8
; NAME/KEY: exon
; LOCATION: 12254..12340
; OTHER INFORMATION: exon 9
; NAME/KEY: exon
; LOCATION: 12854..13023
; OTHER INFORMATION: exon 10
; NAME/KEY: exon
; LOCATION: 13308..13429
; OTHER INFORMATION: exon 11
; NAME/KEY: exon
; LOCATION: 16567..16667
; OTHER INFORMATION: exon 12
; NAME/KEY: exon
; LOCATION: 16775..16945
; OTHER INFORMATION: exon 13
; NAME/KEY: exon
; LOCATION: 17063..17554
; OTHER INFORMATION: exon 14
; NAME/KEY: misc feature
; LOCATION: 17555..20674
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1128
; OTHER INFORMATION: 10-508-191 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 1182
; OTHER INFORMATION: 10-508-245 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 1559
; OTHER INFORMATION: 10-509-284 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 1570
; OTHER INFORMATION: 10-509-295 : deletion of C
; NAME/KEY: allele
; LOCATION: 1827
; OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTT
; NAME/KEY: allele
; LOCATION: 2048
; OTHER INFORMATION: 10-511-62 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 2323
; OTHER INFORMATION: 10-511-337 : insertion of T
; NAME/KEY: allele
; LOCATION: 2341
; OTHER INFORMATION: 10-512-36 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 2623
; OTHER INFORMATION: 10-512-318 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2832
; OTHER INFORMATION: 10-513-250 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2844
; OTHER INFORMATION: 10-513-262 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 2934
; OTHER INFORMATION: 10-513-352 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2947
; OTHER INFORMATION: 10-513-365 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 3802
; OTHER INFORMATION: 12-206-81 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 4062
; OTHER INFORMATION: 10-343-231 : deletion of C
; NAME/KEY: allele
; LOCATION: 4088
; OTHER INFORMATION: 12-206-366 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 4109
; OTHER INFORMATION: 10-343-278 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 4170
; OTHER INFORMATION: 10-343-339 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 5903
; OTHER INFORMATION: 10-346-23 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6019
; OTHER INFORMATION: 10-346-141 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6141
; OTHER INFORMATION: 10-346-263 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 6183
; OTHER INFORMATION: 10-346-305 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 6338
; OTHER INFORMATION: 10-347-74 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6375
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 6429
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OTHER INFORMATION: 10-347-165 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 6467
 OTHER INFORMATION: 10-347-203 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 6484
 OTHER INFORMATION: 10-347-220 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 6534
 OTHER INFORMATION: 10-347-271 : polymorphic base A or T
 NAME/KEY: allele
 LOCATION: 6611
 OTHER INFORMATION: 10-347-348 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 7668
 OTHER INFORMATION: 10-348-391 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 8608
 OTHER INFORMATION: 10-349-47 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 8658
 OTHER INFORMATION: 10-349-97 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 8703
 OTHER INFORMATION: 10-349-142 : polymorphic base G or C
 NAME/KEY: allele
 LOCATION: 8777
 OTHER INFORMATION: 10-349-216 : deletion of CTG
 NAME/KEY: allele
 LOCATION: 8785
 OTHER INFORMATION: 10-349-224 : polymorphic base G or T
 NAME/KEY: allele
 LOCATION: 8926
 OTHER INFORMATION: 10-349-368 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 12171
 OTHER INFORMATION: 10-350-72 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 12429
 OTHER INFORMATION: 10-350-332 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 13341
 OTHER INFORMATION: 10-507-170 : polymorphic base A or G
 NAME/KEY: allele
 LOCATION: 13492
 OTHER INFORMATION: 10-507-321 : polymorphic base A or C
 NAME/KEY: allele
 LOCATION: 13524
 OTHER INFORMATION: 10-507-353 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 13535

Query Match 4.5%; Score 56.8; DB 4; Length 20674;
 Best Local Similarity 46.3%; Pred. No. 0.0021;
 Matches 187; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 845 CATTATTGAGACTACCAAAATAAATGCTTAATTTCAATTTGCTACCTTTTAT 904
 DB 11062 CTTTATTTAATAGCTAAGAAATATTTAATTTAATTTAATTTAATTTA 11121

QY 905 TATGCCCTTGAAAGTTCACCTTAATGACATTTTAAAGTTATGATACATCTGAT 964
 DB 11122 TATTAATAATTAAATTTTAAATTTAATTTAATTTAATTTAATTTAATTT 11181

QY 965 GAAAGCAAGCTAAATATGTTTACAGACAAAGTGATTTACACGTGTTTAAATCT 1024
 DB 11182 AAAATTTAAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 11241

QY 1025 AGCATTAATCATTTTCTTCAATCAAAAGGTTTCAATTTTATTTAGTTGTTAGA 1084
 DB 11242 TTAATTTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 11301

QY 1085 TACTTTCTGATACATCTCTCAACCTTAATTTGGAATATGTTGGGCTTTTG 1144

DB 11302 TAATTAACCTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 11361
 QY 1145 TTTTCTCTTAGATAGACATTTTAAATAAATAAGCTACCAATCTTTGACAT 1204
 DB 11362 TATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 11421

QY 1205 TGTAATGTTAGAAATTTTATATCTGTTAAATAAATTA 1248
 DB 11422 AATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 11465

RESULT 23
 US-10-170-097-651
 Sequence 651; Application US/10170097
 Patent No. 6794143
 GENERAL INFORMATION:
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Bougueterec, Lydie
 APPLICANT: Chumakov, Ilya
 APPLICANT: Cohen, Annick
 TITLE OF INVENTION: BIOMOLECULAR MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
 FILE REFERENCE: GEN-T114XC2D1
 CURRENT FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: US/10/170,097
 PRIOR FILING DATE: 2000-08-16
 PRIOR APPLICATION NUMBER: US 09/502,330
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: US 60/133,200
 PRIOR FILING DATE: 1999-05-07
 PRIOR APPLICATION NUMBER: US 09/275,267
 PRIOR FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: US 60/119,917
 PRIOR FILING DATE: 1999-02-12
 NUMBER OF SEQ ID NOS: 1304
 SOFTWARE: Patent.pm
 SEQ ID NO 651
 LENGTH: 20674
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: 1123..3123
 OTHER INFORMATION: 5'regulatory region
 FEATURE:
 NAME/KEY: exon
 LOCATION: 3124..3297
 OTHER INFORMATION: exon 1
 FEATURE:
 NAME/KEY: exon
 LOCATION: 3871..4072
 OTHER INFORMATION: exon 2
 FEATURE:
 NAME/KEY: exon
 LOCATION: 5552..5633
 OTHER INFORMATION: exon 3
 FEATURE:
 NAME/KEY: exon
 LOCATION: 5758..5880
 OTHER INFORMATION: exon 4
 FEATURE:
 NAME/KEY: exon
 LOCATION: 5966..6099
 OTHER INFORMATION: exon 5
 FEATURE:
 NAME/KEY: exon
 LOCATION: 6349..6509
 OTHER INFORMATION: exon 6
 FEATURE:
 NAME/KEY: exon
 LOCATION: 7379..7522

OTHER INFORMATION: exon 7
FEATURE:
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
FEATURE:
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
FEATURE:
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
FEATURE:
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
FEATURE:
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
FEATURE:
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
FEATURE:
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
FEATURE:
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
FEATURE:
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
FEATURE:
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTT
FEATURE:
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
FEATURE:
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G

FEATURE:
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
FEATURE:
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G

Query Match 4.5%; Score 56.8; DB 4; Length 20674;
Best Local Similarity 46.3%; Pred. No. 0.0021;
Matches 187; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 845 CATTATTGAGAGACTACCAAAATGCTTTAATTTTCATTGCTACCTCTTTTAT 904
| | | | |
Db 11062 CTTTATTAAATGCTAAGGAAATATTTAATATTTTAAATTTTAAATTTTAA 11121
| | | | |
QY 905 TATGCTTGGAATGTTCACTTAATGACATTTTAATAGTTATGTAACATCGAAT 964
| | | | |
Db 11122 TATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 11181
| | | | |
QY 965 GAAAGCAAGCTAATATGTTTACAGCAAGTGTGATTTCACTGTTTAAATCT 1024
| | | | |
Db 11182 AAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 11241
| | | | |
QY 1025 AGCATTAATCAATTTGCTTCAATCAAAAGTGTTCATATTTTAAAGTTAGTA 1084
| | | | |
Db 11242 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 11301
| | | | |
QY 1085 TACTTTCTCAATGACATTTCTCAACCTTAATTTGGAATTTGTGTGCTTTTG 1144
| | | | |
Db 11302 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTTTA 11361
| | | | |
QY 1145 TTTTCTCTTAAGTATGACATTTTAAATAATTAATTAAGTACCAATCTTTGTA 1204
| | | | |
Db 11362 TATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTTGCTTC 11421
| | | | |
QY 1205 TGTAAAGTTAAGAAATTTTAAATCTGTTAAATTAATTAATTAATTAATTA 1248
| | | | |
Db 11422 AATTAATTAATTAATTAATTAATTTTAAATTTTAAATTAATTAATTAATTA 11465
| | | | |

RESULT 24

US-09-370-838-153/c
; Sequence 153, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Radoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 153
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-153

Query Match 4.4%; Score 55.2; DB 4; Length 2109;

Best Local Similarity 51.2%; Pred. No. 0.0017;

Matches 129; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 6 GAGGCGCGGGGTAAAGCGCATTTGATGACGCTGCGGCGGCGCTCGAGCGCGGCGAG 65
| | | | |
Db 1140 GAGCGGACCGGGGCTGCTCGGCGCTCCCGGGGCGCGGCGCGCGCGCGCGCG 1081
| | | | |
QY 66 CCAAGCGCTGACCAAGTTCTCTCTCGGTCCTCTCGGCTTCAGCTCGGCGCTCCG 125
| | | | |
Db 1080 CGCGCGCGCTCG 1021
| | | | |
QY 126 CAGCGCGGAGCGATGCGACCCCGAGGCGCGCGCGCTCCCGCAGCGGCTCCGCGGCTC 185
| | | | |
Db 1020 CGGCGCGGCGCTCCCGCGCGCGCGCTCCCGCGCAGCGCGCGCGCGCGCGCTC 961
| | | | |
QY 186 CTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
| | | | |
Db 960 CACGCGGCG 901
| | | | |

QY 246 AAGCAAAAGCGG 257
| | | | |
Db 900 CAGCGAGGCGG 889
| | | | |

RESULT 25

US-09-854-133-153/c
; Sequence 153, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Radoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 153
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-153

Query Match 4.4%; Score 55.2; DB 4; Length 2109;

Best Local Similarity 51.2%; Pred. No. 0.0017;

Matches 129; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 6 GAGGCGCGGGGTAAAGCGCATTTGATGACGCTGCGGCGGCGCTCGAGCGCGGCGAG 65
| | | | |
Db 1140 GAGCGGACCGGGGCTGCTCGGCGCTCCCGGGGCGCGGCGCGCGCGCGCGCG 1081
| | | | |
QY 66 CCAAGCGCTGACCAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 125
| | | | |
Db 1080 CGCGCGCGCTCG 1021
| | | | |
QY 126 CAGCGCGGAGCGATGCGACCCCGAGGCGCGCGCGCTCCCGCAGCGGCTCCGCGGCTC 185
| | | | |
Db 1020 CGGCGCGGCGCTCCCGCGCGCGCGCTCCCGCGCAGCGCGCGCGCGCGCGCTC 961
| | | | |
QY 186 CTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
| | | | |
Db 960 CACGCGGCG 901
| | | | |
QY 246 AAGCAAAAGCGG 257
| | | | |
Db 900 CAGCGAGGCGG 889
| | | | |

RESULT 26

US-08-817-926-27

; Sequence 27, Application US/08817926

; Patent No. 6001590

; GENERAL INFORMATION:

; APPLICANT: Komeda, Toshinori

; APPLICANT: Suda, Hisako

; APPLICANT: Tamai, Yukio

; APPLICANT: Iwamatsu, Akihiro

; APPLICANT: Kato, No. 6001590uo

; APPLICANT: Sakai, Yasuyoshi

; TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINI

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,926
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02597
FILING DATE: 12-SEP-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 234133/1995
FILING DATE: 12-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 42536/1996
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4818 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: Candida boldinii
US-08-817-926-27

Query Match 4.4%; Score 55; DB 3; Length 4818;

Best Local Similarity 45.5%; Pred. No. 0.0029; Mismatches 235; Indels 0; Gaps 0;

Matches 196; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

QY 821 TGGATGGAATTCAGTTTCGATCATTTATGGAAGACCAAAATTAATGCTTAAT 880
DB 4077 TTGTTAATTTCAATGATTAATTTCTTGATTTTAAATAATTTCTCTTT 4136
QY 881 TTCAATTCGACCTCTTTTATTAATGCTTGAATGCTTCACTTAATGACATTTTA 940
DB 4137 TTTATTTCTTCTTTCTTTCAATTTAAATGATGATGAAGAATTAATATATATA 4196
QY 941 ATTAAGTTATGATACATCTGAATGAAGCAAGCAAGCTAAATATGTTTACAGCAAAAGT 1000
DB 4197 TTAATTTATTAATTAATTAATGCTCAAGCTTTAAAGAAAGTATTAATTAACATC 4256
QY 1001 TGAATTCACAGCTGTTTAAATCTAGCATTTATTTGCTTCATCAAAAGTGTTTC 1060
DB 4257 TTTGAGTTAATAGTAATGTAATACAGATTTAATATACCTTTTTCCTCAATTTTTC 4316
QY 1061 AATAATTTTATTAATGTTAGTAATCTTCTTCATAGTCAATCTCTCAACTTAAT 1120
DB 4317 AATTATTTCAATTTGATTTGTTAATTAATGTAATTAATTAATTAATTAATTTCTGT 4376
QY 1121 TTGGAATATGTTGAGTCTTTTGTCTTTCTTGATAGATTTTAAATAATA 1180
DB 4377 TCTTTTGTTGTTTATCTGTTTATTTTGTGATCAATCTTAATTAATGTTT 4436
QY 1181 AAGACCAATCTTGTGCAATTTGAATGTAATGTAATGTAATGTAATGTAATGTAAT 1240
DB 4437 AATTTTATTAATTAATCTAATTTTAATTAATTAATTAATTAATTAATTAATTAAT 4496
QY 1241 AAAAAATTAAT 1251
DB 4497 ATTTCTAATTT 4507

RESULT 27

US-08-487-826B-13/C

; Sequence 13, Application US/08487826B

; Patent No. 593827

; GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.

; APPLICANT: Chitnis, Chetan

; APPLICANT: Miller, Louis H.

; APPLICANT: Peterson, David S.

; APPLICANT: Su, Xin-shaun

; APPLICANT: Wellens, Thomas E.

; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

; NUMBER OF SEQUENCES: 45 AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe Martens Olson & Bear

; STREET: 620 Newport Center Drive 16th floor

; CITY: Newport Beach

; STATE: California

; COUNTRY: US

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,826B

; FILING DATE: 10-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelson, Ned

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER: NIH121.001CP1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19124 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-487-826B-13

Query Match 4.3%; Score 54.2; DB 2; Length 19124;

Best Local Similarity 46.5%; Pred. No. 0.0085; Mismatches 238; Indels 2; Gaps 1;

Matches 209; Conservative 0; Mismatches 238; Indels 2; Gaps 1;

QY 788 TTGTTCAATTCACCAAAAGAGATGCTCTACGAGGAAATTCAGTTTCGATCAT 847
DB 15954 TTTTATTTATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15895
QY 848 TATTAAGAACTACCAAAATTAATGCTTAATTTCAATTTGCTACCTTTTATTAAT 907
DB 15894 TTTTATTTATTAATTAATTTTATTTATTTATTTATTTATTTATTTATTTTAT 15835
QY 908 GCCTTGAATGTTCACTTAATGACATTTTAAATTAAGTTTATGATACATCTGAATGA 967
DB 15834 TTAATTAATTTTATTTTAAATTAATTTT- -TTTATTTAATGATATATTTT 15777
QY 968 AAGCAAGCTAAATAGTTTACAGCAAGGATGATTTCACTGTTTAAATCTAGC 1027
DB 15776 AACATTTTATTAATTTTATTTTATTTATGATATATATTTTATTTATTTTAT 15717
QY 1028 ATTAATCAATTTGCTTCATCAATCAAAAGGTTTCAATATTTTATTTTATTTAGTTAGTAATAAC 1087
DB 15716 CTTTATTTTCTTTTATGATATATATTTTATTTTATTTTATTTTATTTTCTTCT 15657

QY	1088	TTTCTGACAGCTCATCTCTCAACCGATATTTGGAAATTTGTGGTCTTTGTTT	1147
Db	15556	TTTGTTTTTATTTTTTTTAAATCAATTTTTTTTTTAAATAAAATTTTTTTTAAATTTTTT	15597
QY	1148	TTTCTCTTAGATAGCAATTTTAAATAAAATAATAAAGCTACAACTCTTGACAAATTTGG	1207
Db	15596	TTTGATAATCTTTTTCATTTTTTAATTCATACCAAAATTTAATATTTAATAAATTTTAAAT	15533
QY	1208	AAATGTTAAGAAATTTTTTTTAAATCTGTT	1236
Db	15536	ATTTTTTTAAAAAATTTTTCCTTTTTTTT	15508

RESULT 28

```

/ Sequence 62, Application US/10204708
/ Patent No. 6677731
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
/ TITLE OF INVENTION: by Assessing DNA Methylation
/ FILE REFERENCE: 5013.1012
/ CURRENT APPLICATION NUMBER: US/10/204,708
/ CURRENT FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: PCT/EP01/03971
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 62
/ LENGTH: 6801
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
/ US-10-204-708-62

```

Query Match	4.2%;	Score 52.8;	DB 4;	Length 6801;
Best Local Similarity	46.3%;	Pred. No. 0.011;		
Matches 174; Conservative	0;	Mismatches 222;	Indels 0;	Gaps 0

QY	875	TTAATTTTCATTGGTACTCTTTTATTATATAGCTTGGATGGTTCACCTAAATGACA	934
Db	5499	TTAAATAAATATATGAAAAATATATTTATTTATATAGTATAGGAAATGTAAATTAAGAT	5558
QY	935	TTTAAATAAGTTATGTATACATCTGAATGAAAGCAAGCTAAATATAGTTACAGAC	994
Db	5559	AGTGAATATATTTATATATTTTATAGTAAAGTTTATTTTGTAAATTTAAATTTGGTAA	5618
QY	995	AAAGTGTATTTCACTCTTTTAAATCTAGCATATTCATTTTGTCTCAATCAAAAGT	1054
Db	5619	TAAATTTTATTTTATAGTTTTTTTTTTTAAATATATTTTTTTTTTTTTTTTCGGTTTC	5678
QY	1055	GGTTTCAATATTTTTTTTATGTTGGTGAATACTTTCTCATAGTCAATCTCTCAAC	1114
Db	5679	GTATTTTAAATTTTTTATTTGGTTTTTATTTTAAATTTTTTTTTTATATGTAATTCG	5738
QY	1115	TATATATTTGGAATATGTGTGAGCTTTTGTTTTCTCTTAGTATAGCATTTTAAAAA	1174
Db	5739	GTATTTGATTTAAATTTTTTTTTTGTAAAGTATATTTTATTTAAAGCTTTTAAAGT	5798
QY	1175	AATATAAAGCTAACATCTTGTACAAATTTGTAAATGTGAAGAATTTTTTATATATCG	1233
Db	5799	TTTTTTTTTGGAAAGGTGTAGGGTCAAGAGTATAGTTTAAAGTTAATGTTTTTTTTTT	5858

Qy	1235	TTAAATAAAAAATTATT	1250
Db	5859	TTAGTTAAATTTT	5874

RESULT 29

```

US-08-378-313-26
Sequence 26, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASTOS
APPLICANT: SATO, TAKAHITO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 7244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(3056..3226, 3325..3453, 3539..3700, 4582
LOCATION: ..5574)
US-08-378-313-26

```

Query Match	4.2%;	Score 52.8;	DB 3;	Length 7244;
Best Local Similarity	58.1%;	Pred. No. 0.012;		
Matches	93;	Conservative	0;	Mismatches 67;
			Indels	0;
			Gaps	0;

QY	1092	TTCAAGTACACTTCTCCACCAATATTTGGAAATGTGTGGCTTTGTTTTC	1155
Db	6813	TTTAAACCTAGATTAATCCAAAGATATAATTTGATATTTTAAATGATCTTT	6872
QY	1152	TCTTAGTAGCATTTTAAAAAATAATTAAGCCATCTTTGACATTTGAAAT	1211
Db	6873	TTATCATATGACATGTCGAAAAATTAAATTATATTTTAAATATGTTTTAAAT	6932
QY	1212	GTTAAGAAATTTTTTATATCTGTTAATAATAAATATTTT	1251
Db	6933	ATTTAAAAATTTTATTTAAAAATATTAATGAATATATTTT	6972

RESULT 30

US-10-204-708-2
; Sequence 2, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)
US-10-204-708-2

Query Match
Best Local Similarity 48.0%; Score 52.2; DB 4; Length 10467;
Matches 162; Conservative 0; Mismatches 193; Indels 4; Gaps 1;

QY 875 TTAATTTGATTTGCTACCTCTTTTATATGCTGGAAGCTTCACTTAATGACA 934
DB 2464 TTTTGGATTTTATTTAGAGTGTGTTAGTTTATTTGTTGTTATTTGTTGTTG 2523

QY 935 TTTTAAATAGTTTATGATGATCATCTGATGAAAGCAAGCAATATGTTACAGACC 994
DB 2524 TTTTAAATGTTTTTTTTTATGTTAGTTTATTTATTTATTTATTTGTTGTTAA 2583

QY 995 AAGGTGATTTGACACTGTTTTTAAATCAGACTA---TTCATTTGCTCAATCA 1050
DB 2584 GGTTTTAAATTTTTTATTTTATTTATTTAGTGTGTTATTTTATTTTAACT 2643

QY 1051 AAGTGTTCATATTTTTTTTATGTTAGTTAGATCTTTCTTCATAGTCACATCTCTC 1110
DB 2644 TATTTATTTATTTGATTTTATTTTATTTAGATTTTAAATGTTATTTGTTTGA 2703

QY 1111 AACCTAATTTGGAATATTTGTTGCTCTTTTCTTTCTTTAGTATAGCAATTTTA 1170
DB 2704 GATTTTGAATTTTATTTTATTTTATTTTGGGTTTTTTTTTTGAGTTTTTTTAT 2763

QY 1171 AAAAATATTAAGCTACCACTTTTGTACAAATTTGAAATGTTAAGATTTTTTTA 1230
DB 2764 TAGTATTTGTTAAATTTATTTTATTTTGTGATTTAGATTTGATTTTATTTT 2823

QY 1231 TCTGTTAAATTTAAATTTAT 1249
DB 2824 TAGGTATATATATTTCT 2842

RESULT 31
US-09-056-075-1/c
; Sequence 1, Application US/09056075
; Patent No. 5955368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marilee
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium

; TITLE OF INVENTION: Species
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-9166
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note="RP4 origin of DNA transfer (oriT) from
; OTHER INFORMATION: plasmid RP4"
US-09-056-075-1

Query Match
Best Local Similarity 45.7%; Score 52; DB 2; Length 6243;
Matches 181; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 850 TTGAAGACTACCAAAATTAAGCTTTATTTCAATTTGCTACCTTTTTTATATGAC 909
DB 1488 TTTATTAAGCTCATTTTATTTATTTCTTTCTTCAAGTTATATATATATTA 1429

QY 910 CTGGAATGTTCACTTAATGACATTTTAATTAAGTTATGTAATCATCTGAATGAAA 969
DB 1428 TTTTCAACTTTTAATTAATTAATTTTATTTATTTTATTTTATTTTATTTT 1369

QY 970 GCAAGCTTAATATGTTTACAGACCAAGCTGATTTCACTGTTTTTAAATCTGACAT 1029
DB 1368 TTTATTTTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1309

QY 1030 TATTCATTTTGTCTCAATCAAAAGCTTCAATTTTTTTTATGTTGTTGAATCTT 1089
DB 1308 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1249

QY 1090 TCTTCATAGTCACATCTCTCAACCTAATATTTGGAATTTGTTGCTTTTGTGTTT 1149
DB 1248 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1189

QY 1150 TCTCTTAGTAGACATTTTAAATAATTAAGCTACCAATCTTGTACATTTGTAA 1209
DB 1188 CCTCATTTTATTAAGCTGTATTAATAGGTACCTTGTCTTTTATTTTGGGAGG 1129

QY 1210 ATGTTAAGATTTTATTTTATCTGTTAATATTAAT 1245
DB 1128 TTGTAAAGTAATTTTATCTTAGTTAGTTCGAA 1093

RESULT 32

```
US-10-204-708-24/c
; Sequence 24, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPERROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PCT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 24
; LENGTH: 11049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-24

Query Match
Best Local Similarity 4.1%; Score 51.6; DB 4; Length 11049;
Matches 132; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 815 TTCTACGATGAGATTCAGTTCTCGCATCTTATGAGAACACCAATAATGCT 874
DB 1427 TACACCTTATATTAATCTAATCTCTAAATTAATCTTAATTAATCTTAACAAATCAT 1368
QY 875 TTAATTTTCATTTGCTACCTCTTTTATTTATGCTTGAATGCTTCACTTAATGACA 934
DB 1367 ATACCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1308
QY 935 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 994
DB 1307 TTCTCAACACACATATATAAAAAAATCTCTCTATCTATTAATTAATTAATTAATTAAT 1248
QY 995 AAAGTGATTTCAACAGCTTTTAAATCTAGCATTTATTTGCTTCAATCAAAAGT 1054
DB 1247 AAACCTTAAATTTCTACTAACCCTAAATAAATAAATAAATAAATAAATAAATAAATAA 1188
QY 1055 GGTTCATATTTTCTTTTATGTTGTT 1080
DB 1187 TTTTCTTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1162

RESULT 33
US-09-806-708B-23
; Sequence 23, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1055
; TYPE: DNA
```

```
ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1055)
; OTHER INFORMATION: consensus sequence of A.t. and L.a. PAB1 promoters
US-09-806-708B-23

Query Match
Best Local Similarity 4.1%; Score 51; DB 4; Length 1055;
Matches 100; Conservative 127; Mismatches 206; Indels 5; Gaps 2;

QY 816 TCTACTGATGAGATTCAGTTCTCGCATCTTATGAGAACACCAATAATGCTT 875
DB 42 TGKRCYARBMGMMTAYVMTATKMGTTGMAWRTWRMAAMKTRMCMSTAMNNATMTCT 101
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTTATGCTTGAATGCTTCACTTAATGACAT 935
DB 102 ARKWRGTGRMWTKNNNNAATGTRMWTGYMMTNNGCSMTWABRRYKTRRMWCYTAMWYAS 161
QY 936 TTTAATAATAGTTTATGATACATCTGAATGAAGCAAGCTAAATATGTTTACAGCCA 995
DB 162 MAGNASTRTTYTWRKMKCRKSARARATRGARARAYTAWRTGWTAMATYAAWT 221
QY 996 AAGTGATTTCAACAGCTGTTTAAATCTAGCATTTATTTGCTTCAATCAAAAGTG 1055
DB 222 MNNNNNNNAKA---ACKRATTGWRKSNCTCTTAGGTTTKRATCGAWTCGAWMTKKW 277
QY 1056 GTTTCATATTTTCTTTTATGTTGTTAGTAATAATCTTCTCATAGCATTCCTCAACCT 1115
DB 278 KTWKTSAAWMTWNNNNNNNTTTTKA-AMVAAAAMWMSATTTWMAAATSRITWYYGR 336
QY 1116 ATAATTTGAATATGTTGCTGCTTTGTTTCTTTCTTCTAGTATAGCATTTTAAATA 1175
DB 337 KTAAMNNNGTTCWTRMAMWTKMMKTKGTTTNNNGRITYGTWTKXAATTTTAANN 396
QY 1176 ATATPAAAGCTACCAATCTTTGTACAATTTGTAATGTAAGATTTTATATCTGT 1235
DB 397 TTAAMKWTCTMNNNTTAAKATTTWATCWKMSMTGTSYRAAARAYTAWMTBRVAVANN 456
QY 1236 TAAATPAAATTTATTTCC 1253
DB 457 NNTTWTACCTWTTYYKC 474

RESULT 34
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
```



```
QY      830 TTCAAGTTCTGCGCATCATTAATGAAGAACTACCAAAATAATGCTTAATTTTCATTGTC 889
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1122 KKAANNNNNNMGMDVNRMDATKMSATGTAMWTHAKAGATMCWYVYTGIRNRCKMT 1063
QY      890 TACCCTTTTATTAATGCTTGGATGCTTCACTAAATGACATTTTAAATGAAGTTTA 949
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1062 YAMRTWYRSNAWMSCATKBMWTKWYATKYRTMYAMWCMRRNNMWCATGYSKSCA 1003
QY      950 TGTATACATCTGAAGAAGAAAGCTAAATATGTTTACAGACCAAGAGTGATTTGAC 1009
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1002 TNNAMWYATTRMAAYAAAKAMAMAGNNMRYGAAAGKMGCAAAATGMBWADTAGKNC 943
QY      1010 ACTGTTTAAATCTAGACATTAATTCATTTGCTTCATCAATCAAAAGTGTTCAATATTTT 1069
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      942 NNNNNNNWTTDVRBMAMKAKNNNNNNAVYACVNBAAITNNKATTHMKWTHGHSKRRIH 883
QY      1070 TTTAGTTGGTGAATACCTTTCTTCACTGACATCTCTCAACCTATTAATTTGAATAT 1129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      882 HTRTCRRTKYNNNNNNNATVYVYHHAARRMNAWYRTNNNNNNNNNNNACRTRTWMAMW 823
QY      1130 TGTGTGTGCTTTTGTGTTTCTCTTAGATAGACATTTTAAATAAATAAGCTACC 1189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      822 KHSWNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 763
QY      1190 AATCTTTGATGACATTTGTAATGTTAAGATTTTATATCTGTTAATTAATAATTTAT 1249
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      762 TDMCYKTMWMTWYMDMTTMBTTRTNNMTTSNTNNNNNNNNNNNNNNNNNNNNNNNNNN 703
QY      1250 TTCCAACA 1257
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      702 ATNNWGCW 695
```

```
RESULT 37
US-09-801-861-3
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Human
; US-09-801-861-3
```

```
Query Match      3.9%; Score 48.8; DB 4; Length 53332;
Best Local Similarity 49.1%; Pred. No. 0.27;
Matches 157; Conservative 0; Mismatches 162; Indels 1; Gaps 1;
```

```
QY      932 ACATTTTAAATAGTTTATGATACATGCAATGAAGAAAGCAAGTAAATAGTTACAG 991
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31341 ATATTTTATATATTTTATATATAGTTATATTTATATATATATATATATATATATAT 31400
QY      992 ACCAAGTGATTCACACTGTTTAAATCTAGACATTAATTCATTTGCTTCATCAAA 1051
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31401 ATATTTGATATATTTATA-TATTTATATATTTTATATATATTTATATATTTTAT 31459
QY      1052 AGTGTTTCAATATTTTATTTAGTTGGTGAANAATTTCTTCATAGTCACATTCCTCA 1111
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31460 ATATTTTATATATTTATATATATTTTATATATATTTTATATATATATATATAT 31519
QY      1112 ACCATATATTTGGAATATGTTGGTCTTTGTTTCTTCTAGTATAGCATTTTAA 1171
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31520 ATTTATATATATTTATATATATTTATATATATTTATATATATATATATATTTAT 31579
```

```
QY      1172 AAAATATAAAGCTACCAATCTTTGATACATTTGTAAGTTAAGTTATTTTATAT 1231
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31580 ATATTTATATATTTATATATATTTATATATTTATATATATTTATATATATTTTAT 31639
QY      1232 CTGTTAAATAAATATATTT 1251
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31640 TATATATATATATATATGATTT 31659
```

```
RESULT 38
US-10-224-562-3
; Sequence 3, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-224-562-3
```

```
Query Match      3.9%; Score 48.8; DB 4; Length 53332;
Best Local Similarity 49.1%; Pred. No. 0.27;
Matches 157; Conservative 0; Mismatches 162; Indels 1; Gaps 1;
```

```
QY      932 ACATTTTAAATAGTTTATGATACATGCAATGAAGAAAGCAAGTAAATAGTTACAG 991
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31341 ATATTTTATATATTTTATATATAGTTATATTTATATATATTTATATATATTTATAT 31400
QY      992 ACCAAGTGATTCACACTGTTTAAATCTAGACATTAATTCATTTGCTTCATCAAA 1051
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31401 ATATTTGATATATTTATA-TATTTATATATTTTATATATTTTATATATTTTAT 31459
QY      1052 AGTGTTTCAATATTTTATTTAGTTGGTGAANAATCTTCTCATAGTCACATTCCTCA 1111
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31460 ATATTTTATATATTTATATATATTTTATATATATTTTATATATATTTATATAT 31519
QY      1112 ACCATATATTTGGAATATGTTGGTCTTTGTTTCTTCTAGTATAGCATTTTAA 1171
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31520 ATTTATATATATTTATATATATTTTATATATTTTATATATATATATATATATTTAT 31579
QY      1172 AAAATATAAAGCTACCAATCTTTGATACATTTGTAAGTTAAGTTATTTTATAT 1231
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31580 ATATTTATATATTTATATATATTTTATATATTTTATATATATTTATATATATTTTAT 31639
QY      1232 CTGTTAAATAAATATATTT 1251
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      31640 TATATATATATATATGATTT 31659
```

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RESULT 39
US-08-909-742-1/c
; Sequence 1, Application US/08909742
; Patent No. 6007991
; GENERAL INFORMATION:
; APPLICANT: Vimala S. Sivaraman
; APPLICANT: Helen-yu Wang
; APPLICANT: Craig C. Malbon
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
; TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
```

[illegible]

Query Match	3.9%	Score 48.6	DB 3	Length 1866
Best Local Similarity	55.0%	Pred. No. 0.061		
Matches 116	Conservative 0	Mismatches 94	Indels 1	Gaps 1
QY	45	CGGCTTGAGAGCGCGGCGGAGCCAGAGGCTGACACGTTCTCTTCCTGCTCTCGGC	104	
Db	210	CTGCAACTGCTGTAGAGCGCGGCGCCAGAGCTGACAGAGGCTGCCCCCTTCAACACTTCACCTC	151	
QY	105	CTCAGAGTCGCGCGCTGCCCCGCGACGCGGAGCCATGCGAATCCCAAGGAGCCCGCGCGCTCC	164	
Db	150	CCCCGGAGATCCCCGGGCGGAGCCCTCTGCTTCTAGGGGGCTCCCCGCCCCCGCCCTG	91	
QY	165	CCGAGAGCGGCTCGCGGCGCTCTGCTGCTCTGCTGACATTGCCCCGCGCGCTCGAGC	224	
Db	90	AGCGCGCGCGCCGCAATCTCA-CTCCGCGTGTGCTGCTGCTGTGTTGCTGCTCGCTG	32	
QY	225	GCCCTTGAGATCCCAAGGGAGGAGCAACAAAG	255	
Db	31	CCCTCTGGGGCCCCGGCGGCCCAAGAGACG	1	

```

RESULT 41
US-10-204-708-7
; Sequence 7, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 7
; LENGTH: 6020
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-7

Query Match      3.9%;   Score 48.4;   DB 4;   Length 6020;
Best Local Similarity 43.3%;   Fred. NO. 0.12;
Matches 278;   Conservative 0;   Mismatches 361;   Indels 3;   Gaps 1.

QY      607  GGAATTACACATTCAGAGCGTGAATGTCAGACCTTCCTCCCATGAGCTATATATT 666
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 2577 GGAATTAAAGGTGAGTAAAGTGAATTTTGAATGAAATTAAGAAAAATTTTAAT 2636
Qy 667 ATTGGACCAAGAGACCCCTGAATGAAATTAATTAATTAATTCACCTCTCTG 726
Db 2697 TTTTATATTTAGTAAATATAAGATTAATTTTGTGAATTTTGTGTTTGTGTTG 2696
Qy 727 TGAAGACCTTGTGAAGAAATGCTGTGATGATGAGATGCTATCTGGGTGGA 786
Db 2697 GTAGATGAAAAATGAAAGTATTTTGAATGGTGAAGAAAGTAAATGATAGT 2756
Qy 787 CTGTGATGATTAACCAAGAAAGAGATGCTTACAGAGAAATTCAGTTCTCGATCA 846
Db 2757 TGTAAATTTTGTAAATTTTATTTAGTTTGAATGCTGTGTTAAATTAATGAGAT 2816
Qy 847 TTATGGAACCTACCAAAATTAATGCTTAATTTTCATTTCTCACTCTTTTATTA 906
Db 2817 TTGATAGAGGTGATTTTGTAAATTTTATTTAGTTTGAATGGGGTATTAATTTTA 2876
Qy 907 TGCCTGGAATGCTTCACTTAATGACATTTTAATAGTTTAAATGATTAATCACTGAATGA 966
Db 2877 TTTATATAGGGGTATATTAAGTAAATTAATGAAAAATTTTGAAGATTTTAAATTTTA 2936
Qy 967 AAAGCAAGCTAAATATGTTTACAGCAAGAGTGAATTTCACTGTTTAAATCAAG 1026
Db 2937 GAAATTTTGTAAATGGGGTGTGAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 2996
Qy 1027 CATTAATCAATTTGCTTCAATCAAAAGTGTTCATATTTT---TTTAAAGTGTGA 1083
Db 2997 AGTGAATTTTATTTTAAACGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3056
Qy 1084 ATACTTCTTCACTACATCTCTCAACCTAATTAATTTGGAATATGTTGGTCTTT 1143
Db 3057 GATATTTGTAAATTTTGTGTTGGAACGTAAATATATTTGTAATATGTTATTTAT 3116
Qy 1144 GTTTTCTCTAGTATAGCATTTTAAATAATTAATTAAGTCAATCTTGTACAT 1203
Db 3117 TATTTTATTTAGGAAGTATGTAATGTAATGTAATTTTGTGTTGTTGTTGTTGTTG 3176
Qy 1204 TTGTAATGTTAAGAAATTTTATATCTGTTAAATATAAA 1245
Db 3177 GAGTATATTTATTAATTTATTTATTTATTAAGAGAAAA 3218

RESULT 42
US-10-204-708-35
; Sequence 35, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 35
; LENGTH: 9347
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-35
Query Match 3.8%; Score 48.2; DB 4; Length 9347;
Best Local Similarity 51.6%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 110; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
Qy 1035 ATTGCTTCAATCAAAAGTGTTCATATTTTGTAGTGGTGAATACCTTCTC 1094
Db 7491 AATTAAGCTTTTATTTAGATTTTAAATTTTATTTTGTGAAGTAAATGATTA 7550
Qy 1095 ATAGTCATCTCTCAACCTAATTAATTTGGAATATGTTGGTCTTTGTTCTCT 1154
Db 7551 TTGTAATTTTGTATTAATTTTATTTTATTTTGTATTAAGATTTTATTTAT 7610
Qy 1155 TAGATACATTTTAAATAATTAAGCTACCAATCTTGTACAAATTTGTAATGCT 1214
Db 7611 TAGATACAAATGCTTTTAAATTTGTTTAAATAATTTTGTGATTTATTTTAT 7670
Qy 1215 AAGAAATTTTATATCTGTTAAATAAAATTT 1247
Db 7671 TTAGTATTTTATTTTAAATTAATGATTAATTT 7703

RESULT 43
US-10-204-708-40
; Sequence 40, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 40
; LENGTH: 19513
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-40
Query Match 3.8%; Score 48.2; DB 4; Length 19513;
Best Local Similarity 49.3%; Pred. No. 0.23;
Matches 181; Conservative 0; Mismatches 183; Indels 3; Gaps 2;
Qy 865 AATAAGCTTATTTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGTTGAC 924
Db 339 ATGTAAAGTTTATTTTGTAGTTAAGCAATTTTATTTTGTAGTTTGTAGTTGGA 398
Qy 925 TTAATGACATTTTAAATTAAGTTTATGATATGATGAAAGCAAG-CTAAATAT 983
Db 399 ATTAAGCGCTTATTTATTTATTTAGTAAATTTTGTGTTGATGAGACGGGTTT 458
Qy 984 GTTACAGACCAAGTGTGATTCACGTTTAAATCTAGCATTAATTTGCTT 1043
Db 459 TGTATGTGGTATGTTGTTGATTTTGAATTTTGAATTTATTTGCTTTAGTT 518
Qy 1044 CAATCAAAAGT--CGTTCAATATTTTATTTAGTTGTTGAATCTTCTTCATAGTCA 1101

Db 519 TTTTAAGTGTGAGATTAAGTTGAGTTTCGGCTTCGTTTGGTAATTTTTTTA 578
Qy 1102 CATCTCTCAACCTAATTTGGAAATATTGTTGCTTTTGTCTTCTAGTATA 1161
Db 579 TTTTATAAATTTTGTTCGATTTTCGTTTAAATTAATTTATTTAGTTAT 638
Qy 1162 GCATTTTAAAAAATATTAAGCTACCAATCTTTGACAAATTTGTAATTT 1221
Db 639 TGTATATGAAGATTAAGATTAATTTTGTATTAATTTAAATTTTGAATA 698
Qy 1222 TTTTATA 1228
Db 699 ATTTTAA 705

RESULT 44

US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGEMORU, SHUJI
; APPLICANT: MATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 3.8%; Score 47.8; DB 4; Length 640681;
Best Local Similarity 47.9%; Pred.No.1.5; Indels 3; Gaps 1;
Matches 170; Conservative 0; Mismatches 182

Qy 897 TTTTATATATGCTTGAATGCTTCACTTAATGACATTTTAATTAAGTTATGTATAC 956
Db 88808 TTGTATATATTAAGTATTAATTTTCACTTAAGCCATTTTACAGTACATCAATTA 88867
Qy 957 ATCTGAATGAAGCAAGCTAATATGTTTACAGACCAAGTGATTTCACTGTTT 1016
Db 88868 AT--ATTAAATTAATCTCTAAGATTAATATATATGAAATTAATGTTAGTATTT 88924
Qy 1017 TTTAACTAGCATTAATTCATTTGCTTCATCAAAAGTGCTTCAATTTTTTTAGTT 1076
Db 88925 TTAAATTTTTCAGATTAATTCATTTTAAATTAATTAAGAGTGATTAATCTTGTA 88984
Qy 1077 GGTAGAACTCTTCTTCATAGTACATCTCTCAACTAATTTTGAATATTTGTTG 1136
Db 88985 ATTAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 89044
Qy 1137 GCTTTTGTCTTCTTCTAGTATAGCAATTTTAAAAAATATTAATTAAGTACCAATCTTT 1196
Db 89045 AATAATTAATTTTCTTTTAAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 89104
Qy 1197 GTACAAATTTGTAAATTTGAAGATTTTATATCTGTTAAATTAATTAATTTT 1251
Db 89105 ATGTATATTAAGGAGAGAGTGATTTAAATTAATTAATTTTAAATAATTAATTT 89159

RESULT 45

US-08-397-653B-2
; Sequence 2, Application US/08397653B
; Patent No. 6329570
; GENERAL INFORMATION:
; APPLICANT: Martineau, Belinda

;; TITLE OF INVENTION: COTTON MODIFICATION USING
;; TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Calgene, Inc.
;; STREET: 1920 Fifth Street
;; CITY: Davis
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 95616

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0
;; SOFTWARE: Microsoft Word 5.1a
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/397,653B
;; FILING DATE: 28-FEB-1995
;; CLASSIFICATION: 800

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elizabeth Lassen
;; REGISTRATION NUMBER: 31,845
;; NAME: Donna E. Scherer
;; REGISTRATION NUMBER: 34,719
;; NAME: Carl J. Schvedler
;; REGISTRATION NUMBER: 36,924
;; REFERENCE/DOCKET NUMBER: CGNE 112
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (916) 753-6313
;; TELEFAX: (916) 753-1510

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4383 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
US-08-397-653B-2

Query Match 3.8%; Score 47.6; DB 3; Length 4383;
Best Local Similarity 48.0%; Pred.No.0.16;
Matches 166; Conservative 0; Mismatches 179; Indels 1; Gaps 1;

Qy 843 ATCATATTGAAGACATCAAAATAAATGCTTTATTTTCACTTGTGACCTCTTTT 902
Db 3351 ATGAATAAGATCGATCGATCTTTAATTTATGTTTACATTAATTAATCACTTCT 3410
Qy 903 ATTAGCCTTGAATGCTTCACTTAATGACATTTTAATTAATTAATTAATTAATTAAT 962
Db 3411 GTTACATTCATTTATCTAGTTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 3470
Qy 963 ATGAAGAAGCAAGCTAATATGTTTACAGACCAAGTGATTTGACACTGTTTAAAT 1022
Db 3471 TCTTCAAAAGAGAGTACATATGTAAGAGGATTAATTAATTAATTAATTAATTAATTAAT 3530
Qy 1023 CTAGCATTAATTAAT-TTTCCTTCAATCAAAAGTGCTTCAATTTTATTTTATTTAGTGT 1081
Db 3531 TTCGATATATTCATATTTGATCTCAAAATTAAGATTAATTAATTAATTTATTTTGTAGGAGA 3590
Qy 1082 GAATACCTTCTTCATAGTACATCTCTCAACTAATTTGGAATATTTGTTGTTGTT 1141
Db 3591 AATTTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1187
Qy 1142 TTGTTTCTCTTCTAGTATAGCAATTTTAAAAAATTAATTAAGCTA 1187
Db 3651 TAATATTAATGAATCTCTGTTGCTGAATTTATTAATTAATTAATTAATTAATTAATTAATTAAT 3696

RESULT 46

US-08-397-653B-2
; Patent No. 5175095
; APPLICANT: Martineau, Belinda M.; Houck, Catherine M.

;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 98
;; SEQ ID NO 50
;; LENGTH: 6306
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-50

Query Match 3.8%; Score 47.6; DB 4; Length 6306;
Best Local Similarity 45.5%; Pred. No. 0.19;
Matches 211; Conservative 0; Mismatches 249; Indels 4; Gaps 1;

QY 788 TTGTCAGATTCACCAAGAGATGCTCTGATGGAATGCTTCGCAATC 847
DB 4858 TTTTGTATATGTAAGAAAAATGATTTTAAATGCTGATAGCTTAATTTTAAAT 4917
QY 848 TATTCAGAACTACCAAAATGCTTAATTTTCATTTGCTACCTTTTAAAT 907
DB 4918 TGGAGTATAGATAGATTTATGTTATTTTGTAAATTTTGGAGTTT 4977
QY 908 GCGTTCGAATGCTTCACTTAATGACATTTTAAATGTTATGATACCTGAATGA 967
DB 4978 TTAATTTGATGATAGATGATGTTTGTGCTGATTTTAAATTTGATTTTGAATAT 5037
QY 968 AAGCAAGCTAATATGTTTACGACCAAGTGTATTTTACACGCTTTTAAATCTAC 1027
DB 5038 TGAAGAGTTGAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 5093
QY 1028 ATTATTCATTTGCTTCAATCAAAAGTGTTCATATTTTAAATTTTAAATTTTAAAT 1087
DB 5094 TTTTTCATTTTATTTTATTTTATGATTTTAAAGATTTTATTTAAAGATTTTAAAT 5153
QY 1088 TTTCTCAGTACATCTCTCAACCTAATTTGAAATGTTGCTTTTGT 1147
DB 5154 TCGTATAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 5213
QY 1148 TTTCTCTGATATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1207
DB 5214 TTTTATTTTATTTTAAAGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 5273
QY 1208 AATATGTAAGATTTTATTTATCTGTTAAATTTAAATTTATTT 1251
DB 5274 AATGAGAGAAAGTTTATTTAAATTTTATTTATGAAATTTT 5317

RESULT 49
US-10-204-708-33
;; Sequence 33, Application US/10204708
;; Patent No. 6677731
;; GENERAL INFORMATION:
;; APPLICANT: OLEK, Alexander
;; APPLICANT: PIEPENROCK, Christian
;; APPLICANT: BERLIN, Kurt
;; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;; FILE REFERENCE: 5013.1012
;; CURRENT APPLICATION NUMBER: US/10/204, 708
;; CURRENT FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: PCT/EP01/03971
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: DE 10019058.8
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: DE 10019173.8
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: DE 10032529.7
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: DE 10043826.1
;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 98
;; SEQ ID NO 33
;; LENGTH: 5455

;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-33

Query Match 3.8%; Score 47.4; DB 4; Length 5455;
Best Local Similarity 48.1%; Pred. No. 0.2;
Matches 195; Conservative 0; Mismatches 206; Indels 4; Gaps 2;

QY 847 TATTCAGAACTACCAAAATGCTTAATTTTCATTTGCTACCTTTTAAATTA 906
DB 726 TTTTAAAGTTTAAATTTTATTTGTTTATTTTAAATTTTAAATTTTAAATTTTAAAT 785
QY 907 TCCCTGAAATGCTTCAATTAATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 966
DB 786 TTTTGAAGCGTTTATTTAT 844
QY 967 AAGCAAGCTAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAG 1026
DB 845 TATTTTATTTATGTTATTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTGAG 904
QY 1027 CATATTCATTTGCTTCAATCAAAAGTGTTCATATTTTAAATTTTAAATTTTAAATTTTAAAT 1086
DB 905 TTTTATTTTGTTTTAAATTTTGTGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 964
QY 1087 CTTTCTCATCTCATCTCTCAACCTAATTTTGAATTTGTTGCTTTTGT 1146
DB 965 TTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1024
QY 1147 TTTTCTCAGTATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1206
DB 1025 GTTGTGAAATTTGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1081
QY 1207 TAAATGTAAGATTTTATTTATCTGTTAAATTTAAATTTATTT 1251
DB 1082 TATTTGTAATAGTAAATGTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1126

RESULT 50
US-10-204-708-14
;; Sequence 14, Application US/10204708
;; Patent No. 6677731
;; GENERAL INFORMATION:
;; APPLICANT: OLEK, Alexander
;; APPLICANT: PIEPENROCK, Christian
;; APPLICANT: BERLIN, Kurt
;; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
;; FILE REFERENCE: 5013.1012
;; CURRENT APPLICATION NUMBER: US/10/204, 708
;; CURRENT FILING DATE: 2003-05-06
;; PRIOR APPLICATION NUMBER: PCT/EP01/03971
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: DE 10019058.8
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: DE 10019173.8
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: DE 10032529.7
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: DE 10043826.1
;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 98
;; SEQ ID NO 14
;; LENGTH: 6113
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-14

Query Match 3.8%; Score 47.4; DB 4; Length 6113;
Best Local Similarity 49.1%; Pred. No. 0.21;

